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(54) Title: METHODS OF DIAGNOSIS OF PROSTATE CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF PROSTATE CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in prostate cancer. Also described are such genes whose expression is further up-regulated or down-regulated in drug-resistant prostate cancer cells. Related methods and compositions that can be used for diagnosis and treatment of prostate cancer are disclosed. Also described herein are methods that can be used to identify modulators of prostate cancer.

**METHODS OF DIAGNOSIS OF PROSTATE CANCER,
COMPOSITIONS AND METHODS OF SCREENING FOR
MODULATORS OF PROSTATE CANCER**

5

CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority from the following applications: USSN 09/687,576 filed October 13, 2000, USSN 60/276,791 filed March 16, 2001; USSN 60/288,589, filed May 4, 2001; USSN 09/733,742, filed December 8, 2000; USSN 10 09/733,288, filed December 8, 2000; USSN 09/847,046, filed April 30, 2001; USSN 60/276,888, filed March 16, 2001; USSN 60/286,214, filed April 24, 2001; USSN 60/281,922, filed April 6, 2001; USSN 60/263,957, filed January 24, 2001, which are incorporated herein by reference in their entirety.

15

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in prostate cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis and therapy of prostate cancer. The invention further relates to methods for 20 identifying and using agents and/or targets that inhibit prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer is the most commonly diagnosed internal malignancy and second most common cause of cancer death in men in the U.S., resulting in approximately 25 40,000 deaths each year (Landis et al., *CA Cancer J. Clin.* 48:6-29 (1998); Greenlee et al., *CA Cancer J. Clin.* 50(1):7-13 (2000)), and incidence of prostate cancer has been increasing rapidly over the past 20 years in many parts of the world (Nakata et al., *Int. J. Urol.* 7(7):254-257 (2000); Majeed et al., *BJU Int.* 85(9):1058-1062 (2000)). It develops as the

result of a pathologic transformation of normal prostate cells. In tumorigenesis, the cancer cell undergoes initiation, proliferation and loss of contact inhibition, culminating in invasion of surrounding tissue and, ultimately, metastasis.

Deaths from prostate cancer are a result of metastasis of a prostate tumor.

5 Therefore, early detection of the development of prostate cancer is critical in reducing mortality from this disease. Measuring levels of prostate-specific antigen (PSA) has become a very common method for early detection and screening, and may have contributed to the slight decrease in the mortality rate from prostate cancer in recent years (Nowroozi et al., *Cancer Control* 5(6):522-531 (1998)). However, many cases are not diagnosed until the
10 disease has progressed to an advanced stage.

Treatments such as surgery (prostatectomy) , radiation therapy, and cryotherapy are potentially curative when the cancer remains localized to the prostate. Therefore, early detection of prostate cancer is important for a positive prognosis for treatment. Systemic treatment for metastatic prostate cancer is limited to hormone therapy
15 and chemotherapy. Chemical or surgical castration has been the primary treatment for symptomatic metastatic prostate cancer for over 50 years. This testicular androgen deprivation therapy usually results in stabilization or regression of the disease (in 80% of patients), but progression of metastatic prostate cancer eventually develops (Panvichian et al., *Cancer Control* 3(6):493-500 (1996)). Metastatic disease is currently considered incurable,
20 and the primary goals of treatment are to prolong survival and improve quality of life (Rago, *Cancer Control* 5(6):513-521 (1998)).

Thus, methods that can be used for diagnosis and prognosis of prostate cancer and effective treatment of prostate cancer, and including particularly metastatic prostate cancer, would be desirable. Accordingly, provided herein are methods that can be used in
25 diagnosis and prognosis of prostate cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate, e.g., treat, prostate cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in prostate cancer and other cancers.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in prostate cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate prostate cancer, such as hormones or antibodies. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a prostate cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

In one embodiment, the present invention provides a method of determining the level of a prostate cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting a prostate cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1-16.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat prostate cancer. In another embodiment, the patient is suspected of having metastatic prostate cancer.

In one embodiment, the patient is a human.

In one embodiment, the patient is suspected of having a taxol-resistant cancer.

In one embodiment, the prostate cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of prostate cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a prostate cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic prostate cancer. In a further embodiment, the patient has a drug resistant (e.g., taxol resistant) form of prostate cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the prostate cancer-associated transcript to a level of the prostate cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate prostate cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-16.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-16.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-16.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

5 In one aspect, the present invention provides a method of detecting a prostate cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to prostate cancer in a patient, the method comprising contacting a
10 biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1-16.

In another aspect, the present invention provides a method for identifying a compound that modulates a prostate cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a prostate cancer-associated polypeptide, the
15 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

20 In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting
25 proliferation of a prostate cancer-associated cell to treat prostate cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay
30 comprising the steps of: (i) administering a test compound to a mammal having prostate cancer or to a cell sample isolated therefrom; (ii) comparing the level of gene expression of a

polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of prostate cancer.

In one embodiment, the control is a mammal with prostate cancer or a cell sample therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In one embodiment, the test compound is administered in varying amounts or concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-16 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

In another aspect, the present invention provides a method for treating a mammal having prostate cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having prostate cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in a prostate cancer. In one embodiment, a gene is selected from Tables 1-16. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug

candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate prostate cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the prostate cancer modulatory protein, or an animal lacking the prostate cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-16, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with prostate cancer is provided. The method comprises determining the expression of a gene of Tables 1-16, in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with prostate cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in prostate cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a prostate cancer modulating protein (prostate cancer modulatory protein) or a fragment thereof and an antibody which binds to said prostate cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining a prostate cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said prostate cancer modulatory protein or fragment thereof. The method further includes determining the binding of said prostate cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits prostate cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an

individual a composition comprising a prostate cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-16.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a prostate cancer modulating protein, preferably encoded by a nucleic acid of Tables 1-16, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a prostate cancer modulating protein, preferably selected from the nucleic acids of Tables 1-16, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of a prostate cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-16.

In another aspect of the invention, a method of treating an individual for prostate cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of a prostate cancer modulating protein. In another embodiment, the method comprises administering to a patient having prostate cancer an antibody to a prostate cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for prostate cancer (PC), including metastatic prostate cancer, as well as methods for screening for compositions which modulate prostate cancer. Also provided are methods for treating prostate cancer.

In addition to the other nucleic acid and peptide sequences, the present invention also relates to the identification of PAA2 as a gene that is highly over expressed in prostate cancer patient tissues. PAA2 sequence is identical to the zinc transporter ZNT4. Results presented herein demonstrate that PAA2/ZNT4 is highly expressed in prostate cancer cells. The prostate gland is unique in that it has the highest capacity of any organ in the body

to accumulate zinc. Zinc uptake is regulated by prolactin and testosterone, which induce the expression of a member of the ZIP family of zinc transporters (Costello et al., 1999, J. Biol. Chem. 274:17499-17504). Zinc accumulation in the prostate functions to inhibit citrate oxidation, which results in a decrease in cellular ATP production (Costello and Franklin, 5 1998, Prostate 35:285-296). Cancer cells are more sensitive to decreased ATP production and have evolved to prevent zinc accumulation. Without wishing to be bound by theory, the up-regulation of ZNT4 in prostate cancer cells may result in protection of the cells from high zinc levels by its ability to pump accumulated zinc out of the cells.

The present invention also relates to nucleic acid sequences encoding PBH1. 10 PBH1 is related to human TRPC7 (transient receptor potential-related channels, NP_003298), a putative calcium channel highly expressed in brain (Nagamine et al., Genomics 54:124-131 (1998)). Trp is related to melastatin, a gene down-regulated in metastatic melanomas (Duncan et al., Cancer Res. 58:1515-1520 (1998)), and MTR1, a gene localized to within the Beckwith-Wiedemann syndrome/Wilm's tumor susceptibility region (Prawitt et al., Hum. 15 Mol. Genet. 9:203-216 (2000)). Without wishing to be bound by theory, it is believed that PBH1 functions as a calcium channel.

As a calcium channel, PBH1 is an ideal target for a small molecule therapeutic, or a therapeutic antibody that disrupts channel function. CD20, the target of Rituximab in non-Hodgkin's lymphoma (Maloney et al., Blood 90:2188-2195 (1997); Leget 20 and Czuczman, Curr. Opin. Oncol. 10:548-551 (1998)), is a plasma membrane calcium channel expressed in B cells (Tedder and Engel, Immunol. Today 15:450-454 (1994)). Similarly, a small molecule, or antibody that inhibits or alters a calcium signal mediated by PBH1, will result in the death of prostate cancer cells.

PBH1, and other genes of the invention, are also be useful as targets for 25 cytotoxic T-lymphocytes. Genes that are tumor specific, or that are expressed in immune-privileged organs, are currently being used as potential vaccine targets (Van den Eynde and Boon, Int. J. Clin. Lab. Res. 27:81-86 (1997)). The expression pattern of PBH1 indicates that it is an ideal target for cytotoxic T-lymphocytes. Thus, therapies that utilize PBH1-specific cytotoxic T-lymphocytes to induce prostate cancer cell death are also provided by this 30 invention. See, e.g., U.S. Patent No. 6,051,227 and WO 00/32231, the disclosures of which are herein incorporated by reference.

The present invention is also related to the identification of PAA3 as a gene that is important in the modulation of prostate cancer and or breast cancer.

Tables 1-16 provide unigene cluster identification numbers, exemplar accession numbers, or genomic nucleotide position numbers for the nucleotide sequence of
5 genes that exhibit increased or decreased expression in prostate cancer samples.

Definitions

The term "prostate cancer protein" or "prostate cancer polynucleotide" or "prostate cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic
10 variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200,
15 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-16 and conservatively modified variants
20 thereof or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables
25 1-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "prostate cancer polypeptide" and a "prostate cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" prostate cancer protein or nucleic acid refers to a prostate
30 cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type prostate cancer

polynucleotide or polypeptide sequences. For example, a full length prostate cancer nucleic acid will typically comprise all of the exons that encode for the full length, naturally occurring protein. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

5 "Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a prostate cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes,
10 blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish.

15 "Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues, having treatment or outcome history, will
20 be particularly useful.

 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%,
25 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.,* NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to
30 be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions

and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is
5 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default
10 program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of
15 from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and
25 visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). BLAST and BLAST 2.0 are used, with the parameters
30 described herein, to determine percent sequence identity for the nucleic acids and proteins of

the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, $M=5$, $N=-4$ and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (*see, e.g.*, the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding

naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the

only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

- 5 As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid.
- 10 Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5)
- 15 Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g., Creighton, Proteins* (1984)).

- Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see,*
- 20 *e.g., Alberts et al., Molecular Biology of the Cell* (3rd ed., 1994) and Cantor & Schimmel, *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* (1980). "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that
- 25 often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary
- 30 units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, *Carbohydrate Modifications in Antisense Research*, Sanghui & Cook, eds.. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g. to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, for example, phosphoramidate (Beaucage et al., *Tetrahedron* 49(10):1925 (1993) and references therein; Letsinger, *J. Org. Chem.* 35:3800 (1970); Sprinzl et al., *Eur. J. Biochem.* 81:579 (1977); Letsinger et al., *Nucl. Acids Res.* 14:3487 (1986); Sawai et al, *Chem. Lett.* 805 (1984), Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); and Pauwels et al., *Chemica Scripta* 26:141 91986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., *J. Am. Chem. Soc.* 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, *J. Am. Chem. Soc.* 114:1895 (1992); Meier et al., *Chem. Int. Ed. Engl.* 31:1008 (1992); Nielsen, *Nature*, 365:566 (1993); Carlsson et al., *Nature* 380:207 (1996), all

of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp 169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and

combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified
5 nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g. the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical
10 means. For example, useful labels include fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The radioisotope may be, for example, ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I . In some cases, particularly using antibodies against the
15 proteins of the invention, the radioisotopes are used as toxic moieties, as described below. The labels may be incorporated into the prostate cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981);
20 and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982). The lifetime of radiolabeled peptides or radiolabeled antibody compositions may extended by the addition of substances that stabilize the radiolabeled peptide or antibody and protect it from degradation. Any substance or combination of substances that stabilize the radiolabeled peptide or antibody may be used including those substances disclosed in US Patent No. 5,961,955.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope
30 tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method
5 using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually
10 through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.
15 It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe,
20 one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a
25 native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using
30 polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear

form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a

particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

5 The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence that is determinative of the presence of the nucleotide sequence, in a heterogeneous population of nucleic acids and other biologics (e.g., total cellular or library DNA or RNA). Similarly, the phrase "specifically (or selectively) binds" to an antibody or "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction that
10 is determinative of the presence of the protein, in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay or nucleic acid hybridization conditions, the specified antibodies or nucleic acid probes bind to a particular protein nucleotide sequences at least two times the background and more typically more than 10 to 100 times background.

15 Specific binding to an antibody under such conditions requires an antibody that is selected for its specificity for a particular protein. For example, polyclonal antibodies raised to a particular protein, polymorphic variants, alleles, orthologs, and conservatively modified variants, or splice variants, or portions thereof, can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the desired prostate cancer
20 protein and not with other proteins. This selection may be achieved by subtracting out antibodies that cross-react with other molecules. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual*
25 (1988) for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and
30 will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in

Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background; preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize

under moderately stringent hybridization conditions. Exemplary “moderately stringent hybridization conditions” include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and Current Protocols in Molecular Biology, ed. Ausubel, *et al.*

The phrase “functional effects” in the context of assays for testing compounds that modulate activity of a prostate cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the prostate cancer protein or nucleic acid, e.g., a functional, physical, or chemical effect, such as the ability to decrease prostate cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of prostate cancer cells. “Functional effects” include *in vitro*, *in vivo*, and *ex vivo* activities.

By “determining the functional effect” is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a prostate cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the prostate cancer protein; measuring binding activity or binding assays, e.g. binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on prostate cancer can also be performed using prostate cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of prostate cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for prostate cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

“Inhibitors”, “activators”, and “modulators” of prostate cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of prostate cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of prostate cancer proteins, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. “Activators” are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate prostate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of prostate cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the prostate cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of prostate cancer can also be identified by incubating prostate cancer cells with the test compound and determining increases or decreases in the expression of 1 or more prostate cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more prostate cancer proteins, such as prostate cancer proteins encoded by the sequences set out in Tables 1-16.

Samples or assays comprising prostate cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%,

preferably 50%, more preferably 25-0%. Activation of a prostate cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

5 The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, 10 ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. *See, e.g., Freshney, Culture of Animal Cells a Manual of Basic Technique* pp. 231-241 (3rd ed. 1994).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers 15 to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, 20 aberrant growth control, nonmorphological changes, and/or malignancy (*see, Freshney, Culture of Animal Cells a Manual of Basic Technique* (3rd ed. 1994)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, 25 epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. *See Paul,* 30 *Fundamental Immunology.*

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (*see Fundamental Immunology* (Paul ed., 3d ed. 1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990)).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (*see, e.g., Kohler & Milstein, Nature* 256:495-497 (1975); Kozbor *et al., Immunology Today* 4:72 (1983); Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy* (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that

specifically bind to selected antigens (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990); Marks *et al., Biotechnology* 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site
5 (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.,* an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

10

Identification of prostate cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the
15 sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue (*e.g.,* normal prostate or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the prostate, or prostate cancer tissue or metastatic prostate cancerous tissue can be compared with tissue
20 samples of prostate and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different prostate cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in prostate
25 cancer versus non-prostate cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate prostate cancer, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be
30 analyzed to determine the stage of prostate cancer in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to

mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the prostate cancer expression profile. This may be done by making biochips comprising sets of the important prostate cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the prostate cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the prostate cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the prostate cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in prostate cancer, herein termed "prostate cancer sequences." As outlined below, prostate cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in prostate cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the prostate cancer sequences are from humans; however, as will be appreciated by those in the art, prostate cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other prostate cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets, e.g., (dogs, cats, etc.). Prostate cancer sequences from other organisms may be obtained using the techniques outlined below.

Prostate cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, prostate cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the prostate cancer sequences can be generated.

A prostate cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the prostate cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying prostate cancer-associated sequences, the prostate cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing prostate cancer
5 samples with metastatic cancer samples from other cancers, such as lung, breast, gastrointestinal cancers, ovarian, etc. Samples of different stages of prostate cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are
10 commercially available, e.g. from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal prostate, but also including, and not limited to lung, heart, brain, liver, breast, kidney,
15 muscle, colon, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the prostate cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

20 In a preferred embodiment, prostate cancer sequences are those that are up-regulated in prostate cancer; that is, the expression of these genes is higher in the prostate cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All unigene cluster identification numbers
25 and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, *see, e.g.*, Benson, DA, *et al.*, Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).

30 In another preferred embodiment, prostate cancer sequences are those that are down-regulated in prostate cancer; that is, the expression of these genes is lower in prostate

cancer tissue as compared to non-cancerous tissue (*see, e.g.*, Tables 8, 12 and 14). "Down-regulation" as used herein often means at least about a 1.5-fold change more preferably a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being most preferred.

5

Informatics

The ability to identify genes that are over or under expressed in prostate cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with prostate cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (*see* Anderson, *Pharmaceutical Proteomics: Targets, Mechanism, and Function*, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (*see* U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

30

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing prostate cancer, i.e., the identification of prostate cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount *et al.*, *Bioinformatics* (2001); *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* (Durbin *et al.*, eds., 1999); *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (Baxeavanis & Oeullette eds., 1998)); Rashidi & Buehler, *Bioinformatics: Basic Applications in Biological Science and Medicine* (1999); *Introduction to Computational Molecular Biology* (Setubal *et al.*, eds 1997); *Bioinformatics: Methods and Protocols* (Misener & Krawetz, eds, 2000); *Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach* (Higgins & Taylor, eds., 2000); Brown, *Bioinformatics: A Biologist's Guide to Biocomputing and the Internet* (2001); Han & Kamber, *Data Mining: Concepts and Techniques* (2000); and
10 Waterman, *Introduction to Computational Biology: Maps, Sequences, and Genomes* (1995).

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

15 In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for prostate cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each
20 target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of
25 target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or
30 transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment,

the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides
5 a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may
10 be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or
15 hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line,
20 ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes
25 generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for
30 comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the

degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of prostate cancer-associated proteins

Prostate cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the prostate cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such

proteins often results in unregulated or dysregulated cellular processes (*see, e.g., Molecular Biology of the Cell* (Alberts, ed., 3rd ed., 1994)). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (*see, e.g., Bateman et al., Nuc. Acids Res.* 28:263-266 (2000); Sonnhammer *et al.*, *Proteins* 28:405-420 (1997); Bateman *et al.*, *Nuc. Acids Res.* 27:260-262 (1999); and Sonnhammer *et al.*, *Nuc. Acids Res.* 26:320-322- (1998)).

In another embodiment, the prostate cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described

for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (*see, e.g.* PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor,

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also

bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

5 Prostate cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ*. Alternatively, antibodies can also label intracellular proteins, in which case samples are
10 typically permeabilized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

15 In another embodiment, the prostate cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in
20 an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Prostate cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, *e.g.*,
25 for blood, plasma, serum, or stool tests.

Use of prostate cancer nucleic acids

As described above, prostate cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the prostate
30 cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either

homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The prostate cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the prostate cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, *et al.*, *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once the prostate cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire prostate cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant prostate cancer nucleic acid can be further-used as a probe to identify and isolate other prostate cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant prostate cancer nucleic acids and proteins.

The prostate cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the prostate cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense applications. Alternatively, the prostate cancer nucleic acids that include coding regions of prostate cancer proteins can be put into expression vectors for the expression of prostate cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to prostate cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the prostate cancer nucleic acids, *i.e.* the target sequence (either the target

sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical

equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to,

amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g. using linkers as are known in the art; e.g.,
5 homo-or hetero-bifunctional linkers as are well known (*see* 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art,
10 and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which
15 bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described
20 in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of prostate cancer-associated sequences. These assays are typically performed in
25 conjunction with reverse transcription. In such assays, a prostate cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of prostate cancer-associated RNA. Methods of
30 quantitative amplification are well known to those of skill in the art. Detailed protocols for

quantitative PCR are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be
5 extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of
10 amplification (*see*, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (*see* Wu & Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), and Barringer *et al.*, *Gene* 89:117 (1990)), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), self-sustained sequence replication
15 (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)), dot PCR, and linker adapter PCR, etc.

Expression of prostate cancer proteins from nucleic acids

In a preferred embodiment, prostate cancer nucleic acids, e.g., encoding
20 prostate cancer proteins are used to make a variety of expression vectors to express prostate cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (*see*, e.g., Ausubel, *supra*, and *Gene Expression Systems* (Fernandez & Hoeffler, eds, 1999)) and are used to express proteins. The expression vectors may be either self-replicating
25 extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the prostate cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a
30 promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation.

Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the prostate cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g. in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct.

The integrating vector may be directed to a specific locus in the host cell by selecting the

appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez & Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The prostate cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a prostate cancer protein, under the appropriate conditions to induce or cause expression of the prostate cancer protein. Conditions appropriate for prostate cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the prostate cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (*see, e.g.,* Fernandez & Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory

regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, prostate cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the prostate cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez & Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, prostate cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, prostate cancer protein is produced in yeast cells.

- 5 Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

- The prostate cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the prostate cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the prostate cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the prostate cancer protein is a prostate cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.
- 10
15

- In a preferred embodiment, the prostate cancer protein is purified or isolated after expression. Prostate cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the prostate cancer protein may be purified using a standard anti-prostate cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, *Protein Purification* (1982). The degree of purification necessary will vary depending on the use of the prostate cancer protein. In some instances no purification will be necessary.
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Once expressed and purified if necessary, the prostate cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of prostate cancer proteins

In one embodiment, the prostate cancer proteins are derivative or variant prostate cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative prostate cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the prostate cancer peptide.

Also included within one embodiment of prostate cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the prostate cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant prostate cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the prostate cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed prostate cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of prostate cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger

insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to
5 minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the prostate cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will
10 elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the prostate cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the prostate cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by
15 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the
20 polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side
25 chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

Covalent modifications of prostate cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a prostate cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a prostate
30 cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking prostate cancer polypeptides to a water-insoluble support matrix or surface for

use in the method for purifying anti-prostate cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl
5 esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues,
10 methylation of the amino groups of the lysine, arginine, and histidine side chains (Creighton, *Proteins: Structure and Molecular Properties*, pp. 79-86 (1983)), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the prostate cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern
15 of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence prostate cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence prostate cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express prostate cancer-associated
20 sequences can result in different glycosylation patterns.

Addition of glycosylation sites to prostate cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence prostate cancer polypeptide (for O-linked glycosylation sites). The prostate cancer
25 amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the prostate cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the prostate cancer polypeptide is by chemical or enzymatic coupling of glycosides to the
30 polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin & Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the prostate cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin,
5 *et al.*, *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge *et al.*, *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura *et al.*, *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of prostate cancer comprises linking the
10 prostate cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Prostate cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a prostate cancer polypeptide fused to another,
15 heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a prostate cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the prostate cancer polypeptide. The presence of such epitope-tagged forms of a prostate cancer polypeptide can be detected using
20 an antibody against the tag polypeptide. Also, provision of the epitope tag enables the prostate cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a prostate cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of
25 the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field *et al.*, *Mol. Cell. Biol.* 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and
30 9E10 antibodies thereto (Evan *et al.*, *Molecular and Cellular Biology* 5:3610-3616 (1985)); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky *et al.*,

Protein Engineering 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (Hopp *et al.*, *BioTechnology* 6:1204-1210 (1988)); the KT3 epitope peptide (Martin *et al.*, *Science* 255:192-194 (1992)); tubulin epitope peptide (Skinner *et al.*, *J. Biol. Chem.* 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth *et al.*,
5 *Proc. Natl. Acad. Sci. USA* 87:6393-6397 (1990)).

Also included are other prostate cancer proteins of the prostate cancer family, and prostate cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related prostate cancer proteins from humans or other
10 organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the prostate cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols,
15 *supra*).

Antibodies to prostate cancer proteins

In a preferred embodiment, when the prostate cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the prostate cancer protein
20 should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller prostate cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment; the epitope is unique; that is,
25 antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, *supra*; and Harlow & Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple
30 subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It

may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete
5 adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler &
10 Milstein, *Nature* 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-
15 16 fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*,
20 pp. 59-103 (1986)). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme
25 hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding
30 specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a

protein encoded by a nucleic acid Tables 1-16 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

5 In a preferred embodiment, the antibodies to prostate cancer protein are capable of reducing or eliminating a biological function of a prostate cancer protein, as is described below. That is, the addition of anti-prostate cancer protein antibodies (either polyclonal or preferably monoclonal) to prostate cancer tissue (or cells containing prostate cancer) may reduce or eliminate the prostate cancer. Generally, at least a 25% decrease in
10 activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

 In a preferred embodiment the antibodies to the prostate cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric
15 molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-
20 human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise
25 substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human
30 immunoglobulin (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)). Humanization

can be essentially performed following the method of Winter and co-workers (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are
5 chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom & Winter, *J. Mol. Biol.* 227:381 (1991);
10 Marks *et al.*, *J. Mol. Biol.* 222:581 (1991)). The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, p. 77 (1985) and Boerner *et al.*, *J. Immunol.* 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous
15 immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10:779-
20 783 (1992); Lonberg *et al.*, *Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995).

By immunotherapy is meant treatment of prostate cancer with an antibody raised against prostate cancer proteins. As used herein, immunotherapy can be passive or
25 active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which
30 antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic

acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the prostate cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted prostate cancer protein.

In another preferred embodiment, the prostate cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the prostate cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane prostate cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the prostate cancer protein. The antibody is also an antagonist of the prostate cancer protein. Further, the antibody prevents activation of the transmembrane prostate cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the prostate cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, prostate cancer is treated by administering to a patient antibodies directed against the transmembrane prostate cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labelling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the prostate cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the prostate cancer protein. The therapeutic moiety

may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with prostate cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to prostate cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with prostate cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against prostate cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane prostate cancer proteins not only serves to increase the local concentration of therapeutic moiety in the prostate cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the prostate cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the prostate cancer protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The prostate cancer antibodies of the invention specifically bind to prostate cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of prostate cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the prostate cancer phenotype. Expression levels of genes in normal tissue

(i.e., not undergoing prostate cancer) and in prostate cancer tissue (and in some cases, for varying severities of prostate cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus prostate cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, *Nature Biotechnology* 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the prostate cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to prostate cancer genes, i.e., those identified as being important in a prostate cancer phenotype, can be evaluated in a prostate cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In this embodiment, the prostate cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of prostate cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the prostate cancer protein are detected. Although DNA or RNA encoding the prostate cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a prostate cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a prostate cancer protein is detected by binding the digoxigenin with an anti-digoxigenin

secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The prostate cancer proteins, antibodies, nucleic acids, modified proteins and cells containing prostate cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, prostate cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of prostate cancer. Detection of these proteins in putative prostate cancer tissue allows for detection or diagnosis of prostate cancer. In one embodiment, antibodies are used to detect prostate cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the prostate cancer protein is detected, e.g., by immunoblotting with antibodies raised against the prostate cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the prostate cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the prostate cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the prostate cancer protein(s) contains a detectable label, e.g. an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of prostate cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing prostate cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of prostate cancer proteins. Antibodies can be used to detect a prostate cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous prostate cancer protein.

In a preferred embodiment, *in situ* hybridization of labeled prostate cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including prostate cancer tissue and/or normal tissue, are made. *In situ* hybridization (*see, e.g., Ausubel, supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the prostate cancer proteins, antibodies, nucleic acids, modified proteins and cells containing prostate cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to prostate cancer, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, prostate cancer probes may be attached to biochips for the detection and quantification of prostate cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The prostate cancer

proteins, antibodies, nucleic acids, modified proteins and cells containing prostate cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, *et al.*, *Science* 279:84-8 (1998); Heid, *Genome Res* 6:986-94, 1996).

In a preferred embodiment, the prostate cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified prostate cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the prostate cancer phenotype or an identified physiological function of a prostate cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in prostate cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the prostate cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing prostate cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in prostate cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in prostate cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the prostate cancer protein and standard

immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

In this embodiment, the prostate cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of prostate cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more prostate cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-16. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate prostate cancer, modulate prostate cancer proteins, bind to a prostate cancer protein, or interfere with the binding of a prostate cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the prostate cancer phenotype or the expression of a prostate cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a prostate cancer phenotype, e.g. to a normal tissue fingerprint. In another embodiment, a modulator induced a prostate cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of

more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a prostate cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a prostate cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound

length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop *et al.*, *J. Med. Chem.* 37(9):1233-1251 (1994)).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent No. 5,010,175, Furka, *Pept. Prot. Res.* 37:487-493 (1991), Houghton *et al.*, *Nature*, 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho, *et al.*, *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658 (1994)). *See, generally*, Gordon *et al.*, *J. Med. Chem.* 37:1385 (1994), nucleic acid libraries (*see, e.g.*, Strategene, Corp.), peptide nucleic acid libraries (*see, e.g.*, U.S. Patent 5,539,083), antibody libraries (*see, e.g.*, Vaughn *et al.*, *Nature Biotechnology* 14(3):309-314 (1996), and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al.*, *Science* 274:1520-1522 (1996), and U.S. Patent No. 5,593,853), and small organic molecule libraries (*see, e.g.*, benzodiazepines, Baum, C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka,

Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices
5 (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, *etc.*).

10 The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of prostate cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

 High throughput assays for the presence, absence, quantification, or other
15 properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, *e.g.*, U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (*i.e.*, in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high
20 throughput methods of screening for ligand/antibody binding.

 In addition, high throughput screening systems are commercially available (*see, e.g.*, Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, *etc.*). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid
25 dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, *e.g.*, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene
30 transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, *e.g.*, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention.

- 5 Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, *e.g.*, substrates for enzymes or ligands and receptors.

- 10 In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally
15 these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

- 20 In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, *e.g.*, of hydrophobic amino acids;
25 hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

- 30 Modulators of prostate cancer can also be nucleic acids, as defined below. As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For

example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In certain embodiments, the activity of a prostate cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, *i.e.*, a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA
5 nucleic acid sequence, *e.g.*, a prostate cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise
10 naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the prostate cancer
15 protein mRNA. *See, e.g.*, Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

20 Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, *e.g.*, be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for prostate cancer molecules. Antisense or sense
25 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, *e.g.*, Stein & Cohen (*Cancer Res.* 48:2659 (1988) and van der Krol *et al.* (*BioTechniques* 6:958 (1988)).

30 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of prostate cancer-associated nucleotide sequences. A ribozyme is an

RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (*see, e.g., Castanotto et al., Adv. in Pharmacology* 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel *et al., Nucl. Acids Res.* 18:299-304 (1990); European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (*see, e.g., WO 94/26877; Ojwang et al., Proc. Natl. Acad. Sci. USA* 90:6340-6344 (1993); Yamada *et al., Human Gene Therapy* 1:39-45 (1994); Leavitt *et al., Proc. Natl. Acad. Sci. USA* 92:699-703 (1995); Leavitt *et al., Human Gene Therapy* 5:1151-120 (1994); and Yamada *et al., Virology* 205: 121-126 (1994)).

Polynucleotide modulators of prostate cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of prostate cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

As noted above, gene expression monitoring is conveniently used to test candidate modulators (*e.g., protein, nucleic acid or small molecule*). After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription

with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of
5 detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an
10 epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple
15 probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under
20 conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by
25 altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain
30 steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g. albumin, detergents, *etc.* which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, *etc.*, may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the prostate cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, *e.g.*, for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a prostate cancer expression pattern leading to a normal expression pattern, or to modulate a single prostate cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated prostate cancer tissue reveals genes that are not expressed in normal tissue or prostate cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for prostate cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the

agent induced proteins and used to target novel therapeutics to the treated prostate cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of prostate cancer cells, that have an associated prostate cancer expression profile. By
5 “administration” or “contacting” herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of
10 the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is
15 generated, as outlined herein.

Thus, e.g., prostate cancer tissue may be screened for agents that modulate, e.g., induce or suppress the prostate cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on prostate cancer activity. By defining such a signature for the prostate cancer phenotype, screens for
20 new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular
25 differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as “prostate cancer proteins” or a “prostate cancer modulatory protein”. The prostate cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic
30 acids of Tables 1-16. Preferably, the prostate cancer modulatory protein is a fragment. In a preferred embodiment, the prostate cancer amino acid sequence which is used to determine

sequence identity or similarity is encoded by a nucleic acid of Tables 1-16. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of Tables 1-16. In another embodiment, the sequences are sequence variants as further described herein.

5 Preferably, the prostate cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in
10 coupling, i.e., to cysteine.

 In one embodiment the prostate cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the prostate cancer protein is conjugated to BSA.

 Measurements of prostate cancer polypeptide activity, or of prostate cancer or
15 the prostate cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the prostate cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or
20 animals, one can also measure a variety of effects such as, in the case of prostate cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian
25 prostate cancer polypeptide is typically used, e.g., mouse, preferably human.

 Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a prostate cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the prostate cancer polypeptide levels are determined *in vitro* by measuring the level of
30 protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the prostate cancer

polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids,
5 radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the prostate cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or
10 activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of
15 differentially expressed genes are sometimes referred to herein as "prostate cancer proteins." The prostate cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
20 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or
25 isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the prostate cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a prostate
30 cancer protein and a candidate compound, and determining the binding of the compound to the prostate cancer protein. Preferred embodiments utilize the human prostate cancer protein,

although other mammalian proteins may also be used, e.g. for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative prostate cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the prostate cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to “sticky” or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the prostate cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the prostate cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the prostate cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the prostate cancer protein to a solid support, adding a labeled candidate agent (e.g., a
5 fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophore
10 for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (i.e., a prostate cancer protein), such as an antibody, peptide, binding partner,
15 ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and
20 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test
25 compound. Displacement of the competitor is an indication that the test compound is binding to the prostate cancer protein and thus is capable of binding to, and potentially modulating, the activity of the prostate cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the
30 presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the prostate cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the prostate cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the prostate cancer proteins. In this embodiment, the methods comprise combining a prostate cancer protein and a competitor in a first sample. A second sample comprises a test compound, a prostate cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the prostate cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the prostate cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native prostate cancer protein, but cannot bind to modified prostate cancer proteins. The structure of the prostate cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a prostate cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background

interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

5 In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a prostate cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising prostate cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a prostate cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

10 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g. hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

15 In this way, compounds that modulate prostate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the prostate cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

20 In one embodiment, a method of inhibiting prostate cancer cell division is provided. The method comprises administration of a prostate cancer inhibitor. In another embodiment, a method of inhibiting prostate cancer is provided. The method comprises administration of a prostate cancer inhibitor. In a further embodiment, methods of treating cells or individuals with prostate cancer are provided. The method comprises administration of a prostate cancer inhibitor.

25 In one embodiment, a prostate cancer inhibitor is an antibody as discussed above. In another embodiment, the prostate cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

30 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example,

transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of prostate cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed., 1994), herein incorporated by reference. *See also*, the methods section of Garkavtsev *et al.* (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. *See* Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a prostate cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. *See*, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (*see, e.g.,* Temin, *J. Natl. Cancer Inst.* 37:167-175 (1966); Eagle *et al.*, *J. Exp. Med.* 131:836-879 (1970)); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (*see, e.g.,* Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth. in Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. *See, e.g.,* Folkman, *Angiogenesis and Cancer, Sem Cancer Biol.* (1992)).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, *see, Unkless et al.*, *J. Biol. Chem.* 249:4295-4305 (1974); Strickland & Beers, *J. Biol. Chem.* 251:5694-5702 (1976); Whur *et al.*, *Br. J. Cancer* 42:305-312 (1980); Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth. in Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985); Freshney *Anticancer Res.* 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate prostate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some

other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. *See, e.g., Freshney (1984), supra.*

5

Tumor growth in vivo

Effects of prostate cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the prostate cancer gene is disrupted or in which a prostate cancer gene is inserted. Knock-
10 out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous prostate cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous prostate cancer gene with a mutated version of the prostate cancer gene, or by mutating the endogenous prostate cancer gene, e.g., by exposure to carcinogens.

15

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic
20 lesion (*see, e.g., Capecchi et al., Science 244:1288 (1989)*). Chimeric targeted mice can be derived according to Hogan *et al., Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

Alternatively, various immune-suppressed or immune-deficient host animals
25 can be used. For example, genetically athymic "nude" mouse (*see, e.g., Giovanella et al., J. Natl. Cancer Inst. 52:921 (1974)*), a SCID mouse, a thymectomized mouse, or an irradiated mouse (*see, e.g., Bradley et al., Br. J. Cancer 38:263 (1978); Selby et al., Br. J. Cancer 41:52 (1980)*) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while
30 normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a prostate cancer-associated sequences are injected subcutaneously. After a

suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 **Methods of identifying variant prostate cancer-associated sequences**

Without being bound by theory, expression of various prostate cancer sequences is correlated with prostate cancer. Accordingly, disorders based on mutant or variant prostate cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant prostate cancer genes, e.g., determining all or
10 part of the sequence of at least one endogenous prostate cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the prostate cancer genotype of an individual, e.g., determining all or part of the sequence of at least one prostate cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation
15 of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced prostate cancer gene to a known prostate cancer gene, i.e., a wild-type gene.

The sequence of all or part of the prostate cancer gene can then be compared to the sequence of a known prostate cancer gene to determine if any differences exist. This
20 can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the prostate cancer gene of the patient and the known prostate cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the prostate cancer genes are used as probes to
25 determine the number of copies of the prostate cancer gene in the genome.

In another preferred embodiment, the prostate cancer genes are used as probes to determine the chromosomal localization of the prostate cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the prostate
30 cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a prostate cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will
5 depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery*; Lieberman, *Pharmaceutical Dosage Forms* (vols. 1-3, 1992), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd, *The Art, Science and Technology of Pharmaceutical Compounding* (1999); and Pickar, *Dosage Calculations*
10 (1999)). As is known in the art, adjustments for prostate cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application N. 09/687,576, further discloses the use of
15 compositions and methods of diagnosis and treatment in prostate cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal,
20 preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the prostate cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In
25 some instances, e.g., in the treatment of wounds and inflammation, the prostate cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a prostate cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as
30 pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the

biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that prostate cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, *etc.*) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a prostate cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may

be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., *Remington's Pharmaceutical Science* (15th ed., 1980) and Goodman & Gillman, *The Pharmacological Basis of Therapeutics* (Hardman *et al.*, eds., 1996)).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., *Remington's Pharmaceutical Science* and Goodman and Gillman, *The Pharmacological Basis of Therapeutics*, *supra*.

The compositions containing modulators of prostate cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, *etc.* Such prophylactic

treatments may be used, *e.g.*, in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

5 It will be appreciated that the present prostate cancer protein-modulating compounds can be administered alone or in combination with additional prostate cancer modulating compounds or with other therapeutic agent, *e.g.*, other anti-cancer agents or treatments.

10 In numerous embodiments, one or more nucleic acids, *e.g.*, polynucleotides comprising nucleic acid sequences set forth in Tables 1-16, such as antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of prostate cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or organism-based) recombinant expression systems.

15 The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see*,
20 *e.g.*, Berger & Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology* volume 152 (Berger), Ausubel *et al.*, eds., *Current Protocols* (supplemented through 1999), and Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual* (2nd ed., Vol. 1-3, 1989).

25 In a preferred embodiment, prostate cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, prostate cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the prostate cancer coding regions) can be administered in a gene therapy application. These prostate cancer genes can include antisense applications, either as gene therapy (*i.e.* for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

30 Prostate cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine

compositions can include, e.g., lipidated peptides (*see, e.g., Vitiello, A. et al., J. Clin. Invest.* 95:341 (1995)), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g., Eldridge, et al., Molec. Immunol.* 28:287-294, (1991); Alonso *et al., Vaccine* 12:299-306 (1994); Jones *et al., Vaccine* 13:675-681 (1995)), peptide compositions
5 contained in immune stimulating complexes (ISCOMS) (*see, e.g., Takahashi et al., Nature* 344:873-875 (1990); Hu *et al., Clin Exp Immunol.* 113:235-243 (1998)), multiple antigen peptide systems (MAPs) (*see, e.g., Tam, Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413 (1988); Tam, *J. Immunol. Methods* 196:17-32 (1996)), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery
10 vectors (Perkus, *et al., In: Concepts in vaccine development* (Kaufmann, ed., p. 379, 1996); Chakrabarti, *et al., Nature* 320:535 (1986); Hu *et al., Nature* 320:537 (1986); Kieny, *et al., AIDS Bio/Technology* 4:790 (1986); Top *et al., J. Infect. Dis.* 124:148 (1971); Chanda *et al., Virology* 175:535 (1990)), particles of viral or synthetic origin (*see, e.g., Kofler et al., J. Immunol. Methods.* 192:25 (1996); Eldridge *et al., Sem. Hematol.* 30:16 (1993); Falo *et al., Nature Med.* 7:649 (1995)), adjuvants (Warren *et al., Annu. Rev. Immunol.* 4:369 (1986); Gupta *et al., Vaccine* 11:293 (1993)), liposomes (Reddy *et al., J. Immunol.* 148:1585 (1992); Rock, *Immunol. Today* 17:131 (1996)), or, naked or particle absorbed cDNA (Ulmer, *et al., Science* 259:1745 (1993); Robinson *et al., Vaccine* 11:957 (1993); Shiver *et al., In: Concepts in vaccine development* (Kaufmann, ed., p. 423, 1996); Cease & Berzofsky, *Annu. Rev. Immunol.* 12:923 (1994) and Eldridge *et al., Sem. Hematol.* 30:16 (1993)). Toxin-targeted
20 delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide
25 or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or
30 aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides;

polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or
5 RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery,
10 cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of
15 vaccinia virus, *e.g.*, as a vector to express nucleotide sequences that encode prostate cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are
20 described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (*see, e.g.*, Shata *et al.*, *Mol Med Today* 6:66-71 (2000); Shedlock *et al.*, *J Leukoc Biol* 68:793-806 (2000); Hipp *et al.*, *In Vivo* 14:571-85 (2000)).
25

Methods for the use of genes as DNA vaccines are well known, and include placing a prostate cancer gene or portion of a prostate cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a prostate cancer patient. The prostate cancer gene used for DNA vaccines can encode full-length prostate cancer
30 proteins, but more preferably encodes portions of the prostate cancer proteins including peptides derived from the prostate cancer protein. In one embodiment, a patient is

immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a prostate cancer gene. For example, prostate cancer-associated genes or sequence encoding subfragments of a prostate cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the prostate cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment prostate cancer genes find use in generating animal models of prostate cancer. When the prostate cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the prostate cancer gene will also diminish or repress expression of the gene. Animal models of prostate cancer find use in screening for modulators of a prostate cancer-associated sequence or modulators of prostate cancer. Similarly, transgenic animal technology including gene knockout technology, e.g. as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the prostate cancer protein. When desired, tissue-specific expression or knockout of the prostate cancer protein may be necessary.

It is also possible that the prostate cancer protein is overexpressed in prostate cancer. As such, transgenic animals can be generated that overexpress the prostate cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of prostate cancer and are additionally useful in screening for modulators to treat prostate cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits

may include any or all of the following: assay reagents, buffers, prostate cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative prostate cancer polypeptides or polynucleotides, small molecules inhibitors of prostate cancer-associated sequences *etc.* A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (i.e., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of prostate cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a prostate cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing prostate cancer-associated activity. Optionally, the kit contains biologically active prostate cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Tissue Preparation, Labeling Chips, and Fingerprints

5 Purifying total RNA from tissue sample using TRIzol Reagent

The sample weight is first estimated. The tissue samples are homogenized in 1 ml of TRIzol per 50 mg of tissue using a homogenizer (e.g., Polytron 3100). The size of the generator/probe used depends upon the sample amount. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. A larger generator (e.g., 20 mm) is suitable for tissue samples weighing more than 0.6 g. Fill tubes should not be overfilled. If the working volume is greater than 2 ml and no greater than 10 ml, a 15 ml polypropylene tube (Falcon 2059) is suitable for homogenization.

Tissues should be kept frozen until homogenized. The TRIzol is added directly to the frozen tissue before homogenization. Following homogenization, the insoluble material is removed from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. The cleared homogenate is then transferred to a new tube(s). Samples may be frozen and stored at -60 to -70°C for at least one month or else continue with the purification.

The next process is phase separation. The homogenized samples are incubated for 5 minutes at room temperature. Then, 0.2 ml of chloroform per 1ml of TRIzol reagent is added to the homogenization mixture. The tubes are securely capped and shaken vigorously by hand (do not vortex) for 15 seconds. The samples are then incubated at room temp. for 2-3 minutes and next centrifuged at 6500 rpm in a Sorvall superspeed for 30 min. at 4°C.

The next process is RNA Precipitation. The aqueous phase is transferred to a fresh tube. The organic phase can be saved if isolation of DNA or protein is desired. Then 0.5 ml of isopropyl alcohol is added per 1ml of TRIzol reagent used in the original homogenization. Then, the tubes are securely capped and inverted to mix. The samples are then incubated at room temp. for 10 minutes and centrifuged at 6500 rpm in Sorvall for 20 min. at 4°C.

The RNA is then washed. The supernatant is poured off and the pellet washed with cold 75% ethanol. 1 ml of 75% ethanol is used per 1 ml of the TRIzol reagent used in the initial homogenization. The tubes are capped securely and inverted several times to loosen pellet without vortexing. They are next centrifuged at <8000 rpm (<7500 x g) for 5 minutes at 4°C.

The RNA wash is decanted. The pellet is carefully transferred to an Eppendorf tube (sliding down the tube into the new tube by use of a pipet tip to help guide it in if necessary). Tube(s) sizes for precipitating the RNA depending on the working volumes. Larger tubes may take too long to dry. Dry pellet. The RNA is then resuspended in an appropriate volume (e.g., 2 -5 ug/ul) of DEPC H₂O. The absorbance is then measured.

The poly A+ mRNA may next be purified from total RNA by other methods such as Qiagen's RNeasy kit. The poly A⁺ mRNA is purified from total RNA by adding the oligotex suspension which has been heated to 37°C and mixing prior to adding to RNA. The Elution Buffer is incubated at 70°C. If there is precipitate in the buffer, warm up the 2 x Binding Buffer at 65°C. The the total RNA is mixed with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook and next incubated for 3 minutes at 65°C and 10 minutes at room temperature.

The preparation is centrifuged for 2 minutes at 14,000 to 18,000 g, preferably, at a "soft setting," The supernatant is removed without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. The supernatant is saved until satisfactory binding and elution of poly A⁺ mRNA has been found.

Then, the preparation is gently resuspended in Wash Buffer OW2 and pipetted onto the spin column and centrifuged at full speed (soft setting if possible) for 1 minute.

Next, the spin column is transferred to a new collection tube and gently resuspended in Wash Buffer OW2 and centrifuged as described herein.

Then, the spin column is transferred to a new tube and eluted with 20 to 100 ul of preheated (70°C) Elution Buffer. The Oligotex resin is gently resuspended by pipetting up and down. The centrifugation is repeated as above and the elution repeated with fresh elution buffer or first eluate to keep the elution volume low.

The absorbance is next read to determine the yield, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA is precipitated before proceeding with cDNA synthesis, as components leftover or in the Elution Buffer from the

5 Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA. 0.4 vol. of 7.5 M NH₄OAc + 2.5 vol. of cold 100% ethanol is added and the preparation precipitated at -20°C 1 hour to overnight (or 20-30 min. at -70°C), and centrifuged at 14,000-16,000 x g for 30 minutes at 4°C. Next, the pellet is washed with 0.5 ml of 80% ethanol (-20°C) and then centrifuged at 14,000-16,000 x g for 5 minutes at room temperature.

10 The 80% ethanol wash is then repeated. The last bit of ethanol from the pellet is then dried without use of a speed vacuum and the pellet is then resuspended in DEPC H₂O at 1 µg/ul concentration.

Alternatively the RNA may be purified using other methods (e.g., Qiagen's RNeasy kit).

15 No more than 100 µg is added to the RNeasy column. The sample volume is adjusted to 100 µl with RNase-free water. 350 µl Buffer RLT and then 250 µl ethanol (100%) are added to the sample. The preparation is then mixed by pipetting and applied to an RNeasy mini spin column for centrifugation (15 sec at >10,000 rpm). If yield is low, reapply the flowthrough to the column and centrifuge again.

20 Then, transfer column to a new 2 ml collection tube and add 500 µl Buffer RPE and centrifuge for 15 sec at >10,000 rpm. The flowthrough is discarded. 500 µl Buffer RPE and is then added and the preparation is centrifuged for 15 sec at >10,000 rpm. The flowthrough is discarded. and the column membrane dried by centrifuging for 2 min at maximum speed. The column is transferred to a new 1.5-ml collection tube. 30-50 µl of

25 RNase-free water is applied directly onto column membrane. The column is then centrifuged for 1 min at >10,000 rpm and the elution step repeated.

The absorbance is then read to determine yield. If necessary, the material may be ethanol precipitated with ammonium acetate and 2.5X volume 100% ethanol.

30 First Strand cDNA Synthesis

The first strand can be made using using Gibco's "SuperScript Choice System for cDNA Synthesis" kit. The starting material is 5 ug of total RNA or 1 ug of polyA+ mRNA. For total RNA, 2 ul of SuperScript RT is used; for polyA+ mRNA, 1 ul of SuperScript RT is used. The final volume of first strand synthesis mix is 20 ul. The RNA should be in a volume no greater than 10 ul. The RNA is incubated with 1 ul of 100 pmol T7-T24 oligo for 10 min at 70°C followed by addition on ice of 7 ul of: 4ul 5X 1st Strand Buffer, 2 ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. The preparation is then incubated at 37°C for 2 min before addition of the SuperScript RT followed by incubation at 37°C for 1 hour.

Second Strand Synthesis

For the second strand synthesis, place 1st strand reactions on ice and add: 91 ul DEPC H₂O; 30 ul 5X 2nd Strand Buffer; 3 ul 10mM dNTP mix; 1 ul 10 U/ul E.coli DNA Ligase; 4 ul 10 U/ul E.coli DNA Polymerase; and 1 ul 2 U/ul RNase H. Mix and incubate 2 hours at 16°C. Add 2 ul T4 DNA Polymerase. Incubate 5 min at 16°C. Add 10 ul of 0.5M EDTA.

Cleaning up cDNA

The cDNA is purified using Phenol:Chloroform:Isoamyl Alcohol (25:24:1) and Phase-Lock gel tubes. The PLG tubes are centrifuged for 30 sec at maximum speed. The cDNA mix is then transferred to PLG tube. An equal volume of phenol:chloroform:isamyl alcohol is then added, the preparation shaken vigorously (no vortexing), and centrifuged for 5 minutes at maximum speed. The top aqueous solution is transferred to a new tube and ethanol precipitated by adding 7.5X 5M NH₄OAc and 2.5X volume of 100% ethanol. Next, it is centrifuged immediately at room temperature for 20 min, maximum speed. The supernatant is removed, and the pellet washed with 2X with cold 80% ethanol. As much ethanol wash as possible should be removed before air drying the pellet; and resuspending it in 3 ul RNase-free water.

In vitro Transcription (IVT) and labeling with biotin

In vitro Transcription (IVT) and labeling with biotin is performed as follows:

Pipet 1.5 ul of cDNA into a thin-wall PCR tube. Make NTP labeling mix by combining 2 ul T7 10xATP (75 mM) (Ambion); 2 ul T7 10xGTP (75 mM) (Ambion); 1.5 ul T7 10xCTP (75 mM) (Ambion); 1.5 ul T7 10xUTP (75 mM) (Ambion); 3.75 ul 10 mM Bio-11-UTP (Boehringer-Mannheim/Roche or Enzo); 3.75 ul 10 mM Bio-16-CTP (Enzo); 2 ul 10x T7 transcription buffer (Ambion); and 2 ul 10x T7 enzyme mix (Ambion). The final volume is 20 ul. Incubate 6 hours at 37°C in a PCR machine. The RNA can be further cleaned. Clean-up follows the previous instructions for RNeasy columns or Qiagen's RNeasy protocol handbook. The cRNA often needs to be ethanol precipitated by resuspension in a volume compatible with the fragmentation step.

Fragmentation is performed as follows. 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer (5 x Fragmentation buffer is 200 mM Tris-acetate, pH 8.1; 500 mM KOAc; 150 mM MgOAc). The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65°C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range.

For hybridization, 200 ul (10 ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made. The hybridization mix is: fragment labeled RNA (50 ng/ul final conc.); 50 pM 948-b control oligo; 1.5 pM BioB; 5 pM BioC; 25 pM BioD; 100 pM CRE; 0.1 mg/ml herring sperm DNA; 0.5 mg/ml acetylated BSA; and 300 ul with 1xMES hyb buffer.

The hybridization reaction is conducted with non-biotinylated IVT (purified by RNeasy columns) (see example 1 for steps from tissue to IVT): The following mixture is prepared:

IVT antisense RNA; 4 µg:	µl
Random Hexamers (1 µg/µl):	4 µl
H ₂ O:	<u> µl </u>
	14 µl

- 5 Incubate the above 14 µl mixture at 70°C for 10 min.; then put on ice.

The Reverse transcription procedure uses the following mixture:

0.1 M DTT:	3 µl
50X dNTP mix:	0.6 µl
H ₂ O:	2.4 µl
10 Cy3 or Cy5 dUTP (1mM):	3 µl
SS RT II (BRL):	1 µl
	<u> </u>
	16 µl

The above solution is added to the hybridization reaction and incubated for 30 min., 42°C.

- 15 Then, 1 µl SSII is added and incubated for another hour before being placed on ice.

The 50X dNTP mix contains 25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP and is made by adding 25 µl each of 100mM dATP, dCTP, and dGTP; 10 µl of 100mM dTTP to 15 µl H₂O.]

- RNA degradation is performed as follows. Add 86 µl H₂O, 1.5 µl 1M NaOH/
20 2 mM EDTA and incubate at 65°C, 10 min.. For U-Con 30, 500 µl TE/sample spin at 7000 g for 10 min, save flow through for purification. For Qiagen purification, suspend u-con recovered material in 500 µl buffer PB and proceed using Qiagen protocol. For DNase digestion, add 1 ul of 1/100 dilution of DNase/30 ul Rx and incubate at 37°C for 15 min. Incubate at 5 min 95°C to denature the DNase.

25

Sample preparation

For sample preparation, add Cot-1 DNA, 10 µl; 50X dNTPs, 1 µl; 20X SSC, 2.3 µl; Na pyro phosphate, 7.5 µl; 10 mg/ml Herring sperm DNA; 1 ul of 1/10 dilution to 21.8 final vol. Dry in speed vac. Resuspend in 15 µl H₂O. Add 0.38 µl 10% SDS. Heat

95°C, 2 min and slow cool at room temp. for 20 min. Put on slide and hybridize overnight at 64°C. Washing after the hybridization: 3X SSC/0.03% SDS: 2 min., 37.5 ml 20X SSC+0.75ml 10% SDS in 250ml H₂O; 1X SSC: 5 min., 12.5 ml 20X SSC in 250ml H₂O; 0.2X SSC: 5 min., 2.5 ml 20X SSC in 250ml H₂O. Dry slides and scan at appropriate PMT's and channels.

Example 2: Taxol resistant Xenograft Model of Human Prostate Cancer

Treatment regimens that include paclitaxel (Taxol; Bristol-Myers Squibb Company, Princeton, NJ) have been particularly successful in treating hormone-refractory prostate cancer in the phase II setting (Smith et al., Semin. Oncol. 26(1 Suppl 2):109-11 (1999)). However, many patients develop tumors which are initially, or later become, resistant to taxol. To identify genes that may be involved with resistance to taxol, or are regulated in response to taxol resistance, and therefore may be used to treat, or identify, taxol resistance in patients, the following experiments were carried out.

The androgen-independent human cell line CWR22R was grown as a xenograft in nude mice (Nagabhushan et al., Cancer Res. 56(13):3042-3046 (1996); Agus et al., J. Natl. Cancer Inst. 91(21):1869-1876 (1999); Bubendorf et al., J. Natl. Cancer Inst. 91(20):1758-1764 (1999)). Initially, these xenograft tumors were sensitive to therapeutic doses of taxol. The mice were treated continuously with sub-therapeutic doses, and the tumors were allowed to grow for 3-4 weeks, before surgical removal of the tumors. The tumor from an individual mouse was then minced, and a small portion was then injected into a healthy nude mouse, establishing a second passage of the tumor. This mouse was then treated continuously with the same sub-therapeutic dose of taxol. This process was repeated 14 times, and a portion of each generation of xenograft tumor was collected. There was increasing resistance to therapeutic doses of taxol with each generation. By the end of the process, the tumors were fully resistant to therapeutic doses of taxol. RNA from each generation of tumor was then isolated, and individual mRNA species were quantified using a custom Affymetrix GeneChip® oligonucleotide microarray, with probes to interrogate approximately 35,000

unique mRNA transcripts. Genes were selected that showed a statistically significant up-regulation, or down-regulation, during the subsequent generations of increasingly taxol-resistant tumors. Only one gene was significantly up-regulated, whereas 24 genes were down-regulated; these are presented in Table 10.

The gene sequences identified to be overexpressed in prostate cancer may be used to identify coding regions from the public DNA database. The sequences may be used to either identify genes that encode known proteins, or they may be used to predict the coding regions from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev, 2000, Genome Res. 10:516-522). In addition, one of ordinary skill in the art would understand how to obtain the unigene cluster identification and sequence information according to the exemplar accession numbers provided in Tables 1-16. (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

15

TABLE1: shows genes, including expression sequence tags, differentially expressed in prostate tumor tissue compared to normal tissue as analyzed using the Affymetrix/Eos Hu01 GeneChip array. Shown are the relative amounts of each gene expressed in prostate tumor samples and various normal tissue samples showing the highest expression of the gene.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal body tissue			
15					
	Pkey	UnigeneID	ExAccn	Unigene Title	R1
	131919	Hs.272458	AA121266	ESTs	37.2
	120328	Hs.290905	AA196979	ESTs; Weakly similar to (define not ava	32.6
20	105201	Hs.31412	AA195626	ESTs	30.1
	101486	Hs.1852	M24902	acid phosphatase; prostate	25.2
	119073	Hs.279477	R32894	ESTs	24.8
	133428	Hs.183752	M34376	microseminoprotein; beta-	23.8
	128180	Hs.171995	AA595348	kallikrein 3; (prostate specific antigen	21.4
25	104080	Hs.57771	AA402971	Homo sapiens mRNA for serine protease (T	18.9
	127537	Hs.162859	AA569531	ESTs	18.6
	131665	Hs.30343	R22139	ESTs	17.4
	101050	Hs.1832	K01911	neuropeptide Y	17.3
	130771	Hs.1915	N48056	folate hydrolase (prostate-specific memb	17
30	108153	Hs.40808	AA054237	ESTs	16.9
	107485	Hs.262476	W63793	S-adenosylmethionine decarboxylase 1	16.7
	106155	Hs.33287	AA425309	ESTs	16.5
	129534	Hs.11260	R73640	ESTs	16.4
	100569	Hs.171995	HG2261-HT2351	Antigen, Prostate Specific, Alt. Splice	16
35	101889	Hs.181350	S39329	kallikrein 2; prostatic	15.4
	135389	Hs.99872	U05237	fetal Alzheimer antigen	15
	101506	Hs.62192	M27436	coagulation factor III (thromboplastin;	13.9
	134374	Hs.8236	D62633	ESTs	12.7
	133944	Hs.7780	AA045870	ESTs	12.5
40	109141	Hs.193380	AA176428	ESTs	12.3
	130974	Hs.2178	X57985	H2B histone family; member Q	11.8
	114768	Hs.182339	AA149007	ESTs	11.8
	104394	Hs.172129	H46617	yp19h1.r1 Soares breast 3NbHBst Homo sap	11.8
	125299	Hs.102720	Z39436	ESTs	11.6
45	104660	Hs.14846	AA007160	ESTs	11.4
	100116	Hs.78045	D00654	actin; gamma 2; smooth muscle; enteric	11
	131061	Hs.268744	N64328	ESTs; Moderately similar to KIAA0273 [H.	10.9
	126645	126645	AI167942	Homo sapiens BAC clone RG041D11 from 7q2	10.7
	135153	Hs.95420	N40141	Homo sapiens mRNA for JM27 protein; comp	10.6
50	107033	Hs.113314	AA599629	ESTs	10.6
	118417		N66048	ESTs; Weakly similar to polymerase [H.sa	10.5
	126758	Hs.293960	W37145	ESTs	10.2
	115674	Hs.8364	AA406542	ESTs	10.1
	134969	Hs.92381	AA236324	ESTs; Weakly similar to !!!! ALU CLASS A	10.1
55	107102	Hs.30652	AA609723	ESTs	10.1
	116787	Hs.15641	H28581	ESTs	10.1
	115719	Hs.59622	AA416997	ESTs	10
	123209	Hs.203270	AA489711	ESTs	9.9
	101664	Hs.121017	M60752	H2A histone family; member A	9.8
60	112971	Hs.83883	T17185	ESTs	9.7
	102519	Hs.80296	U52969	Purkinje cell protein 4	9.7
	117984	Hs.106778	N51919	ESTs	9.7
	105840	Hs.22209	AA398533	ESTs	9.4
	129523	Hs.274509	M30894	T-cell receptor; gamma cluster	9.4
65	132964	Hs.167133	AA031360	ESTs	9.2
	121853	Hs.98502	AA425887	ESTs	9

	115764	Hs.91011	AA421562	anterior gradient 2 (Xenopus laevis; sec	8.9
	119617	Hs.55999	W47380	ESTs	8.9
	100552	Hs.301946	HG2167-HT2237	Protein Kinase Ht31, Camp-Dependent	8.9
	105627	Hs.23317	AA281245	ESTs	8.8
5	101461	Hs.76422	M22430	phospholipase A2; group IIA (platelets;	8.7
	131725	Hs.31148	AA456264	ESTs; Highly similar to (define not ava	8.5
	124526	Hs.293185	N62096	yz61c5.s1 Soares_multiple_sclerosis_2NbH	8.5
	118528	Hs.49397	N67889	ESTs	8.2
	133845	Hs.76704	T68510	ESTs	8.2
10	133354	Hs.334762	AA055552	ESTs; Weakly similar to KIAA0319 [H.sapi	8.1
	105912	Hs.20415	AA402000	ESTs; Weakly similar to GS3786 [H.sapien	8
	119018	Hs.278695	N95796	ESTs	8
	100394	Hs.66052	D84276	CD38 antigen (p45)	8
	114132	Hs.24192	Z38688	ESTs	7.9
15	116786	Hs.301527	H25836	tumor necrosis factor (ligand) superfam	7.7
	106579	Hs.23023	AA456135	ESTs	7.6
	128790	Hs.105700	AA291725	secreted frizzled-related protein 4	7.5
	114965	Hs.72472	AA250737	ESTs	7.4
	112033	Hs.22627	R43162	ESTs	7.1
20	102398		U42359	Human N33 protein form 1 (N33) gene, exo	7
	101201	Hs.2256	L22524	matrix metalloproteinase 7 (matrilysin;	6.9
	109272	Hs.288462	AA195718	ESTs	6.9
	103145	Hs.169849	X66276	myosin-binding protein C; slow-type	6.9
	101803	Hs.155691	M86546	pre-B-cell leukemia transcription factor	6.8
25	120562	Hs.302267	AA280036	ESTs; Weakly similar to W01A6.c [C.elega	6.8
	109112	Hs.257924	AA169379	ESTs	6.8
	109795	Hs.326416	F10707	ESTs	6.7
	107532	Hs.173684	Z19643	ESTs; Weakly similar to (define not ava	6.7
	130336	Hs.171995	X07730	kallikrein 3; (prostate specific antigen	6.6
30	131425	Hs.26691	AA219134	ESTs	6.6
	120588	Hs.16193	AA281591	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	6.6
	132902	Hs.59838	AA490969	ESTs	6.6
	125674	Hs.323378	W28078	H.sapiens mRNA for transmembrane protein	6.6
	133724	Hs.75746	U07919	aldehyde dehydrogenase 6	6.5
35	130343	Hs.278628	AA490262	ESTs; Moderately similar to APXL gene pr	6.5
	120215	Hs.108787	Z41050	Homo sapiens Mod4p homolog mRNA; complet	6.5
	129215	Hs.126085	AA176867	ESTs	6.5
	131881	Hs.3383	AA010163	upstream regulatory element binding prot	6.5
	133376	Hs.7232	T23670	ESTs	6.4
40	105376	Hs.8768	AA236559	ESTs; Weakly similar to neuronal thread	6.4
	104874	Hs.26289	AA009527	ESTs	6.4
	100727	Hs.334786	X07290	Human HF.12 gene mRNA	6.3
	130150	Hs.15113	AF000573	homogenisate 1,2-dioxygenase (homogenti	6.3
	121770	Hs.278428	AA421714	Homo sapiens mRNA for KIAA0896 protein;	6.3
45	123475	Hs.250528	AA599267	ESTs; Weakly similar to ANKYRIN; BRAIN V	6.3
	133061	Hs.296638	AB000584	prostate differentiation factor	6.3
	116429	Hs.279923	AA608710	ESTs; Weakly similar to similar to GTP-b	6.2
	101233	Hs.878	L29008	sorbitol dehydrogenase	6.2
	104691	Hs.37744	AA011176	ESTs	6.2
50	127248		AA325029	EST27953 Cerebellum II Homo sapiens cDNA	6.2
	127775	Hs.179902	H04106	ESTs; Weakly similar to (define not ava	6.2
	105500	Hs.222399	AA256485	ESTs	6.1
	131463	Hs.2714	X74142	forkhead (Drosophila)-like 1	6.1
	132116	Hs.40289	AA234767	ESTs	6
55	130828	Hs.203213	AA053400	ESTs	5.9
	115357	Hs.72988	AA281793	ESTs	5.8
	105496	Hs.301997	AA256323	ESTs	5.7
	116334	Hs.48948	AA491457	ESTs	5.7
	107968	Hs.61539	AA034020	ESTs	5.7
60	120132	Hs.125019	Z38839	ESTs; Weakly similar to !!!! ALU SUBFAM	5.6
	106375	Hs.289072	AA443993	ESTs	5.6
	132550	Hs.170195	AA029597	bone morphogenetic protein 7 (osteogenic	5.6
	124777	Hs.140237	R41933	ESTs; Weakly similar to neuronal thread	5.6
	100311	Hs.337616	D50640	phosphodiesterase 3B; cGMP-inhibited	5.6
65	101791	Hs.62354	M83822	Human beige-like protein (BGL) mRNA; par	5.5
	117698	Hs.45107	N41002	ESTs	5.5
	132387	Hs.281434	R70914	heat shock 70kD protein 1	5.5
	122041	Hs.98732	AA431407	Homo sapiens Chromosome 16 BAC clone CIT	5.5
	133723	Hs.262476	AA088851	S-adenosylmethionine decarboxylase 1	5.5

	113938	W81598	ESTs	5.4
	133015	Hs.246315 AA047036	ESTs	5.4
	125745	Hs.75722 A1283493	ribophorin II	5.4
	107295	Hs.80120 T34527	UDP-N-acetyl-alpha-D-galactosamine:polyp	5.4
5	108186	Hs.7780 AA056482	ESTs	5.3
	100184	Hs.21223 D17408	calponin 1; basic; smooth muscle	5.3
	104466	Hs.326392 N25110	Human guanine nucleotide exchange factor	5.3
	104033	Hs.98944 AA365031	ESTs	5.3
	110844	Hs.167531 N31952	ESTs; Weakly similar to (define not ava	5.3
10	129056	Hs.108336 H70627	ESTs; Weakly similar to !!!! ALU SUBFAM	5.3
	102805	Hs.25351 U90304	iroquois-class homeodomain protein	5.3
	133493	Hs.194369 AA284143	Homo sapiens chromosome 1 atrophin-1 rel	5.3
	129184	Hs.109201 W26769	ESTs; Highly similar to (define not ava	5.2
	134158	Hs.79428 U15174	BCL2/adenovirus E1B 19kD-interacting pro	5.2
15	107240	Hs.159872 D59368	ESTs	5.2
	104787	AA027317	ESTs; Weakly similar to !!!! ALU SUBFAM	5.2
	123527	Hs.108327 AA608679	damage-specific DNA binding protein 1 (1	5.2
	116646	Hs.194228 F03048	ESTs; Moderately similar to !!!! ALU SUB	5.2
	101448	Hs.195850 M21389	keratin 5 (epidermolysis bullosa simplex	5.1
20	116188	Hs.184598 AA464728	ESTs; Weakly similar to !!!! ALU SUBFAM	5.1
	126259	Hs.281428 Z21472	ESTs; Moderately similar to !!!! ALU SUB	5.1
	105921	Hs.169119 AA402613	ESTs	5.1
	103375	Hs.54416 X91868	sine oculis homeobox (Drosophila) homolo	5.1
	128871	Hs.106778 AA400271	ESTs; Highly similar to (define not ava	5.1
25	112681	Hs.148932 R87331	ESTs; Moderately similar to semaphorin V	5.1
	105784	Hs.226434 AA350771	ESTs	5.1
	116238	Hs.47144 AA479362	ESTs	5
	102913	Hs.80342 X07696	keratin 15	5
	103011	Hs.326035 X52541	early growth response 1	5
30	126023	H58881	yr36d09.r1 Soares fetal liver spleen 1NF	5
	103709	Hs.13804 AA037316	ESTs	5
	118981	Hs.39288 N93839	ESTs; Weakly similar to !!!! ALU SUBFAM	5
	134807	Hs.89732 X78932	zinc finger protein 273	5
	100079	Hs.23311 AB002365	Human mRNA for KIAA0367 gene; partial cd	4.9
35	132047	Hs.3796 D83492	EphB6	4.9
	132880	Hs.177537 AA444369	ESTs	4.9
	124049	Hs.74519 F10523	primase; polypeptide 2A (58kD)	4.8
	133330	Hs.71119 U42360	Human N33 mRNA; complete cds	4.8
	104776	AA026349	ESTs	4.8
40	122593	Hs.128749 AA453310	Homo sapiens alpha-methylacyl-CoA racema	4.8
	103912	Hs.143087 AA251078	ESTs	4.8
	113961	Hs.26009 W86307	Homo sapiens mRNA for KIAA0860 protein;	4.8
	105288	Hs.3585 AA233168	ESTs; Weakly similar to coded for by C.	4.8
	135035	Hs.284186 H89575	ESTs	4.8
45	104144	Hs.183390 AA447439	ESTs; Weakly similar to ZINC FINGER PROT	4.8
	129389	Hs.288126 AA621604	ESTs	4.8
	125982	R98091	RAE1 (RNA export 1; S.pombe) homolog	4.8
	125162	Hs.26243 W44682	ESTs	4.8
	103023	Hs.117950 X53793	multifunctional polypeptide similar to S	4.7
50	129735	W80701	ESTs; Weakly similar to HERV-E envelope	4.7
	104479	Hs.106390 N36040	ESTs	4.7
	103731	AA070545	zm7c3.r1 Stratagene neuroepithelium (#93	4.7
	126575	Hs.127602 W72416	ESTs	4.7
	124578	Hs.231500 N68321	Human glucose transporter-like protein-1	4.7
55	130817	Hs.1674 M90516	glutamine-fructose-6-phosphate transamin	4.7
	116752	Hs.91622 H06373	Homo sapiens clone 24456 mRNA sequence	4.7
	100279	Hs.82007 D42084	Human mRNA for KIAA0094 gene; partial cd	4.7
	126288	Hs.89576 A1479264	ESTs	4.7
	131836	Hs.32990 AA610086	ESTs	4.7
60	106717	Hs.239489 AA465093	TIA1 cytotoxic granule-associated RNA-bi	4.7
	114542	Hs.91011 AA055768	ESTs	4.6
	103806	AA130614	zo1f2.r1 Stratagene neuroepithelium NT2R	4.6
	130529	AA173238	small inducible cytokine A5 (RANTES)	4.6
	115675	Hs.82065 AA406546	ESTs	4.6
65	111386	Hs.293798 N95326	ESTs	4.6
	106503	Hs.29679 AA452411	ESTs	4.6
	119943	Hs.14158 W86835	copine III	4.6
	104459	Hs.100070 M91493	EST	4.6
	100774	Hs.89603 HG371-HT1063	Mucin 1, Epithelial, Alt. Splice 6	4.6

	100652	Hs.142653	HG2825-HT2949	Ret Transforming Gene	4.6
	132015	Hs.3731	D11900	ESTs	4.6
	126086		H70975	yr73g01.r1 Soares fetal liver spleen 1NF	4.6
	130888	Hs.173094	F03819	ESTs	4.6
5	106390	Hs.20166	AA446964	Prostate stem cell antigen	4.6
	126959		AA199853	ESTs; Moderately similar to !!!! ALU SUB	4.5
	131584	Hs.29117	X91648	H.sapiens mRNA for pur alpha extended 3'	4.5
	104838	Hs.20953	AA039481	ESTs	4.5
	125661		R50319	ESTs	4.5
10	103171	Hs.234726	X68733	alpha-1-antichymotrypsin	4.5
	103928	Hs.199160	AA280085	ESTs	4.5
	102899	Hs.75730	X06272	signal recognition particle receptor (d	4.5
	100892	Hs.180789	HG4557-HT4962	Small Nuclear Ribonucleoprotein U1, 1snr	4.5
	106167	Hs.7956	AA425906	ESTs	4.5
15	129404	Hs.317584	AA172056	ESTs	4.5
	106990	Hs.24758	AA521354	ESTs	4.5
	132316	Hs.44566	U28831	Human protein immuno-reactive with anti-	4.4
	132056	Hs.38176	T89386	Homo sapiens mRNA for KIAA0606 protein;	4.4
	133718	Hs.198760	X15306	neurofilament; heavy polypeptide (200kD)	4.4
20	101470	Hs.1846	M22898	tumor protein p53 (Li-Fraumeni syndrome)	4.4
	131904	Hs.284296	AA143019	ESTs; Highly similar to surface 4 integr	4.4
	105804	Hs.22514	AA383142	ESTs	4.4
	122861	Hs.119394	AA464428	ESTs	4.4
	111336	Hs.29894	N79565	ESTs	4.4
25	121944	Hs.98518	AA429278	ESTs	4.4
	134401	Hs.211577	AA243746	ESTs; Highly similar to CG1 protein [H.s	4.4
	126458	Hs.288969	AA815252	ESTs; Weakly similar to !!!! ALU SUBFAM1	4.4
	133435	Hs.323966	T23983	ESTs; Moderately similar to !!!! ALU SUB	4.4
	105178	Hs.21941	AA187490	ESTs	4.3
30	127315		AA640834	nr27b06.r1 NCI_CGAP_Pr3 Homo sapiens cDN	4.3
	132645	Hs.54424	X87870	H.sapiens mRNA for hepatocyte nuclear fa	4.3
	116162	Hs.282990	AA461487	ESTs; Weakly similar to F52C12.2 [C.eleg	4.3
	118040	Hs.47567	N52876	EST	4.3
	130008	Hs.278427	M31423	cerebellar degeneration-related protein	4.3
35	126607	Hs.114688	W87424	ESTs	4.3
	123061	Hs.105130	AA482030	EST	4.3
	109391	Hs.184245	AA219699	ESTs	4.3
	109175		AA180496	ESTs	4.3
	127003	Hs.173540	AA550806	ESTs; Weakly similar to (define not ava	4.3
40	102547	Hs.46638	U57911	chromosome 11 open reading frame 8	4.3
	134208	Hs.79993	U88871	peroxisomal biogenesis factor 7	4.3
	104258	Hs.5462	AF007216	solute carrier family 4; sodium bicarbon	4.3
	130759	Hs.18946	AA094720	ESTs; Weakly similar to (define not ava	4.3
	132160	Hs.285923	AA281770	seven in absentia (Drosophila) homolog 1	4.3
45	135062	Hs.93872	AA174183	ESTs	4.3
	126510	Hs.334762	R49702	ESTs; Weakly similar to KIAA0319 [H.sapi	4.2
	122055	Hs.98747	AA431732	EST	4.2
	133136	Hs.6574	AF007165	suppressin (nuclear deformed epidermal a	4.2
	109890	Hs.20843	H04649	ESTs	4.2
50	133294	Hs.69997	R79723	H.sapiens mRNA for translin associated z	4.2
	134436	Hs.83190	S80437	fatty acid synthase (3' region) [human,	4.2
	107375	Hs.251064	U88573	NBR2	4.2
	122223	Hs.27413	AA436158	ESTs	4.2
	103044	Hs.248210	X55777	H.sapiens Mahlavu hepatocellular carcino	4.2
55	120125	Hs.59815	W99362	EST	4.2
	128969	Hs.283978	T65327	ESTs; Highly similar to (define not ava	4.2
	129637	Hs.1179	D90359	TATA box binding protein (TBP)-associate	4.2
	106566		AA455921	ESTs; Weakly similar to !!!! ALU SUBFAM1	4.2
	112605	Hs.29852	R79220	ESTs	4.2
60	103364	Hs.279929	X90872	H.sapiens mRNA for gp25L2 protein	4.2
	132811	Hs.57419	U25435	transcriptional repressor	4.2
	126570	Hs.326292	T79274	ESTs	4.2
	116298	Hs.94109	AA489046	ESTs	4.2
	103024	Hs.105938	X53961	lactotransferrin	4.1
65	129133	Hs.108850	R56728	yg95c6.r1 Soares infant brain 1NIB Homo	4.1
	133167	Hs.6641	N98707	kinesin family member 5C	4.1
	126871	Hs.14051	AA351779	ESTs	4.1
	132333	Hs.45032	AA192157	ESTs	4.1
	107376	Hs.327179	U90545	solute carrier family 17 (sodium phospho	4.1

	128517	Hs.100861	AA280617	ESTs; Weakly similar to p60 katanin [H.s]	4.1
	130555	Hs.116774	AA450324	ESTs	4.1
	105765	Hs.24183	AA343514	ESTs	4.1
	126529	Hs.26369	AA133237	ESTs	4.1
5	125928	Hs.181889	H29730	ESTs	4.1
	117280	Hs.172129	N22107	ESTs; Moderately similar to !!!! ALU SUB	4.1
	100234	Hs.3085	D29677	KIAA0054 gene product	4.1
	100959	Hs.118127	J00073	actin; alpha; cardiac muscle	4.1
	107130	Hs.12913	AA620582	ESTs; Weakly similar to (define not ava	4.1
10	105035	Hs.8859	AA128486	ESTs	4.1
	126735	Hs.226795	AA808949	glutathione S-transferase pi	4.1
	113056	Hs.8036	T26471	ESTs; Moderately similar to !!!! ALU SUB	4
	102460	Hs.211582	U48959	Homo sapiens myosin light chain kinase (4
	106968	Hs.26813	AA504631	ESTs; Weakly similar to (define not ava	4
15	123107	Hs.104207	AA486071	ESTs	4
	127256	Hs.267967	AA327550	ESTs; Weakly similar to !!!! ALU SUBFAMI	4
	105329	Hs.22862	AA234561	ESTs	4
	115504	Hs.42736	AA291946	ESTs	4
	120726	Hs.97293	AA293856	ESTs	4
20	103576	Hs.94560	Z26317	desmoglein 2	4
	127889	Hs.144941	AI147408	ESTs	4
	106394	Hs.25320	AA447223	ESTs	4
	128046		AA873285	ESTs	4
	103391	Hs.114366	X94453	pyrroline-5-carboxylate synthetase (glut	4
25	106448	Hs.27004	AA449455	ESTs	4
	126513	Hs.86276	W27601	ESTs; Moderately similar to (define not	4
	129593	Hs.98314	AA487015	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.9
	110151	Hs.31608	H18838	ESTs	3.9
	105344	Hs.8645	AA235303	ESTs	3.9
30	104791	Hs.301871	AA029046	ESTs	3.9
	123442	Hs.111496	AA598803	ESTs	3.9
	127800	Hs.79428	AA521047	BCL2/adenovirus E1B 19kD-interacting pro	3.9
	114555	Hs.167904	AA058594	ESTs	3.9
	122138	Hs.163960	AA435549	ESTs	3.9
35	129565	Hs.198726	X77777	vasoactive intestinal peptide receptor 1	3.9
	103471	Hs.75216	Y00815	protein tyrosine phosphatase; receptor t	3.9
	133908	Hs.325474	M83216	caldesmon 1	3.9
	105635	Hs.301985	AA281508	ESTs	3.9
	134285	Hs.81086	AA460012	solute carrier family 22 (organic cation	3.9
40	134125	Hs.50421	R38102	KIAA0203 gene product	3.9
	125628	Hs.241493	AA418069	natural killer-tumor recognition sequenc	3.9
	103695	Hs.186600	AA018758	ESTs	3.9
	100642	Hs.182183	HG2743-HT3926	Caldesmon 1, Alt. Splice 6, Non-Muscle	3.9
	104334	Hs.78771	D82614	ESTs	3.9
45	110242	Hs.19978	H26417	ESTs	3.9
	125298	Hs.289008	Z39255	ESTs	3.9
	104060	Hs.303193	AA397968	z187a9.r1 Soares_testis_NHT Homo sapiens	3.9
	105823	Hs.293960	AA398197	ESTs	3.9
	126499	Hs.110445	AA315671	ESTs; Moderately similar to unknown [M.m	3.9
50	130752	Hs.18895	D50927	KIAA0137 gene product	3.8
	123494	Hs.112110	AA599786	ESTs	3.8
	104846	Hs.32478	AA040154	ESTs	3.8
	108921	Hs.71721	AA142913	ESTs	3.8
	115506	Hs.45207	AA292537	ESTs	3.8
55	100452	Hs.241552	D87742	Human mRNA for KIAA0268 gene; partial cd	3.8
	104454	Hs.129228	M84443	galactokinase 2	3.8
	108730	Hs.102859	AA126254	ESTs	3.8
	131223	Hs.24427	AA247788	ESTs; Highly similar to (define not ava	3.8
	104784	Hs.269228	AA027055	ESTs	3.8
60	104946	Hs.73848	AA069549	ESTs	3.8
	106932	Hs.9394	AA495926	ESTs	3.8
	101724	Hs.620	M69225	bullous pemphigoid antigen 1 (230/240kD)	3.8
	106140	Hs.14912	AA424524	Homo sapiens mRNA for KIAA0286 gene; par	3.8
	128135	Hs.269721	AA913491	ESTs	3.8
65	120030	Hs.58694	W92051	ESTs	3.8
	126457	Hs.50382	AA007489	zh98g04.r1 Soares_fetal_liver_spleen_1NF	3.8
	123917	Hs.112969	AA621311	EST	3.7
	110714	Hs.17752	H95978	Homo sapiens phosphatidylserine-specific	3.7
	130577	Hs.162	M35410	insulin-like growth factor binding prote	3.7

	117667	Hs.44708	N39214	ser-Thr protein kinase related to the my	3.7
	126104	Hs.39712	N77278	ESTs; Weakly similar to BONE/CARTILAGE P	3.7
	100379	Hs.278721	D82060	Homo sapiens mRNA for membrane protein w	3.7
5	115646	Hs.305971	AA404352	ESTs	3.7
	125792	Hs.193700	AI005388	ESTs; Moderately similar to !!!! ALU SUB	3.7
	102162	Hs.1592	U18291	CDC16 (cell division cycle 16; S. cerevi	3.7
	128530	Hs.183475	AA504343	ESTs; Moderately similar to !!!! ALU SUB	3.7
	119940	Hs.272531	W86779	EST	3.7
10	110769	Hs.23837	N22222	yw34b06.s1 Morton Fetal Cochlea Homo sap	3.7
	132914	Hs.60293	AA496037	ESTs	3.7
	113594	Hs.15683	T92030	ESTs	3.7
	103702	Hs.279952	AA027793	ESTs; Highly similar to (define not ava	3.7
	130780	Hs.19347	AA248406	ESTs	3.7
	123288	Hs.291025	AA495836	EST	3.7
15	120691	Hs.22380	AA291173	ESTs	3.7
	103153	Hs.75295	X66534	guanylate cyclase 1; soluble; alpha 3	3.7
	129201	Hs.109390	H19969	ESTs	3.7
	114788	Hs.54900	AA159181	ESTs	3.7
20	126801	Hs.7337	AA512802	ESTs	3.7
	105503	Hs.31707	AA256616	ESTs	3.7
	104260	Hs.194283	AF008192	Homo sapiens putative GR6 protein (GR6)	3.7
	125980	Hs.35699	R97219	ESTs	3.7
	123255	Hs.105273	AA490890	ESTs	3.6
	103862	Hs.6363	AA206625	ESTs	3.6
25	100696	Hs.121686	HG3162-HT3339	Transcription Factor lia	3.6
	134917	Hs.166994	X87241	FAT tumor suppressor (Drosophila) homolo	3.6
	103520	Hs.10511	Y10511	H.sapiens mRNA for CD176 protein	3.6
	113778	Hs.302738	W15263	ESTs	3.6
30	101838	Hs.75511	M92934	connective tissue growth factor	3.6
	113702	Hs.75511	T97307	ESTs; Moderately similar to !!!! ALU SUB	3.6
	118201	Hs.48428	N59800	EST	3.6
	116519	Hs.68554	C20780	EST	3.6
	105886	Hs.22983	AA400517	ESTs; Moderately similar to UDP-GLUCOSE:	3.6
35	106709	Hs.170291	AA464696	ESTs	3.6
	127858	Hs.27973	AA806365	oc26h07.s1 NCI_CGAP_GCB1 Homo sapiens cD	3.6
	101964	Hs.27973	S81578	dioxin-responsive gene [putative polyade	3.6
	105508	Hs.326416	AA256680	ESTs	3.6
	116844	Hs.337434	H64938	ESTs	3.6
	105372	Hs.142296	AA236481	ESTs	3.6
40	100745	Hs.144630	HG3510-HT3704	V-Erba Related Ear-3 Protein	3.6
	127521	Hs.164018	AA809982	ESTs	3.6
	110758	Hs.274265	N21365	talín	3.6
	107307	Hs.44155	T52099	creatine kinase; mitochondrial 2 (sarcom	3.6
45	133200	Hs.183639	AA432248	ESTs	3.6
	114774	Hs.184325	AA150043	ESTs	3.6
	120265	Hs.270696	AA173759	ESTs; Moderately similar to !!!! ALU SUB	3.6
	134359	Hs.199067	M34309	v-erb-b2 avian erythroblastic leukemia v	3.6
	116250	Hs.44829	AA480975	ESTs; Moderately similar to !!!! ALU SUB	3.6
50	106313	Hs.35841	AA436459	nuclear factor I/X (CCAAT-binding transc	3.6
	131898	Hs.279780	N52232	ESTs	3.6
	133444	Hs.73793	M27281	vascular endothelial growth factor	3.6
	128232	Hs.334841	H06296	ESTs	3.6
	135357	Hs.79572	AA235803	ESTs	3.5
55	457951	Hs.79572	AI369384	arylsulfatase D	3.5
	108407	Hs.79572	AA075519	zm87h9.s1 Stratagene ovarian cancer (#93	3.5
	126659	Hs.79572	T16245	a disintegrin and metalloproteinase doma	3.5
	104189	Hs.301804	AA485805	ESTs	3.5
	125956	Hs.129014	N53276	ESTs	3.5
60	103026	Hs.79386	X54162	Human mRNA for a 64 Kd autoantigen expre	3.5
	133011	Hs.171921	AA042990	sema domain; immunoglobulin domain (lg);	3.5
	131379	Hs.26176	R49035	ESTs	3.5
	126742	Hs.169359	H64106	yr57e06.r1 Soares fetal liver spleen 1NF	3.5
	105560	Hs.306915	AA262783	ESTs	3.5
	118472	Hs.42179	N66818	ESTs	3.5
65	105623	Hs.30127	AA280895	ESTs; Highly similar to !!!! ALU SUBFAM1	3.5
	120262	Hs.145807	AA172076	ESTs; Moderately similar to !!!! ALU SUB	3.5
	105027	Hs.26771	AA126472	ESTs	3.5
	130760	Hs.18953	AA128997	phosphodiesterase 9A	3.5
	117473	Hs.155560	N30157	ESTs	3.5

	102663	Hs.168075	U70322	karyopherin (importin) beta 2	3.5
	126349	Hs.13531	AA442668	ESTs; Weakly similar to (define not ava	3.5
	132154	Hs.41119	N67179	ESTs	3.5
5	131689	Hs.30696	AA599653	transcription factor-like 5 (basic helix	3.5
	127862	Hs.163191	AA765305	EST	3.5
	126995	Hs.189810	W26950	Human DNA sequence from PAC 388M5 on chr	3.5
	119071		R31180	ESTs	3.5
	103941	Hs.96593	AA282978	ESTs	3.5
10	110721	Hs.31319	H97678	ESTs	3.5
	126586	Hs.43086	AA011247	ESTs	3.5
	103106	Hs.1857	X62025	phosphodiesterase 6G; cGMP-specific; rod	3.5
	116357	Hs.90797	AA504806	Homo sapiens clone 23620 mRNA sequence	3.5
	105309	Hs.4104	AA233790	ESTs	3.5
	130796	Hs.19525	R39390	ESTs	3.5
15	109101	Hs.52184	AA167708	ESTs	3.5
	103134	Hs.2839	X65724	Norrie disease (pseudoglioma)	3.5
	131798	Hs.301449	X86098	adenovirus 5 E1A binding protein	3.5
	118535	Hs.49418	N67968	ESTs	3.5
	102592	Hs.11223	U62389	Human putative cytosolic NADP-dependent	3.4
20	125905	Hs.6456	T69868	chaperonin containing TCP1; subunit 2 (b	3.4
	109160	Hs.301997	AA179387	ESTs	3.4
	105327	Hs.211593	AA234440	ESTs	3.4
	106586	Hs.57787	AA456598	ESTs	3.4
	122635		AA454085	EST	3.4
25	132413	Hs.260116	AA132969	metalloprotease 1 (pitrilysin family)	3.4
	131938	Hs.34956	AA283620	ESTs	3.4
	133871	Hs.182793	AA454597	ESTs	3.4
	107175	Hs.292503	AA621751	ESTs; Weakly similar to KIAA0601 protein	3.4
	101188	Hs.184298	L20320	cyclin-dependent kinase 7 (homolog of Xe	3.4
30	126422	Hs.237658	H48518	ESTs; Highly similar to apolipoprotein A	3.4
	118475		N66845	ESTs; Weakly similar to !!!! ALU CLASS B	3.4
	104558	Hs.88959	R56678	ESTs; Weakly similar to !!!! ALU SUBFAM1	3.4
	128307	Hs.132005	AI453794	ESTs	3.4
	112254	Hs.25829	R51831	ESTs	3.4
35	125408	Hs.89578	N72353	yv37e12.r1 Soares fetal liver spleen 1NF	3.4
	109834	Hs.175955	H00604	ESTs	3.4
	130844	Hs.20191	D12122	seven in absentia (Drosophila) homolog 2	3.4
	127143	Hs.20843	AA533553	nj68h04.s1 NCI_CGAP_Pr10 Homo sapiens cD	3.4
	135309	Hs.42500	D25984	ESTs	3.4
40	125724	Hs.295978	AA083407	stimulated trans-acting factor (50 kDa)	3.4
	127692	Hs.187983	AI021912	ESTs	3.4
	116674	Hs.92127	F04816	ESTs	3.4
	134700	Hs.8868	AA481414	golgi SNAP receptor complex member 1	3.4
	114846	Hs.166186	AA234929	ESTs	3.4
45	103649	Hs.155983	Z70219	H.sapiens mRNA for 5'UTR for unknown pro	3.4
	134835	Hs.89925	L04569	calcium channel; voltage-dependent; L ty	3.4
	130568	Hs.16085	AA232535	ESTs; Highly similar to (define not ava	3.4
	111331	Hs.15978	N78773	ESTs	3.4
	106036	Hs.10653	AA412505	ESTs	3.4
50	130987	Hs.21893	R45698	ESTs	3.4
	112814	Hs.35828	R98192	ESTs	3.4
	127815	Hs.255015	AA876009	ob93c10.s1 NCI_CGAP_GCB1 Homo sapiens cD	3.4
	100144	Hs.75616	D13643	KIAA0018 gene product	3.4
	101129	Hs.247992	L10405	Homo sapiens DNA binding protein for sur	3.4
55	130874	Hs.20621	T08287	ESTs	3.4
	106882	Hs.26994	AA489009	ESTs	3.4
	103855	Hs.302267	AA195179	ESTs	3.4
	125957		H45213	yo03b08.r1 Soares adult brain N2b5HB55Y	3.3
	114048	Hs.146085	W94613	ESTs	3.3
60	109826	Hs.75354	F13702	ESTs	3.3
	125355	Hs.170098	R45630	ESTs; Highly similar to KIAA0372 [H.sapi	3.3
	104182	Hs.143792	AA479990	ESTs; Weakly similar to glioma amplified	3.3
	100294	Hs.75454	D49396	Human mRNA for Apo1_Human (MER5(Aop1-Mou	3.3
	131688	Hs.30692	U24153	p21 (CDKN1A)-activated kinase 2	3.3
65	116256	Hs.88201	AA481256	ESTs; Weakly similar to (define not ava	3.3
	102034	Hs.230	U05291	fibromodulin	3.3
	130072	Hs.14658	R99606	Human chromosome 5q13.1 clone 5G8 mRNA	3.3
	114615	Hs.159456	AA083812	ESTs; Highly similar to (define not ava	3.3
	128707	Hs.104105	AA136474	Meis (mouse) homolog 2	3.3

	115048	Hs.190057	AA252668	ESTs	3.3
	125862	Hs.31110	H12084	ESTs	3.3
	135142	Hs.24192	R31679	ESTs	3.3
5	103119	Hs.2877	X63629	cadherin 3; P-cadherin (placental)	3.3
	104460	Hs.62604	M91504	ESTs	3.3
	100365	Hs.79284	D78611	mesoderm specific transcript (mouse) hom	3.3
	131524	Hs.301804	N39152	ESTs	3.3
	102165	Hs.159627	U18321	Death associated protein 3	3.3
10	126966	Hs.182575	R38438	solute carrier family 15 (H+/peptide tra	3.3
	124839	Hs.140942	R55784	ESTs	3.3
	100709	Hs.100469	HG3264-HT3441	Af-6 (Gb:U02478)	3.3
	132967	Hs.61635	AA032221	Homo sapiens BAC clone RG041D11 from 7q2	3.3
	102927	Hs.65114	X12876	keratin 18	3.3
15	132616	Hs.283558	AA386264	ESTs	3.3
	125132	Hs.129781	W15495	ESTs	3.3
	111225	Hs.31652	N68989	ESTs	3.3
	114956	Hs.87113	AA243681	ESTs	3.3
	122235	Hs.112227	AA436475	ESTs	3.3
20	112325	Hs.12315	R56055	ESTs	3.3
	123360	Hs.178604	AA504784	ESTs	3.3
	105150	Hs.155895	AA169640	Homo sapiens mRNA for KIAA0643 protein;	3.3
	107391	Hs.284294	W02877	ESTs	3.3
	113058	Hs.7569	T26893	EST	3.3
25	134371	Hs.82318	S69790	Brush-1	3.3
	125669	Hs.333256	R51308	ESTs; Moderately similar to !!!! ALU SUB	3.3
	111506	Hs.294105	R07726	ESTs	3.3
	122974	Hs.194215	AA478625	ESTs	3.3
	102369	Hs.299867	U39840	hepatocyte nuclear factor 3; alpha	3.3
30	120408	Hs.190151	AA235045	ESTs	3.3
	117993	Hs.47402	N52039	ESTs; Weakly similar to !!!! ALU SUBFAM1	3.3
	129586	Hs.11500	AA437118	ESTs	3.3
	128138	Hs.126494	AI200825	ESTs	3.3
	127265		AA332751	EST37214 Embryo, 8 week I Homo sapiens c	3.3
35	107674	Hs.41143	AA011027	Homo sapiens mRNA for KIAA0581 protein;	3.2
	104866	Hs.293691	AA045342	ESTs	3.2
	103427	Hs.250655	X97303	H.sapiens mRNA for Ptg-12 protein	3.2
	132990	Hs.334334	AA458761	ESTs	3.2
	127017	Hs.251946	AA740146	ESTs	3.2
40	132313	Hs.44481	U13220	forkhead (Drosophila)-like 6	3.2
	106880	Hs.32425	AA488889	ESTs	3.2
	107039	Hs.169780	AA589751	homologous to yeast nitrogen permease (c	3.2
	120870	Hs.292581	AA357172	ESTs	3.2
	107920	Hs.284207	AA027951	ESTs	3.2
45	104165	Hs.105116	AA459160	EST	3.2
	107012	Hs.63908	AA598745	ESTs	3.2
	103605	Hs.194657	Z35402	H.sapiens gene encoding E-cadherin, exon	3.2
	124006	Hs.270016	D60302	ESTs	3.2
	101300	Hs.74137	L40391	Homo sapiens (clone s153) mRNA fragment	3.2
50	101183	Hs.795	L19779	H2A histone family; member O	3.2
	125596		R25698	yg44h11.12 Soares infant brain 1N1B Homo	3.2
	127261		AA661567	nu86b02.s1 NCI_CGAP_Alv1 Homo sapiens cD	3.2
	120090	Hs.59554	W94591	ESTs	3.2
	129393	Hs.166982	D13435	phosphatidylinositol glycan; class F	3.2
55	120923	Hs.97129	AA382283	ESTs	3.2
	118907	Hs.274256	N91003	ESTs	3.2
	111552	Hs.191185	R09411	ESTs	3.2
	104431	Hs.99913	J03019	adrenergic; beta-1-; receptor	3.2
	133551	Hs.278634	D63480	Human mRNA for KIAA0146 gene; partial cd	3.2
60	131615	Hs.192803	D14533	xeroderma pigmentosum; complementation g	3.2
	126547	Hs.84072	U47732	transmembrane 4 superfamily member 3	3.2
	103172	Hs.116774	X68742	integrin; alpha 1	3.2
	113867	Hs.24095	W68845	ESTs	3.2
	133323	Hs.70937	Z83735	H3 histone family; member K	3.2
	111597	Hs.189716	R11499	ESTs	3.2
65	121515	Hs.104696	AA412133	ESTs	3.2
	107445	Hs.6639	W28406	ESTs	3.2
	106887	Hs.334335	AA489091	ESTs	3.2
	123052	Hs.185766	AA481806	ESTs	3.2
	107072	Hs.130760	AA609113	Homo sapiens mRNA; cDNA DKFZp586N0318 (f	3.2

	102214	Hs.32964	U23752	SRY (sex-determining region Y)-box 11	3.2
	123147		AA487961	ab11h6.s1 Stratagene lung (#93721) Homo	3.2
	125435	Hs.272138	R00940	ye87g03.r1 Soares fetal liver spleen 1NF	3.2
5	116246	Hs.250646	AA479961	ESTs; Highly similar to ubiquitin-conjug	3.2
	105169	Hs.180789	AA180321	Homo sapiens (clone S164) mRNA; 3' end o	3.2
	134001	Hs.78344	AF001548	myosin; heavy polypeptide 11; smooth mus	3.2
	124866	Hs.304389	R68571	ESTs	3.2
	133205	Hs.67619	AA089559	Homo sapiens mRNA; chromosome 1 specific	3.2
10	102986	Hs.182378	X17648	colony stimulating factor 1 (macrophage)	3.2
	101232	Hs.242894	L28997	ADP-ribosylation factor-like 1	3.1
	132906	Hs.234896	AA142857	ESTs; Highly similar to geminin [H.sapie	3.1
	104281	Hs.5669	C14290	ESTs	3.1
	123926	Hs.227933	AA621348	ESTs; Highly similar to (define not ava	3.1
	134464	Hs.239720	N79354	ESTs; Weakly similar to Rga [D.melanogas	3.1
15	105322	Hs.16346	AA234100	ESTs	3.1
	100631	Hs.48332	HG2709-HT2805	Serine/Threonine Kinase (Gb:Z25431)	3.1
	130791	Hs.199263	AA259102	ESTs; Highly similar to (define not ava	3.1
	131220	Hs.300855	R77200	ESTs	3.1
20	113237	Hs.123642	T62857	ESTs	3.1
	125562	Hs.98968	AI494372	ESTs	3.1
	134110	Hs.79138	U41060	Human breast cancer; estrogen regulated	3.1
	132393	Hs.47334	W85888	ESTs; Moderately similar to !!! ALU SUB	3.1
	107439	Hs.296842	W27995	ESTs; Moderately similar to non-muscle m	3.1
25	125863	Hs.40719	AA299096	Homo sapiens mRNA; cDNA DKFZp564M0916 (f	3.1
	105811	Hs.286192	AA394121	ESTs	3.1
	129284	Hs.296141	AA104023	ESTs	3.1
	125321	Hs.178294	T86652	ESTs	3.1
	107332	Hs.183297	T87750	ESTs	3.1
30	123570	Hs.109653	AA608955	ESTs	3.1
	100384	Hs.90800	D83646	matrix metalloproteinase 16 (membrane-in	3.1
	109063	Hs.38972	AA161043	tetraspan 1	3.1
	133284	Hs.182828	U09367	zinc finger protein 136 (clone pHZ-20)	3.1
	131839	Hs.33010	H80622	Homo sapiens mRNA for KIAA0633 protein;	3.1
35	117606	Hs.44698	N35115	ESTs	3.1
	418998	Hs.287849	F13215	ESTs	3.1
	125180	Hs.103120	W58344	ESTs	3.1
	100789		HG3893-HT4163	Phosphoglucosylase 1, Alt. Splice	3.1
	126017	Hs.159440	H60487	ESTs	3.1
40	132452	Hs.247324	AA005262	Homo sapiens DNA sequence from PAC 262D1	3.1
	129077	Hs.108479	H78886	ESTs	3.1
	126563	Hs.181368	W26247	U5 snRNP-specific protein (220 kD); orth	3.1
	129650	Hs.118258	N52554	ESTs	3.1
	123465		AA599033	ESTs	3.1
45	126486	Hs.152316	AA345339	EST51345 Gall bladder II Homo sapiens cD	3.1
	126460	Hs.167031	W01616	za36d05.r1 Soares fetal liver spleen 1NF	3.1
	118697	Hs.43234	N72094	ESTs	3.1
	103860	Hs.38057	AA203742	ESTs	3.1
	127968	Hs.124347	AA971439	ESTs	3.1
50	124984	Hs.223241	T47566	yb15c11.s1 Stratagene placenta (#937225)	3.1
	103903	Hs.15220	AA249334	j312.seq.F Human fetal heart, Lambda ZAP	3.1
	106697	Hs.22242	AA463737	ESTs	3.1
	130892	Hs.20993	AA442604	ESTs; Weakly similar to Ydr374cp [S.cere	3
	114032	Hs.35014	W92779	ESTs	3
55	128835	Hs.106390	W15528	ESTs	3
	103667	Hs.247815	Z80788	H.sapiens H4I gene	3
	126264	Hs.250614	N42897	yy13h06.r1 Soares melanocyte 2NbHM Homo	3
	132628	Hs.21275	D25755	ESTs	3
	131107	Hs.75354	N87590	ESTs	3
	126780	Hs.5811	R12421	ESTs	3
60	127363	Hs.22116	AA307744	Homo sapiens Cdc14B1 phosphatase mRNA; c	3
	103690	Hs.84063	AA016186	ESTs	3
	102589	Hs.8867	U82015	Homo sapiens Cyp61 mRNA, complete cds	3
	125144	Hs.24336	W37999	ESTs	3
65	132977	Hs.301404	U28686	RNA binding motif protein 3	3
	120714	Hs.146170	AA292689	ESTs	3
	101038	Hs.79411	J05249	replication protein A2 (32kD)	3
	102856	Hs.248177	X00090	Human histone H3 gene	3
	105516	Hs.30738	AA257971	ESTs	3
	131137	Hs.33287	U85193	nuclear factor I/B	3

	127221	Hs.241551	AI354332	ESTs	3
	411888	Hs.24104	R26708	ESTs	3
	131684	Hs.3066	U26174	granzyme K (serine protease; granzyme 3;	3
	100629	Hs.21291	HG2706-HT2802	Serine/Threonine Kinase (Gb:Z25428)	3
5	119944	Hs.58915	W86838	EST	3
	113801	Hs.118281	W38418	zinc finger protein 266	3
	133780	Hs.76152	M14219	decorin	3
	104690	Hs.14449	AA010889	ESTs	3
	126371	Hs.304139	N57645	EST	3
10	127635	Hs.116346	AA766903	ESTs	3
	128434	Hs.143880	AI190914	ESTs	3
	435761	Hs.187555	AA701941	ESTs	3
	125025	Hs.50748	T71561	ESTs	3
	124940	Hs.103804	R99599	heterogeneous nuclear ribonucleoprotein	3
15	128742	Hs.251531	D00763	proteasome (prosome; macropain) subunit;	3
	107147	Hs.10450	AA621125	Homo sapiens chromosome 2; 10 repeat reg	3
	112068	Hs.22545	R43910	ESTs	3
	105346	Hs.263727	AA235465	ESTs; Moderately similar to !!!! ALU SUB	3
	130972	Hs.21739	AA370302	Homo sapiens mRNA; cDNA DKFZp58611518 (f	3
20	131230	Hs.274407	AA149987	thymus specific serine peptidase	3
	133743	Hs.75847	N79435	ESTs	3
	127402	Hs.227949	AA358869	ESTs; Highly similar to SEC13-RELATED PR	3
	117483	Hs.44189	N30426	ESTs	3
	123659	Hs.112699	AA609368	ESTs	3
25	103963	Hs.63290	AA298588	EST114219 HSC172 cells II Homo sapiens c	3
	103795	Hs.7367	AA112222	ESTs; Moderately similar to (define not	3
	115092	Hs.80975	AA255903	CD39-like 4	2.9
	134831	Hs.89890	S72370	pyruvate carboxylase	2.9
	128579	Hs.101810	AA093378	ESTs; Weakly similar to !!!! ALU SUBFAM1	2.9
30	134193	Hs.7980	F09570	ESTs	2.9
	123522	Hs.112575	AA608577	ESTs	2.9
	107109	Hs.32793	AA609943	ESTs	2.9
	134694	Hs.88556	D50405	histone deacetylase 1	2.9
	134399	Hs.82689	H99801	tumor rejection antigen (gp96) 1	2.9
35	134632	Hs.174139	AA398710	H. sapiens RNA for CLCN3	2.9
	106683	Hs.14512	AA461495	ESTs	2.9
	108555		AA084963	zn13e12.s1 Stratagene hNT neuron (#93723	2.9
	100953	Hs.2110	HG945-HT945	Nucleic Acid-Binding Protein (Gb:L12693)	2.9
	130597	Hs.16492	AA173998	ESTs; Weakly similar to weakly similar t	2.9
40	101813	Hs.139226	M87338	replication factor C (activator 1) 2 (40	2.9
	106638	Hs.286	AA459950	ESTs	2.9
	129109	Hs.108708	AA491295	calcium/calmodulin-dependent protein kin	2.9
	125819	Hs.251871	AA044840	stromal cell-derived factor 1	2.9
	106282	Hs.9857	AA433946	ESTs; Weakly similar to (define not ava	2.9
45	100386	Hs.301636	D83703	peroxisomal biogenesis factor 6	2.9
	114546	Hs.98074	AA056263	ESTs; Moderately similar to !!!! ALU SUB	2.9
	105914	Hs.9701	AA402224	Homo sapiens growth arrest and DNA-damag	2.9
	108552		AA084912	zn11c7.s1 Stratagene hNT neuron (#937233	2.9
	126505	Hs.190057	W26894	16a11 Human retina cDNA randomly primed	2.9
50	134098	Hs.79086	X06323	Human MRL3 mRNA for ribosomal protein L3	2.9
	129721	Hs.211539	L19161	eukaryotic translation initiation factor	2.9
	100076	Hs.277422	AB000897	Homo sapiens mRNA for cadherin FIB3, par	2.9
	117466	Hs.44104	N29862	ESTs	2.9
	106335	Hs.36688	AA437258	ESTs; Moderately similar to WAP four-dis	2.9
55	134510	Hs.250870	U25265	protein kinase; mitogen-activated; knas	2.9
	105835	Hs.32995	AA398412	ESTs	2.9
	106611	Hs.26267	AA458904	ESTs; Weakly similar to torsinA [H.sapie	2.9
	134087	Hs.173824	U51166	thymine-DNA glycosylase	2.9
	100641	Hs.182183	HG2743-HT2846	Caldesmon 1, Alt. Splice 4, Non-Muscle	2.9
60	104602		R86920	ESTs	2.9
	117203	Hs.42738	H99799	ESTs	2.9
	131889	Hs.34073	AA401912	BH-protocadherin (brain-heart)	2.9
	101707	Hs.155212	M65131	methylmalonyl Coenzyme A mutase	2.9
	115271	Hs.5724	AA279422	ESTs	2.9
65	125812	Hs.287912	H73420	lactin; mannose-binding; 1	2.9
	110740	Hs.19762	H99675	ESTs	2.9
	103406	Hs.285728	X95677	H.sapiens mRNA for ArgBP1B protein	2.9
	104577	Hs.132390	R71539	ESTs	2.9
	102772	Hs.161002	U83115	absent in melanoma 1	2.9

	131710	Hs.30985	AA233225	ESTs; Highly similar to (define not ava	2.9
	125231	Hs.268903	W84714	ESTs	2.9
	127380	Hs.15535	AI417137	Homo sapiens clone 24582 mRNA sequence	2.9
5	104229	Hs.61289	AB002346	inositol phosphate 5'-phosphatase 2 (syn	2.9
	126600	Hs.191385	AA699949	ESTs	2.9
	125175	Hs.303030	W52355	EST	2.9
	103849	Hs.34578	AA187045	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.9
	102126	Hs.78961	U14575	protein phosphatase 1; regulatory (inhib	2.9
10	124906	Hs.107815	R87647	ESTs	2.9
	131148	Hs.303125	C00038	ESTs	2.9
	123158	Hs.218329	AA488658	heat shock 70kD protein 1	2.9
	133667	Hs.75462	U72649	Human BTG2 (BTG2) mRNA; complete cds	2.9
	105182	Hs.18271	AA191014	ESTs; Weakly similar to Ydr372cp [S.cere	2.9
15	133968	Hs.232068	D15050	Human mRNA for transcription factor AREB	2.9
	117425	Hs.336901	N27154	ESTs	2.9
	111087	Hs.37637	N59645	ESTs	2.9
	129641	Hs.11805	N66066	ESTs	2.9
	128639	Hs.102897	N91246	ESTs	2.9
20	133209	Hs.79265	AA114183	ESTs; Moderately similar to glutamate py	2.9
	135154	Hs.267812	AA126433	sorting nexin 4	2.9
	126838	Hs.279609	AA858097	pigment epithelium-derived factor	2.9
	103803	Hs.106149	AA127696	ESTs	2.9
	102139	Hs.2128	U15932	dual specificity phosphatase 5	2.9
25	128104		AA971000	op67g11.s1 Soares_NFL_T_GBC_S1 Homo sapi	2.8
	127834	Hs.337631	AA761415	nz22d08.s1 NCI_CGAP_GCB1 Homo sapiens cD	2.8
	133101	Hs.180952	AA488230	ESTs	2.8
	127250	Hs.217916	AI023717	ESTs	2.8
	135063	Hs.93883	D10537	myelin protein zero (Charcot-Marie-Tooth	2.8
30	126323	Hs.68644	N45014	yy80g06.r1 Soares_multiple_sclerosis_2Nb	2.8
	121873	Hs.145696	AA426270	ESTs	2.8
	122090	Hs.98684	AA432141	ESTs	2.8
	118728	Hs.322645	N73705	ESTs	2.8
	135400	Hs.99915	M23263	androgen receptor (dihydrotestosterone r	2.8
35	125278	Hs.129998	W93523	ESTs	2.8
	124387	Hs.109019	N27637	ESTs	2.8
	124803	Hs.12186	R45480	cyclin K	2.8
	H45968	Hs.32149	H45968	ESTs	2.8
	104261	Hs.5409	AF008442	RNA polymerase I subunit	2.8
40	105366	Hs.282093	AA236356	ESTs	2.8
	106070	Hs.5957	AA417761	Homo sapiens clone 24416 mRNA sequence	2.8
	131356	Hs.25960	M13241	v-myc avian myelocytomatosis viral relat	2.8
	112009	Hs.26255	R42714	EST	2.8
	133199	Hs.250175	AA609773	Homo sapiens clone 23904 mRNA sequence	2.8
45	110379	Hs.33130	H44825	ESTs	2.8
	103890	Hs.72085	AA236843	ESTs; Weakly similar to unknown [S.cerev	2.8
	128152		R20353	yg20f10.r1 Soares infant brain 1NIB Homo	2.8
	107008	Hs.23740	AA598710	ESTs	2.8
	135243	Hs.97101	AA215333	ESTs	2.8
	103058	Hs.184510	X57348	stratiffin	2.8
50	132020	Hs.293845	AA428990	ESTs	2.8
	116354	Hs.292566	AA504262	ESTs	2.8
	125867	Hs.12372	H98141	ESTs	2.8
	120603	Hs.98541	AA282787	ESTs; Highly similar to (define not ava	2.8
55	115119	Hs.46847	AA256524	Human DNA sequence from clone 30M3 on ch	2.8
	133865	Hs.170290	F09315	discs; large (Drosophila) homolog 5	2.8
	109415	Hs.110826	AA227219	Homo sapiens CAGF9 mRNA; partial cds	2.8
	128687	Hs.23767	Z38910	ESTs	2.8
	109984	Hs.10299	H09594	ESTs; Moderately similar to !!!! ALU SUB	2.8
60	133179	Hs.66731	U81599	homeo box B13	2.8
	115998	Hs.336629	AA448488	ESTs; Weakly similar to zinc finger prot	2.8
	112180	Hs.25067	R49116	EST	2.8
	120428	Hs.173694	AA236822	ESTs; Moderately similar to (define not	2.8
	106241	Hs.6019	AA430108	ESTs	2.8
65	131060	Hs.22564	AA160890	myosin VI	2.8
	111383	Hs.40919	N94527	ESTs	2.8
	102123	Hs.1594	U14518	centromere protein A (17kD)	2.8
	102722	Hs.79981	U79242	Human clone 23560 mRNA sequence	2.8
	129887	Hs.274324	W92041	PCAF associated factor 65 alpha	2.8
	126663	Hs.181297	AA714635	ESTs	2.8

	104367	Hs.134342	H17438	ESTs; Weakly similar to seventransmembra	2.8
	107316	Hs.193700	T63174	ESTs; Moderately similar to !!!!! ALU SUB	2.8
	128059	Hs.145096	AA972446	ESTs	2.8
	124447		N48000	ESTs	2.8
5	111398	Hs.125565	R00086	deafness; X-linked 1; progressive	2.8
	134085	Hs.79018	U20979	chromatin assembly factor I (150 kDa)	2.8
	124788	Hs.100912	R43543	ESTs	2.8
	112248	Hs.326416	R51361	ESTs	2.8
	121309	Hs.97312	AA402482	ESTs	2.8
10	103076	Hs.75319	X59618	ribonucleotide reductase M2 polypeptide	2.8
	107071	Hs.35198	AA609053	ESTs	2.8
	104425	Hs.35380	H88496	ESTs	2.8
	132991	Hs.62245	AA446906	solute carrier family 25 (mitochondrial	2.8
	104968	Hs.29669	AA084602	ESTs	2.8
15	121153	Hs.97694	AA399640	ESTs	2.8
	131216	Hs.243901	D31058	ESTs	2.8
	109682	Hs.22869	F09299	ESTs	2.8
	131990	Hs.168818	H77734	ESTs; Moderately similar to roundabout 1	2.8
	132027	Hs.181444	N78844	ESTs; Weakly similar to R12C12.6 [C.eleg	2.8
20	127383	Hs.190478	AA447990	ESTs	2.8
	132598	Hs.530	M81379	collagen; type IV; alpha 3 (Goodpasture	2.8
	101121	Hs.1313	L09753	tumor necrosis factor (ligand) superfam	2.8
	123000	Hs.105640	AA479347	ESTs	2.8
	121329	Hs.1755	AA404324	ESTs	2.8
25	100481	Hs.121489	HG1098-HT1098	Cystatin D	2.7
	113803	Hs.283683	W42789	ESTs	2.7
	110934	Hs.169001	N48708	ESTs; Weakly similar to cytochrome P-450	2.7
	432888		T86823	ESTs	2.7
	121802	Hs.188898	AA424328	ESTs	2.7
30	130396	Hs.155313	AB002331	Human mRNA for KIAA0333 gene; partial cd	2.7
	121103	Hs.97697	AA398936	ESTs; Weakly similar to (define not ava	2.7
	131129	Hs.23240	R27296	ESTs	2.7
	130943	Hs.272429	D50855	calcium-sensing receptor (hypocalciuric	2.7
	134676	Hs.87819	W28051	ESTs; Weakly similar to keratin 9; cytos	2.7
35	111900	Hs.25318	R39044	ESTs	2.7
	106025	Hs.173334	AA412063	ESTs	2.7
	126144	Hs.40639	N39696	yx92a07.r1 Soares melanocyte 2NbHM Homo	2.7
	103248	Hs.75262	X77383	cathepsin O	2.7
	127230	Hs.274170	H30501	Homo sapiens Opa-interacting protein OIP	2.7
40	101584	Hs.84072	M35252	transmembrane 4 superfamily member 3	2.7
	124131	Hs.167489	H19980	ESTs	2.7
	129689	Hs.77873	AA130156	ESTs	2.7
	132892	Hs.9973	W92797	ESTs	2.7
	120827	Hs.132967	AA347717	ESTs	2.7
45	134579	Hs.85963	N23222	ESTs; Moderately similar to !!!!! ALU SUB	2.7
	106149	Hs.256301	AA424881	ESTs	2.7
	132037	Hs.332541	AA203649	ESTs; Weakly similar to HEM45 [H.sapiens	2.7
	130542	Hs.179825	U64675	Human sperm membrane protein BS-63 mRNA,	2.7
	122851	Hs.99598	AA463627	ESTs	2.7
50	134983	Hs.196384	D28235	prostaglandin-endoperoxide synthase 2 (p	2.7
	120537	Hs.160422	AA262790	ESTs	2.7
	131036	Hs.174140	X64330	ATP citrate lyase	2.7
	133889	Hs.211582	AA099391	ESTs	2.7
55	128847	Hs.106529	AA424199	zv81e01.r1 Soares_total_fetus_Nb2HF8_9w	2.7
	112755	Hs.306044	R93802	ESTs	2.7
	423239		AA323591	EST26392 Cerebellum II Homo sapiens cDNA	2.7
	105031	Hs.12321	AA127240	ESTs	2.7
	126021	Hs.187516	AA775894	ESTs	2.7
	102116		U13706	Human ELAV-like neuronal protein 1 isofo	2.7
60	133394	Hs.237225	R16759	ESTs; Weakly similar to (define not ava	2.7
	104267	Hs.278439	C00358	ESTs	2.7
	107614	Hs.40241	AA004878	ESTs; Highly similar to (define not ava	2.7
	129809	Hs.1259	X55283	asialoglycoprotein receptor 2	2.7
	112109	Hs.283309	R45221	ESTs; Weakly similar to !!!!! ALU SUBFAM	2.7
65	128422		T85681	yd60c06.r1 Soares fetal liver spleen 1NF	2.7
	109494	Hs.43899	AA233702	ESTs	2.7
	118696	Hs.292284	N72086	Homo sapiens RNA polymerase III largest	2.7
	106053	Hs.36727	AA416963	ESTs; Highly similar to histone H2A [H.s	2.7
	104440	Hs.284380	L20492	gamma-glutamyltransferase 1	2.7

	129426	Hs.111323	AA412087	EST; Highly similar to (define not avai	2.7
	123798		AA620411	small inducible cytokine A5 (RANTES)	2.7
	106716	Hs.238928	AA464962	ESTs	2.7
5	103663		Z78291	Z78291 Homo sapiens brain fetus Homo sap	2.7
	114162	Hs.22265	Z38909	ESTs	2.7
	113063	Hs.5027	T32438	ESTs	2.7
	127897		AA773857	af80c09.r1 Soares_NhHMPu_S1 Homo sapiens	2.7
	130621	Hs.16803	AA621718	ESTs; Weakly similar to (define not ava	2.7
10	116245	Hs.42796	AA479958	ESTs; Highly similar to (define not ava	2.7
	125499		R11878	yf49d11.r1 Soares infant brain 1NIB Homo	2.7
	133960	Hs.77899	M19267	tropomyosin 1 (alpha)	2.7
	104470	Hs.246358	N28843	ESTs; Weakly similar to Similar to colla	2.7
	134982	Hs.92308	N46086	ESTs	2.7
15	106803	Hs.284295	AA479114	ESTs	2.7
	104899	Hs.285574	AA054726	ESTs	2.7
	125401	Hs.337585	A1204637	ESTs; Moderately similar to KIAA0350 [H.	2.7
	111253	Hs.15768	N70042	ESTs; Moderately similar to !!!! ALU SUB	2.7
	118449	Hs.164478	N66413	ESTs; Weakly similar to (define not ava	2.7
20	134507	Hs.84318	M63488	replication protein A1 (70kD)	2.7
	121609	Hs.98185	AA416867	EST	2.7
	113835	Hs.27475	W56590	ESTs	2.7
	113962	Hs.285290	W86375	ESTs; Highly similar to (define not ava	2.7
	121913	Hs.98558	AA428062	ESTs	2.7
25	108194	Hs.216717	AA057250	ESTs	2.7
	130799	Hs.12696	AA464273	ESTs	2.7
	123184	Hs.18166	AA489072	Homo sapiens mRNA for KIAA0870 protein;	2.7
	103420	Hs.173497	X97065	SEC23-like protein B	2.7
	106186	Hs.6315	AA427398	acetylserotonin N-methyltransferase-like	2.7
30	101349		L77559	Homo sapiens DGS-B partial mRNA	2.7
	112954	Hs.6655	T16559	ESTs	2.7
	133054	Hs.291079	R07876	ESTs; Weakly similar to unknown [S.cerev	2.7
	128131	Hs.25640	A1283162	claudin 3	2.6
	101864	Hs.75777	M95787	transgelin	2.6
35	111948	Hs.26303	R40752	ESTs	2.6
	130145	Hs.151051	U07620	protein kinase mitogen-activated 10 (MAP	2.6
	126507	Hs.23964	A1362218	ESTs	2.6
	117903	Hs.47111	N50740	ESTs	2.6
	116345	Hs.199067	AA495981	ESTs	2.6
40	132227	Hs.4248	AA412620	ESTs	2.6
	125746	Hs.274256	H03574	yj42b06.r1 Soares placenta Nb2HP Homo sa	2.6
	105073	Hs.89463	AA137034	ESTs	2.6
	102764		U82310	Homo sapiens unknown protein mRNA, parti	2.6
	131367	Hs.173933	AA456687	ESTs	2.6
45	130792	Hs.19500	AA307896	nuclear localization signal deleted in v	2.6
	107427	Hs.46736	W26975	ESTs	2.6
	117477	Hs.44175	N30328	ESTs	2.6
	106290	Hs.16364	AA435542	ESTs	2.6
	126829	Hs.7910	R11547	ESTs	2.6
50	118836	Hs.173001	N79820	ESTs	2.6
	100147	Hs.136348	D13666	osteoblast specific factor 2 (fascidin	2.6
	104278	Hs.109253	C02582	ESTs; Highly similar to (define not ava	2.6
	135051	Hs.83484	C15324	ESTs	2.6
	126081	Hs.227835	A1346024	collagen; type I; alpha 1	2.6
55	123579		AA608983	af5d4.s1 Soares_testis_NHT Homo sapiens	2.6
	130115	Hs.149923	M31627	X-box binding protein 1	2.6
	101434	Hs.1430	M20218	coagulation factor XI (plasma thrombopla	2.6
	122962	Hs.104720	AA478429	ESTs; Moderately similar to !!!! ALU SUB	2.6
	126151	Hs.40808	AA324743	ESTs	2.6
60	128925	Hs.21851	D61676	Homo sapiens mRNA; cDNA DKFZp586J2118 (I	2.6
	128919	Hs.103391	L27559	insulin-like growth factor binding prote	2.6
	130296	Hs.154103	R09286	LIM protein (similar to rat protein kina	2.6
	128402	Hs.191637	AA457244	ESTs	2.6
	129273	Hs.109968	W63783	ESTs	2.6
65	125483	Hs.7788	F07759	ESTs	2.6
	132953	Hs.321264	AA029927	ESTs	2.6
	130963	Hs.21639	U57099	nuclear protein; marker for differentiat	2.6
	120614	Hs.194154	AA284281	ESTs; Weakly similar to !!!! ALU SUBFAM1	2.6
	123251	Hs.103267	AA490858	ESTs; Moderately similar to Rabin3 [R.no	2.6
	121710	Hs.96744	AA419011	ESTs	2.6

	125428	Hs.851	W74608	ESTs; Highly similar to (define not ava	2.6
	115906	Hs.82302	AA436616	ESTs	2.6
	108432		AA076626	Homo sapiens clone 23851 mRNA sequence	2.6
5	126191	Hs.191911	H97728	ESTs	2.6
	106164	Hs.281434	AA425773	ESTs	2.6
	111519	Hs.268615	R08165	ESTs	2.6
	134590	Hs.173840	W58612	ESTs	2.6
	102565		U59748	Human desert hedgehog (hDHH) mRNA, parti	2.6
10	129879	Hs.13109	AA194973	ESTs	2.6
	114264	Hs.334609	Z40074	ESTs	2.6
	106236	Hs.21104	AA429951	ESTs	2.6
	135192	Hs.321709	AF000234	purinergic receptor P2X; ligand-gated io	2.6
	109833	Hs.29889	H00580	ESTs	2.6
	105756	Hs.8535	AA303088	ESTs; Weakly similar to transformation-r	2.6
15	121422	Hs.97967	AA406210	ESTs	2.6
	130417	Hs.155485	U58522	Human huntingtin interacting protein (Hl	2.6
	124312	Hs.102329	H94647	ESTs	2.6
	108998	Hs.97199	AA156058	ESTs	2.6
20	127081	Hs.180591	R88362	ESTs; Weakly similar to weak similarity	2.6
	129574	Hs.11463	AA458603	ESTs; Weakly similar to (define not ava	2.6
	112410	Hs.26904	R61680	ESTs	2.6
	123929	Hs.112981	AA621364	ESTs	2.6
	122905	Hs.104835	AA470070	ESTs	2.6
25	116399	Hs.110637	AA599729	Homo sapiens homeobox protein A10 (HOXA1	2.6
	130279	Hs.153934	AA424044	core-binding factor; runt domain; alpha	2.6
	130021	Hs.1435	M24470	guanosine monophosphate reductase	2.6
	100585	Hs.199160	HG2367-HT2463	Trithorax Homolog Hrx	2.6
	104965	Hs.30177	AA084104	ESTs	2.6
30	117711	Hs.46485	N45201	EST	2.6
	124792	Hs.48712	R44357	ESTs	2.6
	111299	Hs.74313	N73808	ESTs	2.6
	103616	Hs.32971	Z46973	phosphoinositide-3-kinase; class 3	2.6
	133629	Hs.195614	D13642	KIAA0017 gene product	2.6
35	126484	Hs.169977	A1086782	ESTs	2.6
	100858		HG4245-HT4515	Forkhead Family Abx1	2.6
	133547	Hs.301927	X02883	T-cell receptor, alpha (V;D;J;C)	2.6
	126680	Hs.133865	F07097	ESTs	2.6
	125739	Hs.92137	AA428557	v-myc avian myelocytomatosis viral oncog	2.6
40	102276	Hs.10247	U30999	Human (memc) mRNA, 3'UTR	2.6
	105586	Hs.191538	AA279137	ESTs	2.6
	103978	Hs.34136	AA307443	ESTs	2.6
	125064	Hs.268601	T80622	ESTs; Weakly similar to (define not ava	2.6
	114212	Hs.21201	Z39338	ESTs; Highly similar to (define not ava	2.6
	116959	Hs.40022	H79310	EST	2.6
45	109228	Hs.306995	AA193366	ESTs	2.6
	133989	Hs.78202	U29175	SWI/SNF related; matrix associated; acti	2.6
	100640	Hs.182183	HG2743-HT2845	Caldesmon 1, Alt. Splice 3, Non-Muscle	2.6
	133093	Hs.285996	AA598749	ESTs	2.6
	114306	Hs.6540	Z40861	ESTs	2.6
50	106060	Hs.171391	AA417287	C-terminal binding protein 2	2.5
	107748	Hs.60772	AA017258	EST	2.5
	100134	Hs.49	D13264	macrophage scavenger receptor 1	2.5
	133969	Hs.78	U13044	GA-binding protein transcription factor;	2.5
55	130992	Hs.74316	AA455001	ESTs	2.5
	127493	Hs.291701	AA080801	oc39a08.s1 NCI_CGAP_GCB1 Homo sapiens cD	2.5
	132869	Hs.203961	N26855	ESTs	2.5
	117570	Hs.44583	N34415	EST	2.5
	124644	Hs.109654	N91279	ESTs	2.5
	103558	Hs.2785	Z19574	keratin 17	2.5
60	132883	Hs.5897	AA047151	ESTs	2.5
	102009	Hs.82643	U02680	protein tyrosine kinase 9	2.5
	116058	Hs.20159	AA454156	ESTs	2.5
	121989	Hs.193784	AA430044	ESTs	2.5
	131257	Hs.24908	AA256042	ESTs	2.5
65	100320	Hs.75275	D50916	homolog of yeast (S. cerevisiae) ufd2	2.5
	102959	Hs.121524	X15722	glutathione reductase	2.5
	132969	Hs.6166	AA047616	ESTs	2.5
	130869	Hs.2057	AA128100	uridine monophosphate synthetase (orotat	2.5
	129645	Hs.118131	L38928	5,10-methenyltetrahydrofolate synthetase	2.5

	126399	Hs.83883	AA128075	zl16d08.r1 Soares_pregnant_uterus_NbHPU	2.5
	134069	Hs.78935	U29607	Homo sapiens eIF-2-associated p67 homolo	2.5
	109816	Hs.61960	F11013	ESTs; Weakly similar to KIAA0176 (H.sapi	2.5
5	134801	Hs.89695	X02160	insulin receptor	2.5
	104232	Hs.10587	AB002351	Human mRNA for KIAA0353 gene; partial cd	2.5
	107361	Hs.159486	U72513	Human RPL13-2 pseudogene mRNA; complete	2.5
	106057	Hs.289074	AA417067	ESTs	2.5
	134252	Hs.80720	AA031782	Homo sapiens mRNA; cDNA DKFZp586B1722 (I	2.5
10	128062	Hs.105547	AA379500	ESTs	2.5
	110009	Hs.6614	H10933	ESTs	2.5
	111375	Hs.20432	N93696	ESTs	2.5
	122642	Hs.99361	AA454186	ESTs	2.5
	127999	Hs.69851	AA837495	ESTs; Weakly similar to Wiskott-Aldrich	2.5
15	105029	Hs.13268	AA126855	ESTs	2.5
	105082	Hs.26765	AA143763	ESTs; Weakly similar to Similarity to S.	2.5

TABLE 1A show the accession numbers for those primekeys lacking unigeneID's for Table 1. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey:		Unique Eos probeset identifier number
CAT number:		Gene cluster number
Accession:		Genbank accession numbers
Pkey	CAT number	Accessions
108552	111555_1	AA071210 AA069899 AA071438 AA084912 AA084803 AA079371 AA079370
126023	1596090_1	H57661 H58881
126086	1606216_1	H75681 H70975
102565	32479_1	AB010994 U59748 AA064660
101964	48158_-7	S81578
125499	1562851_1	H10543 R11878
125596	1708455_1	R25698 R56582 R56018
118417	37186_1	AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547 AI680833 AI633818 N29986 U87592 U87593 U87590 U87591 S46404 U87587 AA463992 AW206802 AI970376 AI583718 AI672574 N25695 AW665466 AI818326 AA126128 AI480345 AW013827 AA248638 AI214968 AA204735 AA207155 AA206262 AA204833 AW003247 AW496808 AI080480 AI631703 AI651023 AI867418 AW818140 AA502500 AI206199 AI671282 AI352545 BE501030 AI652535 BE465762 AA206331 AW451866 AA471088 AA206342 AA204834 AA206100 AW021661 AA332922 N66048 AA703396 H92278 AW139734 H92683 U87589 U87595 H69001 U87594 BE466420 AI624817 BE466611 AI206344 AA574397 AA348354 AI493192
125661	327827_1	AA491830 R50173 R55192 R50320 AI732306 AI732305 AI820727 AI820728 R55191 R50319 R50227
125957	1583542_1	H41694 H45213
125982	1766315_1	R98091 W92898
127248	227560_1	AA364195 AA325029 AW962050
103731	112052_1	AA070545 AA131490 AA131373
127261	231687_1	AA330501 AA661567
127265	232391_1	AA331503 AA332751 AW962542
126659	1541209_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
127315	37838_1	AF116622 AI114507 AA640834 AA377999
103806	112618_1	AA130614 AA071410
128104	502608_1	AA906093 AA971000
104602	524482_2	H47610 R86920
128152	297868_1	F07973 R20353 AA442660
128422	1811283_1	T77794 T85681
127897	446527_1	AA773681 AA773857
106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI033658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
129735	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AI134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
123147	219802_-2	AA487961
130529	158447_1	AA178953 AA192740
123579	genbank_AA608983	AA608983
109175	genbank_AA180496	AA180496
100789	tigr_HT4163	S67698
100858	tigr_HT4515	U10072

	123798	579959_1	AA620411	AA287491
	102116	entrez_U13706	U13706	
	102398	entrez_U42359	U42359	
	102764	entrez_U82310	U82310	
5	118475	genbank_N66845	N66845	
	104776	genbank_AA026349	AA026349	
	104787	genbank_AA027317	AA027317	
	113702	genbank_T97307	T97307	
	113938	genbank_W81598	W81598	
10	122635	genbank_AA454085	AA454085	
	108407	genbank_AA075519	AA075519	
	108432	genbank_AA076626	AA076626	
	108555	genbank_AA084963	AA084963	
	101349	entrez_L77559	L77559	
15	124447	genbank_N48000	N48000	
	119071	genbank_R31180	R31180	
	103520	entrez_Y10511	Y10511	
	103663	genbank_Z78291	Z78291	
	128046	877605_1	AA873285	AI025762
20	126959	546044_1	AA199853	AA206355
	123465	genbank_AA599033	AA599033	

MISSING AT THE TIME OF PUBLICATION

TABLE 2: shows a preferred subset of the Accession numbers for genes found in Table 1 which are differentially expressed in prostate tumor tissue compared to normal prostate tissue.

5

10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue (Relaxed ratio (87/70))

15	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	131919	AA121266	Hs.272458	ESTs	37.2
	120328	AA196979	Hs.290905	ESTs; Weakly similar to (define not ava	32.6
	101486	M24902	Hs.1852	acid phosphatase; prostate	25.2
	119073	R32894	Hs.279477	ESTs	24.8
20	133428	M34376	Hs.183752	microsaminoprotein; beta-	23.8
	128180	AA595348	Hs.171995	kallikrein 3; (prostate specific antigen	21.4
	104080	AA402971	Hs.57771	Homo sapiens mRNA for serine protease (T	18.9
	127537	AA569531	Hs.162859	ESTs	18.6
	131665	R22139	Hs.30343	ESTs	17.4
25	101050	K01911	Hs.1832	neuropeptide Y	17.3
	130771	N48056	Hs.1915	folate hydrolase (prostate-specific memb	17
	107485	W63793	Hs.262476	S-adenosylmethionine decarboxylase 1	16.7
	106155	AA425309	Hs.33287	ESTs	16.5
	129534	R73640	Hs.11260	ESTs	16.4
30	100569	HG2261-HT2351		Antigen, Prostate Specific, Alt. Splice	16
	101889	S39329	Hs.181350	kallikrein 2; prostatic	15.4
	135389	U05237	Hs.99872	fetal Alzheimer antigen	15
	133944	AA045870	Hs.7780	ESTs	12.5
	130974	X57985	Hs.2178	H2B histone family; member Q	11.8
35	114768	AA149007	Hs.182339	ESTs	11.8
	104660	AA007160	Hs.14846	ESTs	11.4
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.	10.9
	126645	AI167942	Hs.61635	Homo sapiens BAC clone RG041D11 from 7q2	10.7
	135153	N40141	Hs.95420	Homo sapiens mRNA for JM27 protein; comp	10.6
40	107033	AA599629	Hs.113314	ESTs	10.6
	118417	N66048		ESTs; Weakly similar to polymerase [H.sa	10.5
	126758	W37145	Hs.293960	ESTs	10.2
	107102	AA609723	Hs.30652	ESTs	10.1
	116787	H28581	Hs.15641	ESTs	10.1
45	115719	AA416997	Hs.59622	ESTs	10
	123209	AA489711	Hs.203270	ESTs	9.9
	101664	M60752	Hs.121017	H2A histone family; member A	9.8
	112971	T17185	Hs.83883	ESTs	9.7
	117984	N51919	Hs.106778	ESTs	9.7
50	129523	M30894	Hs.274509	T-cell receptor; gamma cluster	9.4
	132964	AA031360	Hs.167133	ESTs	9.2
	121853	AA425887	Hs.98502	ESTs	9
	119617	W47380	Hs.55999	ESTs	8.9
	105627	AA281245	Hs.23317	ESTs	8.8
55	101461	M22430	Hs.76422	phospholipase A2; group IIA (platelets;	8.7
	124526	N62096	Hs.293185	yz61c5.s1 Soares_multiple_sclerosis_2NbH	8.5
	133845	T68510	Hs.76704	ESTs	8.2
	133354	AA055552	Hs.334762	ESTs; Weakly similar to KIAA0319 [H.sapi	8.1
	119018	N95796	Hs.278695	ESTs	8
60	100394	D84276	Hs.66052	CD38 antigen (p45)	8
	106579	AA456135	Hs.23023	ESTs	7.6
	114965	AA250737	Hs.72472	ESTs	7.4
	112033	R43162	Hs.22627	ESTs	7.1
	102398	U42359		Human N33 protein form 1 (N33) gene, exo	7
65	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	6.9
	101803	M86546	Hs.155691	pre-B-cell leukemia transcription factor	6.8
	120562	AA280036	Hs.302267	ESTs; Weakly similar to W01A6.c [C.elega	6.8

	109112	AA169379	Hs.257924	ESTs	6.8
	109795	F10707	Hs.326416	ESTs	6.7
	130336	X07730	Hs.171995	kallikrein 3; (prostate specific antigen	6.6
	131425	AA219134	Hs.26691	ESTs	6.6
5	132902	AA490969	Hs.59838	ESTs	6.6
	133724	U07919	Hs.75746	aldehyde dehydrogenase 6	6.5
	120215	Z41050	Hs.108787	Homo sapiens Mcd4p homolog mRNA; complet	6.5
	131881	AA010163	Hs.3383	upstream regulatory element binding prot	6.5
	100727	X07290	Hs.334786	Human HF.12 gene mRNA	6.3
10	121770	AA421714	Hs.278428	Homo sapiens mRNA for KIAA0896 protein;	6.3
	123475	AA599267	Hs.250528	ESTs; Weakly similar to ANKYRIN; BRAIN V	6.3
	133061	AB000584	Hs.296638	prostate differentiation factor	6.3
	116429	AA009710	Hs.279923	ESTs; Weakly similar to similar to GTP-b	6.2
	101233	L29008	Hs.878	sorbitol dehydrogenase	6.2
15	104691	AA011176	Hs.37744	ESTs	6.2
	127248	AA325029	EST27953	Cerebellum II Homo sapiens cDNA	6.2
	105500	AA258485	Hs.222399	ESTs	6.1
	130828	AA053400	Hs.203213	ESTs	5.9
	115357	AA281793	Hs.72988	ESTs	5.8
20	116334	AA491457	Hs.48948	ESTs	5.7
	120132	Z38839	Hs.125019	ESTs; Weakly similar to !!!! ALU SUBFAMI	5.6
	106375	AA443993	Hs.289072	ESTs	5.6
	124777	R41933	Hs.140237	ESTs; Weakly similar to neuronal thread	5.6
	101791	M83822	Hs.62354	Human beige-like protein (BGL) mRNA; par	5.5
25	117698	N41002	Hs.45107	ESTs	5.5
	122041	AA431407	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	5.5
	133723	AA088851	Hs.262476	S-adenosylmethionine decarboxylase 1	5.5
	113938	W81598	ESTs		5.4
	133015	AA047036	Hs.246315	ESTs	5.4
30	108186	AA056482	Hs.7780	ESTs	5.3
	104466	N25110	Hs.326392	Human guanine nucleotide exchange factor	5.3
	104033	AA365031	Hs.98944	ESTs	5.3
	110844	N31952	Hs.167531	ESTs; Weakly similar to (define not ava	5.3
	129056	H70627	Hs.108336	ESTs; Weakly similar to !!!! ALU SUBFAMI	5.3
35	133493	AA284143	Hs.194369	Homo sapiens chromosome 1 atrophin-1 rel	5.3
	129184	W26769	Hs.109201	ESTs; Highly similar to (define not ava	5.2
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	5.1
	116188	AA464728	Hs.184598	ESTs; Weakly similar to !!!! ALU SUBFAMI	5.1
	105921	AA402613	Hs.169119	ESTs	5.1
40	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	5.1
	128871	AA400271	Hs.106778	ESTs; Highly similar to (define not ava	5.1
	116238	AA479362	Hs.47144	ESTs	5
	102913	X07696	Hs.80342	keratin 15	5
	103011	X52541	Hs.326035	early growth response 1	5
45	118981	N93839	Hs.39288	ESTs; Weakly similar to !!!! ALU SUBFAMI	5

TABLE 2A shows the accession numbers for those primekeys lacking unigeneID's for Table 2. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey:	Unique Eos probeset Identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
15	<hr/>	
	Pkey	CAT number Accession
20	118417	37186_1 AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547 AI680833 AI633818 N29986 U87592 U87593 U87590 U87591 S46404 U87587 AA463992 AW206802 AI970376 AI583718 AI672574 N25695 AW665466 AI818326 AA126128 AJ480345 AW013827 AA248638 AI214968 AA204735 AA207155 AA206262 AA204833 AW003247 AW496808 AJ080480 AI631703 AI651023 AI867418 AW818140 AA502500 AI206199 AI871282 AI352545 BE501030 AI652535 BE465762 AA206331 AW451866 AA471088 AA206342 AA204834 AA206100 AW021661 AA332922 N66048 AA703396 H92278 AW139734 H92683 U87589 U87595 H69001 U87594 BE466420 AI624817 BE466611 AI206344 AA574397 AA348354 AI493192
25	127248	227560_1 AA364195 AA325029 AW962050
	107033	235652_1 AI141999 AA730176 R44544 R41778 AW300793 AW966157 AA918501 AA599629 AI082195 AI198537 AW006520 AW236663 AW151420 AI826987 AI810832 AI669102 AI201981 N27331 AA335566 T84622 BE085347 BE085269
	102398	entrez_U42359 U42359
	113938	genbank_W81598 W81598

TABLE 3: shows genes, including expression sequence tags, differentially expressed in prostate tumor tissue compared to normal tissue as analyzed using the Affymetrix/Eos Hu02 GeneChip array. Shown are the relative amounts of each gene expressed in prostate tumor samples and various normal tissue samples showing the highest expression of the gene.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal body tissue			
15					
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
20	100131	D12485	Hs.11951	phosphodiesterase 1/nucleotide pyrophosph	6.3
	100235	D29954	Hs.13421	KIAA0056 protein	5.1
	100570	HG2261-HT2352	Hs.171995	Antigen, Prostate Specific, Alt. Splice	9
	100819	HG4020-HT4290	Hs.2387	Transglutaminase	10.5
	101063	L00354	Hs.80247	cholecystokinin	8.5
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	4.7
25	101416	M17254	Hs.279477	v-ets avian erythroblastosis virus E26 o	4.7
	101447	M21305		Human alpha satellite and satellite 3 ju	11
	101485	M24736	Hs.89546	selectin E (endothelial adhesion molecu	9.8
	101514	M28214	Hs.123072	RAB3B; member RAS oncogene family	6.2
	101626	M57399	Hs.44	pleiotrophin (heparin binding growth fac	8.4
30	101663	M60750	Hs.2178	H2B histone family; member A	4.9
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	5.4
	101768	M81118	Hs.78989		7.5
	101817	M88163	Hs.152292	SWI/SNF related; matrix associated; acti	5.5
	101888	M99701	Hs.95243	transcription elongation factor A (SII)-	5.7
35	102031	U04898	Hs.2156	RAR-related orphan receptor A	13.2
	102052	U07559	Hs.505	ISL 1 transcription factor; LIM/homeodoma	8.9
	102221	U24576	Hs.3844	LIM domain only 4	5.8
	102233	U26173	Hs.78334	nuclear factor; interleukin 3 regulated	7.4
	102302	U33052	Hs.69171	protein kinase C-like 2	8.2
40	102348	U37519	Hs.87539	aldehyde dehydrogenase 8	5.9
	102457	U48807	Hs.2359	dual specificity phosphatase 4	5.1
	102473	U49957	Hs.180398	LIM domain-containing preferred transloc	5.7
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9
	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	10.6
45	102751	U80034	Hs.68583	mitochondrial intermediate peptidase	15.6
	102823	U90914	Hs.5057	carboxypeptidase D	4.9
	102869	X02544	Hs.572	orosomucoid 1	22.6
	103031	X54667	Hs.123114	cystatin S	4.7
	103043	X55733	Hs.93379	eukaryotic translation initiation factor	4.9
50	103093	X60708	Hs.44926	dipeptidylpeptidase IV (CD26; adenosine	5.8
	103376	X92098	Hs.323378	coated vesicle membrane protein	5.2
	103401	X95240	Hs.54431	specific granule protein (28 kDa); cyste	7.4
	103613	Z46629	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	5.2
	103677	Z83806		H.sapiens mRNA for axonemal dynein heavy	4.9
55	103962	AA298180	Hs.83243	ESTs	6
	104084	AA410529	Hs.30732	ESTs	6.4
	104257	AF006265	Hs.9222	estrogen receptor-binding fragment-assoc	6.8
	104301	D45332	Hs.6783	ESTs	10.5
	104769	AA025887	Hs.283943	ESTs; Weakly similar to !!!!! ALU SUBFAM	6.3
60	104851	AA040882	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	4.9
	104896	AA054228	Hs.23165	ESTs	5.8
	104956	AA074880	Hs.20509	ESTs; Weakly similar to hypothetical pro	6.4
	104957	AA074919	Hs.10026	ESTs; Weakly similar to ORF YJL063c (S.c	4.8
	104967	AA084506	Hs.291000	ESTs	6.5
65	105099	AA150776	Hs.23729	Homo sapiens clone 24405 mRNA sequence	7
	105298	AA233459	Hs.26369	ESTs	5.1

	105304	AA233553	Hs.190325	ESTs	4.7
	105370	AA236476	Hs.22791	ESTs; Weakly similar to transmembrane pr	10.3
	105427	AA251330	Hs.28248	ESTs	5
	105542	AA261858	Hs.266957	ESTs; Weakly similar to heat shock prote	8.8
5	105628	AA281251	Hs.79828	ESTs; Weakly similar to putative zinc fi	5.5
	105640	AA281623	Hs.6685	ESTs; Weakly similar to KIAA0742 protein	8
	105645	AA282138	Hs.11325	ESTs	14
	105691	AA287097	Hs.289068	transcription factor 4	6.3
	105730	AA292701	Hs.5364	DKFZP5641052 protein	4.9
10	105808	AA393808	Hs.286131	KIAA0438 gene product	7
	105826	AA398243	Hs.194477	ESTs; Moderately similar to similar to N	5
	105903	AA401433	Hs.200016	ESTs; Weakly similar to diphosphoinosito	9.9
	105906	AA401633	Hs.22380	ESTs	11.5
	106065	AA417558	Hs.25206	ESTs	5.1
15	106094	AA419461	Hs.23317	ESTs	10.9
	106157	AA425367	Hs.34892	ESTs	6.6
	106184	AA426643	Hs.10762	ESTs	8.5
	106211	AA428240	Hs.126083	ESTs	8.4
	106213	AA428258	Hs.8769	Homo sapiens mRNA; cDNA DKFZp564E153 (fr	5.7
20	106272	AA432074	Hs.323099	ESTs	5.8
	106369	AA443828	Hs.288856	ESTs	6.3
	106400	AA447621	Hs.94109	ESTs	5.4
	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	9.2
	106507	AA452584	Hs.267819	protein phosphatase 1; regulatory (inhib	5.6
25	106523	AA453441	Hs.31511	ESTs	4.7
	106532	AA453628	Hs.37443	ESTs	4.7
	106557	AA455087	Hs.22247	ESTs	5.7
	106575	AA456039	Hs.105421	ESTs	7.2
	106618	AA459249	Hs.8715	ESTs; Weakly similar to Similarity with	5.6
30	106820	AA481037	Hs.12592	ESTs	5.4
	106846	AA485223	Hs.34892	ESTs	5.3
	106973	AA505141	Hs.11923	Human DNA sequence from clone 167A19 on	7.5
	107110	AA609952	Hs.12784	KIAA0293 protein	6.1
	107127	AA620504	Hs.179898	ESTs	7.1
35	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	5.2
	107217	D51095	Hs.35861	DKFZP586E1621 protein	15.1
	107365	U78294	Hs.111256	arachidonate 15-lipoxygenase; second typ	4.7
	107630	AA007218	Hs.60178	ESTs	5.3
	107734	AA016225	Hs.7517	ESTs	4.8
40	107760	AA018042	Hs.252085	EST	7.6
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	10.5
	108012	AA039616	Hs.173334	ESTs	6.5
	108520	AA084138	Hs.46786	ESTs	7.9
	108583	AA088276	Hs.68826	ESTs	5.6
45	108613	AA100967	Hs.69165	ESTs	6
	108664	AA113349	Hs.69588	EST	6.3
	108677	AA115629	Hs.118531	ESTs	5.9
	108807	AA129968	Hs.49376	ESTs; Weakly similar to PROTEIN PHOSPHAT	5.8
	108910	AA136590		ESTs	5
50	108933	AA147224	Hs.337232	ESTs	12.7
	108948	AA149579	Hs.118258	ESTs	6.8
	109014	AA156790	Hs.262038	ESTs	15.3
	109124	AA171529	Hs.183887	ESTs	6.1
	109142	AA176438	Hs.41295	ESTs	5.1
55	109277	AA196332	Hs.86043	ESTs	5.5
	109342	AA213620		Homo sapiens mRNA; cDNA DKFZp586M1418 (fr	16
	109562	F01811	Hs.187931	ESTs; Moderately similar to voltage-gate	10.8
	109565	F01930	Hs.23648	ESTs	7
	109648	F04600	Hs.7154	ESTs	9.9
60	109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; com	6.4
	109859	H02308	Hs.20792	ESTs	5.3
	110181	H20276	Hs.31742	ESTs	16.8
	110854	N32919	Hs.27931	ESTs	10
	110924	N47938	Hs.12940	yy84a09.s1 Soares_multiple_sclerosis_2Nb	5.6
65	111046	N55514	Hs.318584	ESTs	6.9
	111091	N59858	Hs.33032	Homo sapiens mRNA; cDNA DKFZp434N185 (fr	5.2
	111157	N66613	Hs.99364	ESTs	5
	111164	N66857	Hs.122489	ESTs; Weakly similar to !!!! ALU CLASS C	5.8
	111221	N68869	Hs.15119	ESTs	6.2

	111348	N90041	Hs.9585	ESTs	5.4
	111353	N90430	Hs.6616	ESTs	5.3
	111495	R07210	Hs.9683	ESTs	5.8
	111540	R08850	Hs.9786	ESTs	6
5	111579	R10657	Hs.167115	KIAA0830 protein	12.6
	111581	R10684	Hs.5794	ESTs	7.1
	111734	R25375	Hs.128749	ESTs	6.2
	111861	R37460	Hs.25231	ESTs	9.4
	111870	R37778	Hs.18685	ESTs; Weakly similar to hypothetical pro	6.5
10	111937	R40431	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	4.8
	111987	R42036	Hs.6763	KIAA0942 protein	6.4
	112184	R49173	Hs.330242	ESTs	5.6
	112286	R53765	Hs.158135	KIAA0981 protein	9.3
	112380	R59740	Hs.5740	ESTs	4.7
15	112452	R63841	Hs.157461	ESTs	6
	112601	R79111	Hs.78225	annexin A1	5.4
	112753	R93696	Hs.169882	ESTs	5.8
	112902	T09262	Hs.129190	ESTs	5.1
	112984	T23457	Hs.289014	ESTs	4.9
20	113021	T23855	Hs.129836	KIAA1028 protein	10.8
	113083	T40530	Hs.266957	ESTs; Weakly similar to heat shock prote	5.7
	113200	T57773	Hs.10263	ESTs	7.3
	113494	T88878	Hs.86538	ESTs	8.7
	113849	W60439	Hs.8858	ESTs; Moderately similar to cbp146 [M.mu	4.9
25	113883	W72382	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	4.7
	113950	W85765	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.7
	113986	W87482	Hs.21894	ESTs	5.9
	113989	W87544	Hs.268828	ESTs	4.7
	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 protein	21.3
30	114340	Z41395	Hs.143611	ESTs	9.6
	114346	Z41450	Hs.130489	ESTs	5.2
	114435	AA018216	Hs.164975	Bicaudal D (Drosophila) homolog 1	7.4
	114463	AA025370	Hs.40109	KIAA0872 protein	8.2
	114652	AA101416	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	5.4
35	114721	AA131450	Hs.103822	ESTs	4.8
	114730	AA133527	Hs.331328	ESTs; Weakly similar to The KIAA0138 gen	5.1
	114833	AA234362	Hs.87159	ESTs; Moderately similar to CGI-66 prote	5.5
	114860	AA235112	Hs.42179	ESTs; Moderately similar to similar to m	6.3
	114884	AA235811	Hs.293672	ESTs	5.2
40	114895	AA236177	Hs.76591	KIAA0887 protein	4.7
	114908	AA236545	Hs.54973	ESTs	5.2
	114932	AA242751	Hs.16218	KIAA0903 protein	5.7
	115084	AA255566	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	5.2
	115140	AA258030	Hs.279938	ESTs; Weakly similar to supported by GEN	5.9
45	115468	AA287061	Hs.48499	ESTs; Highly similar to Bdeight protein	4.7
	115583	AA398913	Hs.45231	LDOC1 protein	7.6
	115709	AA412519	Hs.58279	ESTs	4.8
	115772	AA423972	Hs.131740	ESTs	5
	115774	AA424029	Hs.288390	ESTs; Moderately similar to dynamin; int	5.4
50	115776	AA424038	Hs.81897	ESTs	5
	115821	AA427528	Hs.130965	ESTs; Weakly similar to ZINC FINGER PROT	13.7
	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q3	10.6
	116024	AA451748	Hs.83883	Human DNA sequence from clone 718J7 on c	6.8
	116108	AA457566	Hs.28777	ESTs	6
55	116117	AA459117	Hs.31575	SEC63; endoplasmic reticulum translocon	7.3
	116146	AA460701	Hs.15423	ESTs	5.5
	116296	AA489033	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (fr	5.7
	116379	AA521472	Hs.71252	ESTs	5.9
	116393	AA599463	Hs.306051	protein phosphatase 2 (formerly 2A); reg	5.9
60	116401	AA599963	Hs.59698	ESTs	7.9
	116416	AA609219	Hs.39982	ESTs	9.2
	116587	D59325	Hs.121429	ESTs	5.2
	116601	D80055	Hs.45140	ESTs	4.9
	116684	F09156	Hs.66095	ESTs	7.2
65	116722	F13654		HSFIH32 Stratagene cat#937212 (1992) Hom	5.5
	116766	H13260	Hs.95097	ESTs	5.9
	117453	N29568	Hs.108319	thyroid hormone receptor-associated prot	6.9
	117557	N33920	Hs.44532	diubiquitin	4.8
	117708	N45114	Hs.126280	ESTs	6.3

	118001	N52151	Hs.47447	ESTs	11.4
	118229	N62339	Hs.166254	heat shock 90kD protein 1; alpha	6.2
	118599	N69207	Hs.203697	ESTs	5.8
5	118645	N70358	Hs.125180	growth hormone receptor	7.1
	118873	N89881	Hs.44577	ESTs	6
	118985	N94303	Hs.55028	ESTs	9.3
	119107	R42424	Hs.63841	ESTs	6
	119126	R45175	Hs.117183	ESTs	17.9
10	119271	T16387	Hs.65328	ESTs	6
	119367	T78324	Hs.250895	ESTs	5
	119721	W69440	Hs.48376	ESTs	15.4
	119741	W70205	Hs.43670	kinesin family member 3A	10.1
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	5.3
15	120217	Z41078	Hs.66035	ESTs	4.8
	120266	AA173939	Hs.205442	ESTs; Weakly similar to inner centromere	8.8
	120294	AA190888	Hs.153881	ESTs; Highly similar to NY-REN-62 antigen	4.9
	120418	AA236010	Hs.26613	Homo sapiens mRNA; cDNA DKFZp566F1323 (f	4.7
	120486	AA253400	Hs.137569	tumor protein 63 kDa with strong homolog	5.6
20	120524	AA261852	Hs.192905	ESTs	4.9
	120571	AA280738	Hs.34892	ESTs	8.8
	120596	AA282074	Hs.237323	ESTs	6.2
	120713	AA292655	Hs.96557	ESTs	9.9
	120992	AA398246	Hs.97594	ESTs	16.4
25	121429	AA406293	Hs.41167	ESTs	6.9
	121503	AA412049	Hs.290347	ESTs	7.6
	121512	AA412105	Hs.193736	ESTs	5.8
	121816	AA424814	Hs.48827	ESTs	4.6
	122027	AA431302	Hs.98721	EST; Weakly similar to N-copine [H.sapie	5.6
30	122294	AA437311	Hs.98927	ESTs	5.7
	122411	AA446859	Hs.99083	ESTs	6.5
	122791	AA460158	Hs.129836	KIAA1028 protein	12.4
	122792	AA460225	Hs.99519	ESTs	5.1
	122969	AA478539	Hs.104336	ESTs	4.9
35	123085	AA485724	Hs.27413	ESTs	5.4
	123100	AA485957	Hs.306219	Homo sapiens clone 25032 mRNA sequence	5
	123295	AA495981	Hs.250830	ESTs	4.7
	123311	AA496252	Hs.105069	ESTs	7.4
	123583	AA609006	Hs.111240	ESTs	9.1
40	123619	AA609200		ESTs	4.7
	123645	AA609310	Hs.188691	ESTs	4.8
	123709	AA609651	Hs.112742	ESTs	7
	123968	C14333	Hs.108327	damage-specific DNA binding protein 1 (1	5
	124178	H45996	Hs.97101	putative G protein-coupled receptor	6.8
45	124352	N21626	Hs.102406	ESTs	10.2
	124357	N22401		yw37g07.s1 Morton Fetal Cochlea Homo sap	10.6
	124515	N58172	Hs.109370	ESTs	14.2
	124911	R88992	Hs.174195	ESTs	4.8
	125154	W38419		ESTs	4.7
50	125892	W01626		za36e07.r1 Soares fetal liver spleen 1NF	5.1
	126802	AA947601	Hs.97056	ESTs	5.1
	126812	Z36290	Hs.173933	ESTs; Weakly similar to NUCLEAR FACTOR 1	4.6
	127080	AA662913	Hs.180173	ESTs	5
	127308	AA507628	Hs.334390	ESTs	4.8
55	127370	AI024352	Hs.70337	immunoglobulin superfamily; member 4	4.7
	127385	AI457411	Hs.106728	ESTs	4.8
	127965	AA828760	Hs.292059	ESTs	4.8
	128172	AI400862	Hs.265130	ESTs	5
	128305	AI039722	Hs.279009	ESTs	5.8
60	128420	AI088155	Hs.41296	ESTs; Weakly similar to unknown [H.sapie	17
	128467	AA176446	Hs.180428	ESTs; Weakly similar to hypothetical 43.	4.8
	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	7.9
	128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapi	8.1
	128651	AA446990	Hs.103135	ESTs	6.5
	129088	AA215971	Hs.194431	KIAA0992 protein	5.2
65	129136	N26391	Hs.250723	ESTs	5.1
	129171	AA234048	Hs.7753	calumenin	5.8
	129229	AA211941	Hs.109643	polyadenylate binding protein-interactin	5.8
	129386	N27524	Hs.260024	Cdc42 effector protein 3	5.2
	129467	AA410311	Hs.44208	ESTs	5.1

	129564	H22136	Hs.75295	guanylate cyclase 1; soluble; alpha 3	16.3
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubiquitin	9.2
	129821	F11019	Hs.12696	cortactin SH3 domain-binding protein	8.6
5	129823	X00948	Hs.105314	relaxin 2 (H2)	9.1
	129847	W46767	Hs.296178	ESTs; Weakly similar to RNA POLYMERASE I	5.4
	129912	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen	6.5
	129958	L20591	Hs.1378	annexin A3	5.1
	129977	J04076	Hs.1395	early growth response 2 (Krox-20 (Drosophila))	8.6
10	130061	U82256	Hs.172851	arginase; type II	7.4
	130241	U78313	Hs.153203	MyoD family inhibitor	4.9
	130466	N21679	Hs.180059	ESTs	5.8
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	6.7
	130619	AA477739	Hs.12532	ESTs	6.4
	130925	N71935	Hs.169378	multiple PDZ domain protein	7.9
15	130938	AA013250	Hs.21398	ESTs; Moderately similar to PUTATIVE GLU	6.2
	130971	H20332	Hs.301444	signal sequence receptor; gamma (translocator)	6.4
	131066	F09006	Hs.22588	ESTs	5
	131126	F09012	Hs.181326	myotubularin related protein 2	6.4
20	131310	J02960	Hs.2551	adrenergic; beta-2-; receptor; surface	7.9
	131487	AA253220	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f5.9)	7.6
	131561	X59841	Hs.294101	pre-B-cell leukemia transcription factor	7.6
	131562	U90551	Hs.28777	H2A histone family; member L	5.1
	131579	N62922	Hs.29088	ESTs	11
25	131629	AA442119	Hs.238809	ESTs	4.9
	131682	AA428368	Hs.30654	ESTs	4.8
	131699	R68657	Hs.90421	ESTs; Moderately similar to !!!! ALU SUB	6.5
	131785	N32724	Hs.32317	Sox-like transcriptional factor	5.6
	132053	H93381	Hs.38085	ESTs; Weakly similar to putative glycine	7.2
	132122	U65092	Hs.40403	Cbp/p300-interacting transactivator; wnt	5.6
30	132191	AA449431	Hs.288361	KIAA0741 gene product	8
	132256	AA608856	Hs.431	murine leukemia viral (bmi-1) oncogene homolog	5.5
	132482	AA429478	Hs.238126	ESTs; Highly similar to CGI-49 protein [6.6
	132533	AA021608	Hs.172510	ESTs	5.8
	132572	AA448297	Hs.237825	signal recognition particle 72kD	6.2
35	132581	R42266	Hs.52256	ESTs; Weakly similar to beta-TrCP protein	16
	132700	N47109	Hs.5521	ESTs	6.8
	132701	AA279359	Hs.55220	BCL2-associated athanogene 2	5.3
	132725	L41887	Hs.184167	splicing factor; arginine/serine-rich 7	7.8
40	132783	N74897	Hs.278894	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	5.9
	132790	X75535	Hs.168670	peroxisomal farnesylated protein	8
	132939	U76189	Hs.61152	exostoses (multiple)-like 2	5.2
	133142	F03321	Hs.65874	ESTs	5.2
	133342	U29589	Hs.7138	cholinergic receptor; muscarinic 3	10.3
45	133434	AA278852	Hs.30212	ESTs	5.8
	133453	M68941	Hs.73826	protein tyrosine phosphatase; non-receptor	4.9
	133520	X74331	Hs.74519	primase; polypeptide 2A (58kD)	13.1
	133544	T33873	Hs.74624	protein tyrosine phosphatase; receptor type I	4.6
	133608	D13315	Hs.75207	glyoxalase I	4.8
50	133626	H75939	Hs.75277	Homo sapiens mRNA; cDNA DKFZp586M141 (f1.5)	5
	133633	D21262	Hs.75337	nucleolar phosphoprotein p130	6.3
	133797	S66431	Hs.76272	retinoblastoma-binding protein 2	6
	133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homologous)	5.4
	134095	U47414	Hs.79069	cyclin G2	5.2
55	134249	N89827	Hs.80667	RALBP1 associated Eps domain containing	6.5
	134321	AA418230	Hs.8172	ESTs	7
	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	4.7
	134542	X57025	Hs.85112	insulin-like growth factor 1 (somatomedin)	7.7
	134570	U66615	Hs.172280	SWI/SNF related; matrix associated; actin	6.4
60	134592	U82613	Hs.289104	Alu-binding protein with zinc finger domain	5.4
	134654	W23625	Hs.8739	ESTs; Weakly similar to ORF YGR200c [S.cerevisiae]	5
	134666	AA482319	Hs.8752	putative type II membrane protein	5.4
	134806	Z49099	Hs.89718	spermine synthase	6.7
	134951	AA431480	Hs.169358	ESTs	9.8
65	135066	X04602	Hs.93913	Interleukin 6 (interferon; beta 2)	5.7
	135155	AA358268	Hs.166556	ESTs; Moderately similar to transcription factor	4.9
	135411	L10333	Hs.99947	reticulin 1	5.3
	300023	M10098		AFFX control: 18S ribosomal RNA	4.6
	300254	AW079607	Hs.55610	ESTs; Weakly similar to ZnT-3 [H.sapiens]	7.8
	300273	AW013907	Hs.167531	ESTs; Moderately similar to predicted human	11.5

	300319	AW157646	Hs.153506	ESTs; Weakly similar to microtubule-acti	8.5
	300566	H86709	Hs.326392	son of sevenless (Drosophila) homolog 1	5.8
	300578	AI989417	Hs.134289	ESTs	4.4
	300671	AI239706	Hs.93810	ESTs	7.9
5	300675	AA039352	Hs.125034	ESTs; Weakly similar to ORF YDL040c [S.c	4.5
	300680	AW468066	Hs.24817	ESTs; Weakly similar to KIAA0986 protein	5.2
	300762	AI497778	Hs.20509	ESTs	6.4
	300810	AI076890	Hs.146847	ESTs	5.8
10	300813	AA406411	Hs.208341	ESTs; Weakly similar to KIAA0989 protein	10.6
	300823	AI863068	Hs.106823	ESTs; Weakly similar to putative zinc fi	5.6
	300834	AF109300	Hs.147924	ESTs	6.7
	300923	AW136372	Hs.1852	ESTs	7.6
	300962	AA593373	Hs.293744	ESTs	5.5
15	301015	AA947682	Hs.20252	ESTs; Weakly similar to Chain A; Cdc42hs	7
	301042	AI659131	Hs.197733	ESTs	24.9
	301242	AW161535	Hs.23782	ESTs	11.8
	301254	AI049624	Hs.283390	EST cluster (not in UniGene) with exon h	4.3
	301262	H29500	Hs.7130	ESTs; Moderately similar to N-copine [H.	4.3
20	301388	AA156879	Hs.262036	ESTs; Weakly similar to ZINC FINGER PROT	6.6
	301563	AI802946	Hs.44208	ESTs; Weakly similar to match to ESTs AA	5.7
	301656	AW008475	Hs.151258	EST cluster (not in UniGene) with exon h	6.8
	301689	Z44810	Hs.301789	ESTs; Weakly similar to similar to C.ele	6.3
	301783	AL046347	Hs.83937	Homo sapiens PAC clone DJ1159O04 from 7p	6.2
25	301805	AI800004	Hs.142846	ESTs; Weakly similar to MesP1 [M.musculu	8.5
	301846	R20002	Hs.6823	ESTs; Weakly similar to intrinsic factor	4.6
	301891	AF131855	Hs.279591	Homo sapiens clone 25056 mRNA sequence	6.3
	302005	AI869666	Hs.123119	ESTs	36.8
	302056	AI457532	Hs.30488	ESTs; Moderately similar to ROSA26AS [M.	9.5
30	302067	H05698	Hs.222399	ESTs; Weakly similar to protein-tyrosine	5.8
	302099	AL021397	Hs.137576	ribosomal protein L34 pseudogene 1	8.8
	302147	AB022660	Hs.151717	KIAA0437 protein	5.9
	302214	AJ001454	Hs.159425	Homo sapiens mRNA for testican-3	4.3
	302236	AI128606	Hs.6557	zinc finger protein 161	4.3
35	302358	D81150	Hs.322848	EST cluster (not in UniGene) with exon h	5.5
	302410	NM_004917	Hs.218366	EST cluster (not in UniGene) with exon h	26.8
	302486	AC003682	Hs.183512	multiple UniGene matches	8.2
	302582	NM_000522	Hs.249195	EST cluster (not in UniGene) with exon h	6.4
	302785	AA425562	Hs.11065	EST cluster (not in UniGene) with exon h	5
40	302792	AA343696	Hs.46821	ESTs; Weakly similar to putative [H.sapi	4.8
	302881	AA508353	Hs.105314	relaxin 1 (H1)	78.8
	302892	N58545	Hs.42346	histone deacetylase 3	8.5
	302970	AW118352	Hs.312679	EST cluster (not in UniGene) with exon h	7.4
	302977	AW263124	Hs.315111	EST cluster (not in UniGene) with exon h	5.5
45	303029	AF199613		EST cluster (not in UniGene) with exon h	4.6
	303125	AF161352	Hs.111782	EST cluster (not in UniGene) with exon h	5.8
	303280	AI571580	Hs.170307	ESTs	4.3
	303306	AA215297	Hs.61441	EST cluster (not in UniGene) with exon h	6.4
	303309	AL134164	Hs.145418	ESTs	6.6
50	303344	AA255977	Hs.250646	ESTs; Highly similar to ubiquitin-conjug	19.5
	303380	AA298471	Hs.326567	EST cluster (not in UniGene) with exon h	6.6
	303401	AA758552	Hs.309497	ESTs	6.8
	303525	AW516519	Hs.273294	ESTs	4.8
	303526	AA348111	Hs.96900	ESTs	12.1
55	303540	AA355607	Hs.309490	ESTs; Weakly similar to MMSET type I [H.	8.2
	303572	AW338520	Hs.242540	ESTs	8.4
	303685	AW500106	Hs.23643	EST cluster (not in UniGene) with exon h	4.9
	303699	D30891	Hs.19525	EST cluster (not in UniGene) with exon h	15.7
	303702	AW500748	Hs.224961	ESTs; Weakly similar to 73 kDa subunit o	6.3
60	303718	AI741397	Hs.114658	ESTs	4.6
	303722	AA521510	Hs.145010	ESTs	12.5
	303732	AW502405	Hs.125759	ESTs; Weakly similar to tumor suppressor	4.3
	303735	AA707750	Hs.169055	ESTs; Weakly similar to cis-Golgi matrix	5.4
	303752	AI017286	Hs.5957	EST cluster (not in UniGene) with exon h	5.3
	303753	AW503733	Hs.9414	ESTs	13
65	303813	AI275850	Hs.114658	EST cluster (not in UniGene) with exon h	7.8
	304053	R00493	Hs.125565	translocase of inner mitochondrial membr	4.8
	304218	N66373	Hs.27973	ESTs; Weakly similar to ZK354.7 [C.elega	6
	305200	AA668128	Hs.45207	EST singleton (not in UniGene) with exon	5.7
	306716	AI024916	Hs.251354	ESTs	5.7

	307848	AI364186	EST singleton (not in UniGene) with exon	7.3
	307871	AI368665	Hs.31476 EST singleton (not in UniGene) with exon	5.4
	308050	AI460004	Hs.31608 EST singleton (not in UniGene) with exon	8.1
5	308362	AI613519	Hs.105749 EST singleton (not in UniGene) with exon	5.5
	308923	AI863051	Hs.279815 ESTs	4.4
	309116	AI927149	Hs.29797 ribosomal protein L10	4.5
	309375	AW075342	Hs.9271 EST singleton (not in UniGene) with exon	7.4
	309674	AW205604	Hs.266009 ESTs; Weakly similar to !!!! ALU SUBFAM1	5
10	310095	AI921750	Hs.144871 ESTs	5
	310098	AI685841	Hs.161354 ESTs	11.6
	310250	AI478629	Hs.158465 ESTs	5.8
	310365	AI262148	Hs.145569 ESTs	9.7
	310382	AI734009	Hs.127699 EST cluster (not in UniGene)	10.4
15	310409	AI612775	Hs.145710 ESTs	4.6
	310431	AI420227	Hs.149358 ESTs	72.9
	310573	AW292180	Hs.156142 ESTs	7.6
	310598	AI338013	Hs.140546 ESTs	9.2
	310639	AW269082	Hs.175162 ESTs	4.5
20	310787	AW262580	Hs.147674 ESTs	4.9
	310816	AI973051	Hs.224965 ESTs	7.6
	311251	AI655662	Hs.197698 ESTs	41.3
	311280	AI767957	Hs.198248 ESTs; Weakly similar to Y38A8.1 gene pro	4.5
	311330	AI679524	Hs.201629 ESTs; Moderately similar to !!!! ALU SUB	4.6
25	311515	AW136713	Hs.23862 ESTs	5.9
	311574	AI824863	Hs.211420 ESTs	4.8
	311587	AI828254	Hs.271019 ESTs	5.8
	311596	AI682088	Hs.79375 ESTs	26.4
	311631	AI809519	Hs.271133 ESTs	6.4
30	311688	AW025661	Hs.240090 ESTs	7.4
	311783	AI682478	Hs.13528 EST	4.6
	311826	AA765470	Hs.85092 ESTs	6.7
	311853	AW014013	Hs.107056 ESTs	5.3
	311901	R16890	Hs.137135 ESTs	5.6
35	311932	AW451654	Hs.257482 ESTs	4.3
	312153	AA759250	Hs.118625 cytochrome b-561	11
	312182	AA834800	Hs.326263 EST cluster (not in UniGene)	16.9
	312242	AI380207	Hs.125276 ESTs	4.7
	312296	C01367	Hs.127128 ESTs	5.3
40	312407	R46180	Hs.153485 ESTs	6.2
	312424	AA847398	Hs.281997 ESTs	4.8
	312425	R49353	Hs.293892 ESTs	5.2
	312480	R68651	Hs.144997 ESTs	9.5
	312518	C17785	Hs.182738 ESTs	6.3
45	312521	AA033609	Hs.239884 ESTs	11.2
	312527	AI695522	Hs.191271 ESTs	4.7
	312539	AI004377	Hs.200360 ESTs	7
	312546	AI623511	Hs.118567 ESTs	5.1
	312563	AA976064	Hs.180842 ESTs	6.5
50	312623	AA694607	Hs.176956 EST cluster (not in UniGene)	10.8
	312857	AA772279	Hs.126914 ESTs	5
	312890	AI813654	Hs.5957 ESTs	5.8
	312903	AA939266	Hs.278626 ESTs	7.7
	312905	H92571	Hs.234478 ESTs	6.5
55	312976	AA836271	Hs.125830 ESTs	4.6
	312983	AI079278	Hs.269899 ESTs	5.1
	312996	AA249018	Hs.154331 EST cluster (not in UniGene)	7
	313035	N36417	Hs.144928 ESTs	6.3
	313165	AI801098	Hs.151500 ESTs	4.3
60	313188	AI039702	Hs.179573 collagen; type I; alpha 2	4.8
	313218	AA827805	Hs.124296 ESTs	5
	313226	AI200281	Hs.123910 ESTs	5.9
	313325	AI420611	Hs.127832 ESTs	4.6
	313326	AI088120	Hs.122329 ESTs	7.4
	313425	AA745689	Hs.186838 ESTs; Weakly similar to similar to zinc	6.3
65	313499	AI261390	Hs.146085 ESTs	5.6
	313540	AI797301	Hs.5740 ESTs	5.9
	313568	AW467376	Hs.129640 ESTs	4.3
	313569	AI273419	Hs.135146 ESTs; Weakly similar to ZK1058.5 [C.eleg	4.6
	313603	AW468119	Hs.287631 EST cluster (not in UniGene)	6.8

	313615	AW295194	Hs.301997	DKFZP434N126 protein	5.2
	313625	AW468402	Hs.254020	ESTs	7.8
	313634	AA688292	Hs.337786	ESTs	4.4
	313635	AA507227	Hs.6390	ESTs	8.1
5	313638	AI753075	Hs.104627	ESTs	6.7
	313670	C16690	Hs.23767	EST cluster (not in UniGene)	4.4
	313671	W49823	Hs.104613	ESTs	4.4
	313676	AA861697	Hs.120591	EST cluster (not in UniGene)	13.4
10	313703	AI161293	Hs.280380	ESTs; Weakly similar to KIAA0525 protein	10
	313712	AA768553	Hs.74170	ESTs	5.2
	313800	AW296132	Hs.55098	ESTs	5.4
	313979	AI535895	Hs.221024	ESTs	4.3
	314121	AI732100	Hs.187619	ESTs	13.6
	314123	AW245993	Hs.223394	ESTs	6.4
15	314171	AI821895	Hs.193481	ESTs	29.4
	314188	AL138431	Hs.164243	ESTs	4.6
	314219	AL036001	Hs.48376	ESTs	5.7
	314236	AA743396	Hs.169023	ESTs	4.9
	314237	AA732359	Hs.96264	ESTs	4.4
20	314284	AA731431	Hs.293464	EST cluster (not in UniGene)	6.4
	314305	AI280112	Hs.125232	ESTs	5.3
	314343	AI754701	Hs.328476	ESTs; Weakly similar to alternatively sp	6.2
	314530	AI052358	Hs.193726	ESTs	4.5
25	314691	AW207206	Hs.136319	ESTs	17
	314695	AW502698	Hs.118152	ESTs	8.9
	314785	AI538226	Hs.32976	ESTs	9.4
	314801	AA481027	Hs.109045	ESTs; Weakly similar to ORF YGR245c [S.c	8
	314864	AA493811	Hs.294068	ESTs	6
30	314907	AI672225	Hs.222886	ESTs	19.3
	314916	AA548906	Hs.122244	ESTs	4.5
	314954	AA521381	Hs.187726	ESTs	5.3
	314981	AA524953	Hs.293334	ESTs	4.6
	315021	AA533447	Hs.312989	EST cluster (not in UniGene)	5.1
35	315051	AW292425	Hs.163484	EST	15.5
	315052	AA876910	Hs.134427	ESTs	20
	315073	AW452948	Hs.257631	ESTs	5.3
	315084	AI821085		ESTs	8.2
	315214	AI915927	Hs.34771	ESTs	5.4
40	315220	AI420753	Hs.66731	ESTs	5.1
	315278	AI985544	Hs.12450	ESTs	5.8
	315282	AI222165	Hs.144923	ESTs	4.5
	315368	AW291563	Hs.104696	ESTs	8
	315369	AA764918	Hs.256531	ESTs	4.8
45	315378	AI263393	Hs.145008	ESTs	6.2
	315379	AI378329	Hs.126629	ESTs	5.4
	315402	AW293424	Hs.75354	ESTs	5.1
	315442	AA977935	Hs.127274	ESTs	6.6
	315443	AW003416	Hs.160604	ESTs	5.5
50	315528	R37257	Hs.184780	ESTs	8.1
	315593	AW198103	Hs.158154	ESTs	9.9
	315634	AA837085	Hs.220585	ESTs	7.8
	315705	AW449285	Hs.313636	ESTs	8.9
	315707	AI418055	Hs.161160	ESTs	5.1
55	315714	AA744015	Hs.298138	EST cluster (not in UniGene)	6.1
	315740	T05558	Hs.156880	EST cluster (not in UniGene)	6.8
	315762	AI391470	Hs.158618	ESTs	5.3
	315769	AA744875	Hs.189413	ESTs	5
	315843	AA679430	Hs.191897	ESTs	5.7
60	315990	AI800041	Hs.190555	ESTs	9.2
	316012	AA764950	Hs.119898	ESTs	4.3
	316036	AA708018	Hs.190389	ESTs	5.9
	316055	AA693680	Hs.6947	EST cluster (not in UniGene)	6.7
	316074	AW517542	Hs.293273	ESTs	5.5
65	316100	AW203986	Hs.213003	ESTs	5.1
	316169	AI127483	Hs.120451	ESTs	8.2
	316442	AA760894	Hs.153023	ESTs	17.1
	316491	AA766025	Hs.186854	EST	4.6
	316504	AW135854	Hs.132458	ESTs	4.3
	316667	AW015940	Hs.232234	ESTs	7.6

	316854	AA831215	Hs.159066	ESTs; Weakly similar to predicted using	5.1
	316905	AW138241	Hs.210846	ESTs	6.4
	317008	AW051597	Hs.143707	ESTs	4.4
5	317019	AA864968	Hs.127699	ESTs	11
	317194	AW445167	Hs.126036	ESTs	13.5
	317224	D56760	Hs.93029	ESTs	8.7
	317404	AI806867	Hs.126594	ESTs	8.7
	317501	AA931245	Hs.137097	ESTs	11.1
10	317548	AI654187	Hs.195704	ESTs	14.2
	317651	AW292779	Hs.169799	ESTs	5.8
	317758	AI733277	Hs.128321	ESTs	5.4
	317850	N29974	Hs.152982	EST cluster (not in UniGene)	11.4
	317869	AW295184	Hs.129142	ESTs; Weakly similar to DEOXYRIBONUCLEAS	13.8
15	317902	AI828602	Hs.211265	ESTs	5.3
	317916	AI565071	Hs.159983	ESTs	7.7
	318239	AI085198	Hs.164226	ESTs	13.1
	318268	AI817736	Hs.182490	ESTs	6.2
	318327	AW294013	Hs.200942	ESTs	4.6
20	318363	R45530	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	6
	318428	AI949409	Hs.194591	ESTs	12.3
	318464	AI151010	Hs.157774	ESTs	4.3
	318524	AW291511	Hs.159066	ESTs	25.9
	318540	T30280	Hs.274803	EST cluster (not in UniGene)	7
25	318591	AW206806	Hs.115325	ESTs	4.8
	318615	AI133617	Hs.10177	ESTs	5.5
	318646	AW175665	Hs.278695	ESTs	5.7
	318667	AI493742	Hs.165210	ESTs	11
	318668	W26276	Hs.136075	ESTs	5.9
30	318753	AA578265	Hs.7130	copine IV	5.5
	319080	Z45131	Hs.23023	ESTs	16.9
	319181	F06504	Hs.27384	EST cluster (not in UniGene)	4.6
	319191	AF071538	Hs.79414	prostate epithelium-specific Ets transcr	6.6
	319233	R21054	Hs.180532	ESTs	4.9
35	319586	D78808	Hs.283683	ESTs	8.2
	319750	AA621606	Hs.117956	ESTs	9.3
	319763	AA460775	Hs.6295	ESTs	14.3
	319824	AA424266	Hs.123642	EST cluster (not in UniGene)	12.8
	319838	AA337642	Hs.95262	nuclear factor related to kappa B bindin	5.1
40	319913	AA179304	Hs.271586	ESTs; Moderately similar to !!!! ALU SUB	4.3
	319964	T80579	Hs.290270	ESTs	5.8
	320076	AI653733	Hs.271593	ESTs	8.5
	320102	AW296219	Hs.115325	RAB7; member RAS oncogene family-like 1	9.8
	320187	T99949	Hs.303428	EST cluster (not in UniGene)	9.8
45	320211	AL039402	Hs.125783	DEME-6 protein	7.9
	320324	AF071202	Hs.139336	ATP-binding cassette; sub-family C (CFTR	56.2
	320455	R49889	Hs.24144	EST cluster (not in UniGene)	8.3
	320464	AI089817	Hs.237146	ESTs	5.4
	320561	NM_006953	Hs.159330	EST cluster (not in UniGene)	7
50	320574	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DKFZp586N2020 (f4.4	6.7
	320576	AL049977	Hs.162209	Homo sapiens mRNA; cDNA DKFZp564C122 (fr	6
	320654	AW263086	Hs.118112	ESTs	13.5
	320796	AF038966	Hs.31218	secretory carrier membrane protein 1	6.2
	320800	AI681006	Hs.71721	ESTs	9.3
55	320813	AW360847	Hs.16578	ESTs	8.1
	320853	AI473796	Hs.135904	ESTs	6
	320856	D59945	Hs.65366	EST cluster (not in UniGene)	9.2
	320899	AA633772	Hs.116796	ESTs	5
	320918	AW195012	Hs.293970	ESTs	5.9
60	320973	HI9732	Hs.247917	ESTs	4.6
	321099	AA018386	Hs.64341	ESTs	5.8
	321190	H52462	Hs.163872	EST cluster (not in UniGene)	8.4
	321318	AB033041	Hs.137507	EST cluster (not in UniGene)	7.3
	321382	AW372449	Hs.175982	EST cluster (not in UniGene)	14.7
65	321441	AW297633	Hs.118498	ESTs	9.2
	321538	H80483	Hs.46903	EST cluster (not in UniGene)	4.8
	321609	H86021	Hs.182538	ESTs; Weakly similar to hMmTRA1b [H.sapi	5.5
	321636	AI791838	Hs.193465	ESTs	4.6
	321638	AI356352	Hs.108932	ESTs	6.6
	321644	AI204177	Hs.237396	ESTs	

	321681	AA233821	Hs.190173	EST cluster (not in UniGene)	4.6
	321726	X91221	Hs.144465	EST cluster (not in UniGene)	5
	321758	U29112	Hs.196151	EST cluster (not in UniGene)	6.2
	321877	AL109784	Hs.189222	EST cluster (not in UniGene)	4.6
5	321899	N55158	Hs.29468	ESTs	4.6
	321902	AA746374	Hs.145010	ESTs	8.2
	322007	AW410646	Hs.164649	ESTs	5.1
	322055	AL137646	Hs.146001	EST cluster (not in UniGene)	4.3
	322092	AF085833	Hs.135624	EST cluster (not in UniGene)	4.3
10	322221	AI890619	Hs.179662	nucleosome assembly protein 1-like 1	4.4
	322278	AF086283		EST cluster (not in UniGene)	5.8
	322303	W07459	Hs.157601	EST cluster (not in UniGene)	22
	322437	AW393804	Hs.170253	ESTs; Weakly similar to rabaptin-4 [H.sa	4.4
	322493	AF143235	Hs.279819	EST cluster (not in UniGene)	7.2
15	322782	AA056060	Hs.202577	EST cluster (not in UniGene)	18.4
	322811	AA782292	Hs.105872	ESTs	6.9
	322818	AW043782	Hs.293616	ESTs	10.7
	322826	AI807883	Hs.180059	ESTs	5
20	322887	AI986306	Hs.86149	ESTs; Weakly similar to KIAA0969 protein	11.9
	322889	AA081924	Hs.124918	ESTs	7.1
	322924	AA669253	Hs.136075	ESTs	4.5
	322982	AI351191	Hs.128430	ESTs	6.6
	322994	AA422116	Hs.191461	ESTs	4.7
	323040	AA336609	Hs.10862	ESTs	6.9
25	323041	AL118747	Hs.26691	EST cluster (not in UniGene)	8.3
	323045	AA148950	Hs.188836	ESTs	4.6
	323048	AL118923	Hs.175110	EST cluster (not in UniGene)	7.5
	323070	AA157726	Hs.264330	ESTs	7.5
	323071	AA157867	Hs.5722	ESTs	4.7
30	323097	Z44354	Hs.296261	guanine nucleotide binding protein (G pr	4.9
	323131	AA176982	Hs.270124	EST cluster (not in UniGene)	6.1
	323136	AL120351	Hs.30177	EST cluster (not in UniGene)	4.3
	323175	AI827137	Hs.336454	ESTs	6.2
35	323218	AF131846	Hs.13396	Homo sapiens clone 25028 mRNA sequence	6.3
	323226	AF055019	Hs.21906	Homo sapiens clone 24670 mRNA sequence	12.6
	323236	AA363148	Hs.293960	ESTs	10.9
	323262	AI829770	Hs.190642	ESTs	7.6
	323276	AA836452	Hs.323822	ESTs	7.6
40	323287	AA639902	Hs.104215	ESTs	24.7
	323335	AI655499	Hs.161712	ESTs	14.1
	323341	AL134875	Hs.108646	ESTs	5.3
	323362	AL135067	Hs.117182	ESTs	6.1
	323486	C05278	Hs.299221	ESTs; Moderately similar to [PYRUVATE DE	8.5
45	323496	AI826801	Hs.300700	ESTs	4.5
	323507	H71721	Hs.128387	ESTs	4.4
	323545	AI814405	Hs.224569	ESTs	5.8
	323623	AA314280	Hs.146589	EST cluster (not in UniGene)	5
	323663	AW283526	Hs.243023	ESTs	7.7
	323691	AA317561	Hs.145599	EST cluster (not in UniGene)	5.9
50	323810	AA740405	Hs.108806	ESTs	6.2
	323846	AA337621	Hs.137635	ESTs	6
	323929	AA354940	Hs.145958	ESTs	10.7
	323959	AI636775	Hs.6831	ESTs	5.4
	323996	AA367032	Hs.217882	ESTs	5.8
55	323997	AA844907	Hs.274454	EST cluster (not in UniGene)	4.4
	324019	AW177009		EST cluster (not in UniGene)	4.6
	324130	AL046575	Hs.130198	ESTs	11
	324295	AI146686	Hs.143691	ESTs	13.7
	324296	AI524039	Hs.192524	ESTs	6.8
60	324307	AA627642	Hs.4994	transducer of ERBB2; 2 (TOB2)	4.9
	324330	AA884766		EST cluster (not in UniGene)	4.3
	324385	F28212	Hs.284247	EST cluster (not in UniGene)	4.7
	324430	AA464018	Hs.184598	EST cluster (not in UniGene)	13.6
	324452	AW014022	Hs.170953	ESTs	7.6
65	324547	AW501974	Hs.74170	ESTs	5.6
	324603	AW016378	Hs.292934	ESTs	24.2
	324617	AA508552	Hs.185839	ESTs	54
	324618	AI346282	Hs.87159	ESTs	4.6
	324620	AA448021	Hs.94109	EST cluster (not in UniGene)	5.7

	324626	AI685464	ESTs	9	
	324658	AI694767	Hs.129179 ESTs	22	
	324676	AW503943	Hs.112451 ESTs	4.9	
	324691	AI217963	Hs.293341 ESTs; Weakly similar to Pro-a2(XI) [H.s.a]	10.6	
5	324696	AA641092	Hs.257339 ESTs	10.2	
	324713	AW340249	Hs.163440 ESTs	5.5	
	324715	AI739168	Hs.131798 EST cluster (not in UniGene)	7.2	
	324718	AI557019	Hs.116467 ESTs	34.4	
10	324720	AA578904	Hs.292437 ESTs	4.8	
	324752	AI279919	Hs.272072 ESTs; Moderately similar to !!!! ALU SUB	7.9	
	324753	AA612626	Hs.144871 EST cluster (not in UniGene)	5.2	
	324790	AI334367	Hs.159337 ESTs	7.6	
	324801	AI819924	Hs.14553 ESTs	12.6	
15	324804	AI692552	ESTs	6.5	
	324845	AA361016	Hs.337533 ESTs	4.5	
	324888	AI564134	Hs.136102 KIAA0853 protein	4.4	
	324929	AI741633	Hs.125350 ESTs	6.5	
	324961	AA613792	EST cluster (not in UniGene)	5.1	
20	325108	AA401863	Hs.22380 ESTs	7.1	
	326816		CH.20_hs gjl6552458	9.6	
	326997		CH.21_hs gjl5867660	4.8	
	327098		CH.21_hs gjl6682516	4.3	
	328492		CH.07_hs gjl5868455	5.8	
25	329362		CH.X_hs gjl5868837	4.3	
	329929		CH.16_p2 gjl6165201	5.5	
	329960		CH.16_p2 gjl5091594	7.6	
	330020		CH.16_p2 gjl6671887	6	
	330211		CH.05_p2 gjl6013592	12.6	
30	330384	M23263	androgen receptor (dihydrotestosterone r	9	
	330430	HG2261-HT2352	Hs.321110	Antigen, Prostate Specific, All. Splice	13.8
	330546	U31382	Hs.299867 guanine nucleotide binding protein 4	6	
	330551	U39840	hepatocyte nuclear factor 3; alpha	4.9	
	330658	AA319514	Hs.30732 ESTs	6	
35	330700	AA037415	Hs.20999 ESTs	5.5	
	330704	AA056557	Hs.6759 ESTs	5.1	
	330705	AA102571	Hs.157078 ESTs	11.7	
	330706	AA121140	Hs.177576 ESTs; Moderately similar to kynurenine a	14.5	
	330712	AA167269	Hs.52620 ESTs	5	
40	330725	AA252033	Hs.24052 ESTs; Weakly similar to !!!! ALU SUBFAM1	7.2	
	330732	AA281092	Hs.35254 ESTs	4.9	
	330762	AA449677	Hs.15251 Human DNA sequence from clone 437M21 on	18.5	
	330763	AA450200	Hs.143187 FK506-binding protein 3 (25kD)	4.3	
	330772	AA479114	Hs.11356 ESTs	5.8	
45	330786	D60374	EST	4.6	
	330892	AA149579	Hs.91202 ESTs	15.3	
	330949	H01458	Hs.142896 ESTs	10.3	
	330977	H20826	Hs.315181 ESTs	4.4	
	331017	N24619	Hs.108920 ESTs	11.8	
50	331099	R36671	Hs.14846 ESTs	11.6	
	331128	R51361	Hs.268714 ESTs	4.8	
	331151	R82331	Hs.268838 ESTs	13	
	331195	T64447	Hs.168439 ESTs	4.9	
	331320	AA262999	Hs.300141 ESTs	4.8	
55	331321	AA278355	Hs.87929 ESTs	6.1	
	331337	AA287662	Hs.118630 ESTs	9.2	
	331348	AA400596	Hs.88143 ESTs	9.9	
	331359	AA416979	Hs.81897 ESTs	4.3	
	331383	AA454543	Hs.43543 ESTs	4.6	
60	331422	F10802	Hs.237339 ESTs; Moderately similar to !!!! ALU SUB	4.9	
	331442	H77381	Hs.41223 ESTs	7.5	
	331466	N21680	Hs.43455 ESTs	5.4	
	331479	N27154	Hs.44076 ESTs	6.5	
	331490	N32912	Hs.291039 ESTs; Weakly similar to hypothetical 43.	12.5	
65	331493	N34357	Hs.93817 ESTs	4.6	
	331561	N62780	Hs.48703 ESTs	9.2	
	331615	N92352	Hs.5472 ESTs	4.6	
	331659	W48868	Hs.334305 ESTs	8.7	
	331698	Z38907	Hs.65949 KIAA0888 protein	10.3	
	331811	AA404500	Hs.187958 ESTs	4.8	

	331848	AA417039	Hs.98268	signal recognition particle 72kD	7.5
	331873	AA429445	Hs.98640	ESTs	6.5
	331889	AA431407	Hs.98802	Homo sapiens Chromosome 16 BAC clone CTT	33.6
5	331967	AA460158	Hs.99589	KIAA1028 protein	6.8
	331974	AA464518	Hs.105322	ESTs	5.3
	332043	AA490831	Hs.201591	ESTs	10.8
	332076	AA599477	Hs.291156	ESTs	4.4
	332173	F09281	Hs.100725	ESTs	5.5
10	332247	N58172		ESTs	14.2
	332249	N62096	Hs.194140	ESTs	7.2
	332325	T79428	Hs.339667	ESTs	5.6
	332396	AA340504		ESTs; Weakly similar to similar to human	21.2
	332434	N75542	Hs.237731	transcription factor 4	15.3
15	332493	N95495	Hs.56729	ESTs; Highly similar to GTP-binding prot	7.1
	332522	L38503	Hs.178357	glutathione S-transferase theta 2	6.6
	332526	AA281753	Hs.17731	inositol 1;4;5-triphosphate receptor; ty	5.8
	332530	M31682	Hs.19280	inhibin; beta B (activin AB beta polypep	5.5
	332533	M99487	Hs.325825	folate hydrolase (prostate-specific memb	38.1
20	332538	N48715	Hs.20991	ESTs	6.5
	332546	D84454	Hs.22587	solute carrier family 35 (UDP-galactose	4.8
	332594	AA279313	Hs.32951	methyl CpG binding protein 2	5.6
	332610	AA412405	Hs.40513	ESTs; Weakly similar to BETA GALACTOSIDA	5.6
	332661	N95742	Hs.6390	ESTs	6.9
25	332697	T94885	Hs.75725	carboxypeptidase E	24.3
	332712	D26070	Hs.79306	inositol 1;4;5-triphosphate receptor; ty	9.9
	332716	L00058	Hs.79630	v-myc avian myelocytomatosis viral oncog	5.6
	332726	R72029	Hs.83428	synaptophysin-like protein	5
	332781	AA233258		ESTs; Weakly similar to D1007.5 [C.elega	4.5
30	332797			CH22_FGENES.6_2	30.8
	332798			CH22_FGENES.6_5	66.8
	332799			CH22_FGENES.6_6	19.8
	332933			CH22_FGENES.38_7	5.6
	332980			CH22_FGENES.54_1	5.5
35	332984			CH22_FGENES.54_6	4.9
	333168			CH22_FGENES.94_1	4.7
	333169			CH22_FGENES.94_2	4.4
	333452			CH22_FGENES.157_1	4.8
	333456			CH22_FGENES.157_5	4.3
	333458			CH22_FGENES.157_7	4.6
40	333611			CH22_FGENES.217_6	4.7
	333621			CH22_FGENES.219_5	5.5
	333814			CH22_FGENES.282_2	7.1
	333849			CH22_FGENES.290_8	6.2
	333949			CH22_FGENES.303_5	4.3
45	333951			CH22_FGENES.303_7	4.9
	333955			CH22_FGENES.303_11	5.6
	334150			CH22_FGENES.339_1	5.1
	334223			CH22_FGENES.360_4	20.3
	334297			CH22_FGENES.372_3	9.4
50	334443			CH22_FGENES.387_2	4.6
	334444			CH22_FGENES.387_4	5.6
	334447			CH22_FGENES.387_7	13.1
	334570			CH22_FGENES.405_11	5.4
	334749			CH22_FGENES.427_1	5.3
55	334777			CH22_FGENES.430_9	4.7
	334960			CH22_FGENES.465_29	5.2
	335179			CH22_FGENES.504_9	8.8
	335293			CH22_FGENES.527_6	4.7
	335550			CH22_FGENES.576_11	5.1
60	335581			CH22_FGENES.581_19	5.7
	335586			CH22_FGENES.581_25	4.3
	335809			CH22_FGENES.617_6	6.2
	335810			CH22_FGENES.617_7	5.8
	335822			CH22_FGENES.619_7	7.1
65	335824			CH22_FGENES.619_11	8.5
	335853			CH22_FGENES.626_5	4.3
	335886			CH22_FGENES.632_4	4.3
	336034			CH22_FGENES.678_5	6.8
	336441			CH22_FGENES.827_7	7.6

	336624	CH22_FGENES.6-3	43.3
	336625	CH22_FGENES.6-4	37.9
	336679	CH22_FGENES.43-7	5.3
	337577	CH22_C65E1.GENSCAN.8-1	4.9
5	338255	CH22_EM:AC005500.GENSCAN.276-3	13.4
	338260	CH22_EM:AC005500.GENSCAN.279-10	4.6
	338561	CH22_EM:AC005500.GENSCAN.421-5	4.6
	338562	CH22_EM:AC005500.GENSCAN.421-6	4.3
	338759	CH22_EM:AC005500.GENSCAN.517-6	5.1
10	338763	CH22_EM:AC005500.GENSCAN.517-16	5.5
	338764	CH22_EM:AC005500.GENSCAN.517-17	7.1

TABLE 3A shows the accession numbers for those primekeys lacking unigeneID's for Table 3. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
15	Pkey	CAT number
		Accession
	123619	371681_1
	116722	143512_1
	103677	41847_1
20	125992	1589048_1
	109342	genbank_AA213620
	125154	genbank_W38419
	101447	entrez_M21305
	124357	genbank_N22401
25	108910	genbank_AA136590
	322278	47271_1
	315084	350959_1
	324019	262792_1
	324330	300543_1
30	324626	336411_1
	303029	37699_1
	324804	398093_1
	324961	376239_1
	329362	c_x_hs
35	336624	CH22_4071FG_6_3_
	336625	CH22_4072FG_6_4_
	336679	CH22_4157FG_43_7_
	338255	CH22_6856FG_LINK_EM:AC00
	338260	CH22_6863FG_LINK_EM:AC00
40	329929	c16_p2
	329960	c16_p2
	338561	CH22_7294FG_LINK_EM:AC00
	338562	CH22_7295FG_LINK_EM:AC00
	338759	CH22_7581FG_LINK_EM:AC00
45	338763	CH22_7585FG_LINK_EM:AC00
	338764	CH22_7586FG_LINK_EM:AC00
	333168	CH22_400FG_94_1_LINK_EM:A
	333169	CH22_401FG_94_2_LINK_EM:A
	333452	CH22_702FG_157_1_LINK_EM:
50	333456	CH22_706FG_157_5_LINK_EM:
	333458	CH22_708FG_157_7_LINK_EM:
	333611	CH22_872FG_217_6_LINK_EM:
	333621	CH22_882FG_219_5_LINK_EM:
	333814	CH22_1083FG_282_2_LINK_EM
55	333849	CH22_1118FG_290_8_LINK_EM
	335179	CH22_2515FG_504_9_LINK_EM
	333949	CH22_1225FG_303_5_LINK_EM
	333951	CH22_1227FG_303_7_LINK_EM
	333955	CH22_1231FG_303_11_LINK_E
60	335293	CH22_2635FG_527_6_LINK_EM
	326816	c20_hs
	326897	c21_hs
	335550	CH22_2905FG_576_11_LINK_E
	335581	CH22_2938FG_581_19_LINK_E
65	335586	CH22_2944FG_581_25_LINK_E

	328492	c_7_hs	
	335809	CH22_3181FG_617_6_LINK_EM	
	335810	CH22_3182FG_617_7_LINK_EM	
5	335822	CH22_3195FG_619_7_LINK_EM	
	335824	CH22_3197FG_619_11_LINK_E	
	335853	CH22_3228FG_626_5_LINK_EM	
	335886	CH22_3261FG_632_4_LINK_EM	
	330020	c16_p2	
	330211	c_5_p2	
10	337577	CH22_5864FG_LINK_C65E1.G	
	307848	AI364186	
	332797	CH22_13FG_6_2_LINK_C4G1.G	
	332798	CH22_14FG_6_5_LINK_C4G1.G	
	332799	CH22_15FG_6_6_LINK_C4G1.G	
15	334150	CH22_1429FG_339_1_LINK_EM	
	332933	CH22_154FG_38_7_LINK_C20H	
	332980	CH22_204FG_54_1_LINK_EM:A	
	332984	CH22_208FG_54_6_LINK_EM:A	
	334223	CH22_1507FG_360_4_LINK_EM	
20	334297	CH22_1588FG_372_3_LINK_EM	
	327098	c21_hs	
	334443	CH22_1742FG_387_2_LINK_EM	
	334444	CH22_1743FG_387_4_LINK_EM	
	334447	CH22_1746FG_387_7_LINK_EM	
25	334570	CH22_1875FG_405_11_LINK_E	
	334749	CH22_2061FG_427_1_LINK_EM	
	334777	CH22_2089FG_430_9_LINK_EM	
	336034	CH22_3418FG_678_5_LINK_DJ	
	334960	CH22_2281FG_465_29_LINK_E	
30	336441	CH22_3861FG_827_7_LINK_DJ	
	330551	9851_2	U39840 NM_004496 AW135607 BE087458 BE087567 AA177116 AW195705 AW750756 AI811008 AI694151 BE348594 AW971075 AI347950 AI201455 AI073898 AA652680 AA613671 AI318364 AA507550 AA693692 AI032599 AA991871 AI269801 AW948974 T74639 AA532907 AW949173 BE379594 AI192455 AL039862 AI744012 AI761735 AW243181 AI743687 AI928223 AI423022 AI627855 AI636059 AI651571 AW802044 AI826995 AI431733 AI539125 AA863056 AW270910 AI768930 AW008835 AW615183 AW591147 AI695294 AI672106 AA506358 AI308060 AA011556 AA962437 AI935488 BE219625 AI004356 AW151394 AI218466 N66178 AI419784 AW242519 AW946907 D60374 AA989263 AI698799 AA470460 AI824167 AA669097 AA513815 AA026798 AA676526 AA704429 AA704269 AW118292 AA579216 N58172 AW579842 BE156562 BE156690 BE156489 BE081033 AK001559 BE149402 M85387 AW367811 AW367798 R17370 AI908947 AA382932 R58449 H18732 AA371231 AW962899 AA713530 AW892946 R53463 H11063 AW068542 Z40761 BE176212 BE176155 W23952 W92188 AW374883 AA303497 AW954769 AA036808 BE168053 AW382073 AW382085 AL041475 H80748 AI078161 BE463983 AI805213 AI761264 W94885 N94502 AI623772 AI419532 AI810302 AI634190 AW002516 AW150777 AI352312 AI367474 AW204807 AI675502 AI337028 AW134715 BE328451 AI123157 AI560020 AI300745 AI608631 AI248873 AA742484 AW051635 H18646 AI245045 AA507111 AI640510 AI925594 AA115747 AA143035 AA151106 AK001764 BE313896 AA380199 AA380151 AA194996 AW118089 AA495871 AW975219 AW085598 AI378909 AW992310 AW992409 AI911857 AA657643 AI804471 AI242589 AI623968 R09556 AI129100 AI206500 AA680094 AA677784 AI023178 AI277519 AA424742 AI240654 AA232846 AI804273 AI382376 AA001729 W90790 BE090656 AW295015 AI674596 AI431734 AI420517 AW769185 AI128355 AI192474 AI820001 AA001929 AA706925 AI076676 AI499119 AI200493 AI695919 AI376217 W69195 W69261 AW305099 W90320 BE048357 AI658856 AA838534 AA233258 AI753393 AA709227 AI674387 AI872616
35	330786	53973_3	
40	332247	372969_1	
	332396	20265_1	
45			
	332781	32044_1	
50			

TABLE 3B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 3. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

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10 Pkey: Unique number corresponding to an Eos probaset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
15	333611	Dunham, I. et al.	Plus	6548368-6548507
	333621	Dunham, I. et al.	Plus	8597414-8597560
	333814	Dunham, I. et al.	Plus	7894165-7894252
	333849	Dunham, I. et al.	Plus	8018323-8018472
20	333949	Dunham, I. et al.	Plus	8589634-8589791
	333951	Dunham, I. et al.	Plus	8592501-8592637
	333955	Dunham, I. et al.	Plus	8597414-8597560
	334150	Dunham, I. et al.	Plus	10529221-10529854
	334297	Dunham, I. et al.	Plus	13420934-13421058
25	334443	Dunham, I. et al.	Plus	14298981-14299056
	334444	Dunham, I. et al.	Plus	14306433-14306492
	334447	Dunham, I. et al.	Plus	14308764-14308824
	334570	Dunham, I. et al.	Plus	14994868-14994943
	334777	Dunham, I. et al.	Plus	16259586-16260166
30	335179	Dunham, I. et al.	Plus	21634405-21634526
	335581	Dunham, I. et al.	Plus	24976198-24976334
	335586	Dunham, I. et al.	Plus	24990333-24990497
	335809	Dunham, I. et al.	Plus	26310772-26310909
	335810	Dunham, I. et al.	Plus	26314767-26314849
35	335822	Dunham, I. et al.	Plus	26364087-26364196
	335824	Dunham, I. et al.	Plus	26376860-26376942
	335886	Dunham, I. et al.	Plus	26934235-26934364
	336034	Dunham, I. et al.	Plus	28014404-28014590
	336441	Dunham, I. et al.	Plus	34187606-34187663
40	337577	Dunham, I. et al.	Plus	595377-595678
	338260	Dunham, I. et al.	Plus	15458919-15459257
	332797	Dunham, I. et al.	Minus	216964-216798
	332798	Dunham, I. et al.	Minus	232147-231974
	332799	Dunham, I. et al.	Minus	232421-232307
45	332933	Dunham, I. et al.	Minus	2035790-2035681
	332980	Dunham, I. et al.	Minus	5136165-5136019
	332984	Dunham, I. et al.	Minus	2632606-2632457
	333168	Dunham, I. et al.	Minus	3729896-3729788
	333169	Dunham, I. et al.	Minus	3730864-3730767
50	333452	Dunham, I. et al.	Minus	5136165-5136019
	333456	Dunham, I. et al.	Minus	2631933-2631797
	333458	Dunham, I. et al.	Minus	5143942-5143806
	334223	Dunham, I. et al.	Minus	12734365-12734269
	334749	Dunham, I. et al.	Minus	16090686-16090106
55	334960	Dunham, I. et al.	Minus	20160968-20160795
	335293	Dunham, I. et al.	Minus	22316408-22316275
	335550	Dunham, I. et al.	Minus	24668714-24668658
	335853	Dunham, I. et al.	Minus	26614629-26614506
	336624	Dunham, I. et al.	Minus	227714-227577
60	336625	Dunham, I. et al.	Minus	229124-229024
	336679	Dunham, I. et al.	Minus	2035790-2035681
	338255	Dunham, I. et al.	Minus	15242294-15242231
	338561	Dunham, I. et al.	Minus	22311866-22311856
	338562	Dunham, I. et al.	Minus	22312594-22312465
65	338759	Dunham, I. et al.	Minus	26582475-26582199
	338763	Dunham, I. et al.	Minus	26628148-26628009
	338764	Dunham, I. et al.	Minus	26641232-26641101

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329960	5091594	Minus	1031-1162
329929	6165201	Minus	156410-156553
330020	6671887	Plus	172397-172491
326816	6552458	Plus	198354-198436
326997	5867660	Minus	71389-72147
327098	6682516	Minus	1061684-1062361
330211	6013592	Plus	59158-59215
328492	5868455	Minus	46094-46241
329362	5868837	Minus	65688-68173

TABLE 4: shows a preferred subset of the Accession numbers for genes found in Table 3 which are differentially expressed in prostate tumor tissue compared to normal prostate tissue.

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
10	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal body tissue			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	100819	HG4020-HT4290Hs.2387		Transglutaminase	10.5
	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	10.6
	102669	X02544	Hs.572	orosomucoid 1	22.6
20	105370	AA236476	Hs.22791	ESTs; Weakly similar to transmembrane pr	10.3
	105645	AA282138	Hs.11325	ESTs	14
	106094	AA419461	Hs.23317	ESTs	10.9
	109014	AA156790	Hs.262036	ESTs	15.3
	109562	F01811	Hs.187931	ESTs; Moderately similar to voltage-gate	10.8
	113021	T23855	Hs.129836	KIAA1028 protein	10.8
25	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 protein	21.3
	122791	AA460158	Hs.129836	KIAA1028 protein	12.4
	124352	N21626	Hs.102406	ESTs	10.2
	301042	AI659131	Hs.197733	ESTs	24.9
	302005	AI869666	Hs.123119	ESTs	36.8
30	302410	NM_004917	Hs.218366	EST cluster (not in UniGene) with exon h	26.8
	302881	AA508353	Hs.105314	relaxin 1 (H1)	78.8
	303344	AA255977	Hs.250646	ESTs; Highly similar to ubiquitin-conjug	19.5
	303753	AW503733	Hs.9414	ESTs	13
	310431	AI420227	Hs.149358	ESTs	72.9
35	311251	AI655662	Hs.197698	ESTs	41.3
	311596	AI682088	Hs.79375	ESTs	26.4
	312153	AA759250	Hs.118625	cytochrome b-561	11
	312521	AA033609	Hs.239884	ESTs	11.2
	313676	AA861697	Hs.120591	EST cluster (not in UniGene)	13.4
40	314171	AI821895	Hs.193481	ESTs	29.4
	314907	AI672225	Hs.222886	ESTs	19.3
	315051	AW292425	Hs.163484	EST	15.5
	315052	AA876910	Hs.134427	ESTs	20
	317548	AI654187	Hs.195704	ESTs	14.2
45	317869	AW295184	Hs.129142	ESTs; Weakly similar to DEOXYRIBONUCLEAS	13.8
	318428	AI949409	Hs.194591	ESTs	12.3
	318524	AW291511	Hs.159066	ESTs	25.9
	319080	Z45131	Hs.23023	ESTs	16.9
	319763	AA460775	Hs.6295	ESTs	14.3
50	320324	AF071202	Hs.139336	ATP-binding cassette; sub-family C (CFTR	56.2
	321441	AW297633	Hs.118498	ESTs	14.7
	322303	W07459	Hs.157601	EST cluster (not in UniGene)	22
	322782	AA056060	Hs.202577	EST cluster (not in UniGene)	18.4
	322818	AW043782	Hs.293616	ESTs	10.7
55	323287	AA639902	Hs.104215	ESTs	24.7
	324603	AW016378	Hs.292934	ESTs	24.2
	324617	AA508552	Hs.195839	ESTs	54
	324658	AI694767	Hs.129179	ESTs	22
	324691	AI217963	Hs.293341	ESTs; Weakly similar to Pro-a2(XI) [H.sa	10.6
60	324696	AA641092	Hs.257339	ESTs	10.2
	324718	AI557019	Hs.116467	ESTs	34.4
	330211			CH.05_p2 gi16013592	12.6
	330430	HG2261-HT2352	Hs.321110	Antigen, Prostate Specific, Alt. Splice	13.8
	330706	AA121140	Hs.177576	ESTs; Moderately similar to kynurenine a	14.5
65	330762	AA449677	Hs.15251	Human DNA sequence from clone 437M21 on	18.5
	330892	AA149579	Hs.91202	ESTs	15.3
	330949	H01458	Hs.142896	ESTs	10.3

	331099	R36671	Hs.14846	ESTs	11.6
	331151	R82331	Hs.268838	ESTs	13
	331889	AA431407	Hs.98802	Homo sapiens Chromosome 16 BAC clone CIT	33.6
5	332247	N58172		ESTs	14.2
	332396	AA340504		ESTs; Weakly similar to similar to human	21.2
	332533	M99487	Hs.325825	folate hydrolase (prostate-specific memb	38.1
	332697	T94885	Hs.75725	carboxypeptidase E	24.3
	332797			CH22_FGENES.6_2	30.8
	332798			CH22_FGENES.6_5	66.8
10	332799			CH22_FGENES.6_6	19.8
	334223			CH22_FGENES.360_4	20.3
	336624			CH22_FGENES.6-3	43.3
	336625			CH22_FGENES.6-4	37.9

TABLE 4A shows the accession numbers for those primekeys lacking unigeneID's for Table 4. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
15	Pkey	CAT number	Accession
	336624	CH22_4071FG_6_3_	
	336625	CH22_4072FG_6_4_	
	330211	c_5_p2	
20	332797	CH22_13FG_6_2_LINK_C4G1.G	
	332798	CH22_14FG_6_5_LINK_C4G1.G	
	332799	CH22_15FG_6_6_LINK_C4G1.G	
	334223	CH22_1507FG_360_4_LINK_EM	
25	332247	372969_1	AA669097 AA513815 AA026798 AA676526 AA704429 AA704269 AW118292 AA579216 N58172
	332396	20265_1	AW579842 BE156562 BE156690 BE156489 BE081033 AK001559 BE149402 M85387 AW367811
			AW367798 R17370 AI908947 AA382932 R58449 H18732 AA371231 AW962899 AA713530 AW892946
			R53463 H11063 AW068542 Z40761 BE176212 BE176155 W23952 W92188 AW374883 AA303497
			AW954769 AA036808 BE168063 AW382073 AW382085 AL041475 H80748 AI078161 BE463983
30			AI805213 AI761264 W94885 N94502 AI623772 AI419532 AI810302 AI634190 AW002516 AW150777
			AI352312 AI367474 AW204807 AI675502 AI337026 AW134715 BE328451 AI123157 AI560020
			AI300745 AI608631 AI248873 AA742484 AW051635 H18646 AI245045 AA507111 AI640510 AI925594
			AA115747 AA143035 AA151106

5 **TABLE 4B** shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 4. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

15	Pkey	Ref	Strand	NL_position
	332797	Dunham, I. et al.	Minus	216964-216798
	332798	Dunham, I. et al.	Minus	232147-231974
	332799	Dunham, I. et al.	Minus	232421-232307
20	334223	Dunham, I. et al.	Minus	12734365-12734269
	336624	Dunham, I. et al.	Minus	227714-227577
	336625	Dunham, I. et al.	Minus	229124-229024
	330211	6013592	Plus	59158-59215

TABLE 5: 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

5 Table 5 shows 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.44. The "average" prostate cancer level was set to the 85th percentile amongst 73 prostate cancers. The "average" normal adult tissue level was set to the 85th percentile
10 amongst 162 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst the 162 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

15	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal tissue			
20	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	86.42
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	66.46
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	58.36
25	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	56.16
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	53.38
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	48.28
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	45.24
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.48
30	420154	AI093155	Hs.95420	JM27 protein	41.12
	433466	AA508353	Hs.105314	relaxin 1 (H1)	39.88
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	38.42
	400292	AA250737	Hs.72472	ESTs	38.00
	432887	AI926047	Hs.162859	ESTs	36.48
35	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	36.45
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	33.20
	437052	AA861697	Hs.120591	ESTs	33.02
	418396	AI765805	Hs.26691	ESTs	32.68
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	32.44
40	407709	AA456135	Hs.23023	ESTs	32.10
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	31.80
	407168	FA5175		ESTs	31.72
	440260	AI972867	Hs.7130	copine IV	30.52
	421513	X00949	Hs.105314	relaxin 1 (H1)	30.10
45	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	29.68
	407122	H20276	Hs.31742	ESTs	29.24
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.90
	432244	AI669973	Hs.200574	ESTs	28.74
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	28.74
50	415989	AI267700	Hs.111128	ESTs	28.34
	418961	AW967646	Hs.23023	ESTs	27.34
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	27.32
	458509	AA654650	Hs.282906	ESTs	27.24
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	27.16
55	428336	AA503115	Hs.183752	microseminoprotein, beta-	26.17
	450096	AI682088	Hs.223368	holocarboxylase synthetase (biotin-prop	25.60
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	24.91
	437571	AA760894	Hs.153023	ESTs	24.74
	453160	AI263307	Hs.146228	H2B histone family, member L	24.66
60	453096	AW294631	Hs.11325	ESTs	24.46
	425075	AA506324	Hs.1852	acid phosphatase, prostate	24.23
	407202	N58172	Hs.109370	ESTs	24.18

	424846	AU077324	Hs.1832	neuropeptide Y	23.57
	453370	AI470523	Hs.182356	ATP-binding cassette, sub-family C (CFTR	23.16
	422805	AA436989	Hs.121017	H2A histone family, member A	22.52
5	444917	R68651	Hs.144997	ESTs	22.26
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	22.02
	413597	AW302885	Hs.117183	ESTs	21.76
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	21.32
	435981	H74319	Hs.188620	ESTs	21.12
10	432966	AA650114		ESTs	21.07
	418848	AI820961	Hs.193465	ESTs	21.06
	405685				20.90
	443271	BE568568	Hs.195704	ESTs	19.98
	418819	AA228776	Hs.191721	ESTs	19.94
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	19.72
15	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	19.56
	429918	AW873986	Hs.119383	ESTs	19.04
	415539	AI733881	Hs.72472	ESTs	18.43
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	18.34
20	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	18.28
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	17.82
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	17.66
	431676	AI685464	Hs.292638	gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	17.64
	410330	AW023630	Hs.46786	ESTs	17.52
	432441	AW292425	Hs.163484	ESTs	17.41
25	452792	AB037765	Hs.30652	KIAA1344 protein	17.39
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	17.00
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	16.82
	430487	D87742	Hs.241552	KIAA0268 protein	16.72
30	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	16.60
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	16.50
	439677	R82331	Hs.164599	ESTs	16.46
	449625	NM_014253	Hs.23796	odx (odd Oz/ten-m, Drosophila) homolog 1	16.32
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	16.28
35	447033	AI357412	Hs.157601	ESTs	16.02
	453006	AI362575	Hs.167133	ESTs	15.74
	431474	AL133990	Hs.190642	ESTs	15.70
	420218	AW958037	Hs.22437	ribosomal protein L4	15.64
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.54
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	15.48
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	15.40
	415263	AA948033	Hs.130853	ESTs	15.38
	432437	W07088	Hs.293585	ESTs	15.26
	428398	AI249368	Hs.98558	ESTs	15.21
	429900	AA460421	Hs.30875	ESTs	14.90
45	449156	AF103907	Hs.171353	prostate cancer antigen 3	14.89
	411086	U80034	Hs.68583	mitochondrial intermediate peptidase	14.81
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	14.76
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	14.76
50	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	14.60
	418601	AA279490	Hs.86368	calmegin	14.56
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	14.55
	445885	AI734009	Hs.127699	KIAA1603 protein	14.44
	452712	AW838616		gb:RCS-LT0054-140200-013-D01 LT0054 Homo	14.22
55	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	14.12
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	13.78
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	13.57
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	13.40
	416445	AL043004	Hs.300678	KIAA0135 protein	13.32
60	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U4 Homo sapiens	13.24
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	13.21
	446720	AI439136	Hs.140546	ESTs	13.06
	434988	AI418055	Hs.161160	ESTs	13.02
	448172	N75276	Hs.135904	ESTs	12.98
65	416182	NM_004354	Hs.79069	cyclin G2	12.94
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	12.79
	445413	AA151342	Hs.12677	CGI-147 protein	12.64
	452588	AA889120	Hs.110637	homeo box A10	12.62
	407819	R42185	Hs.274803	ESTs	12.60
	433444	AW975324	Hs.129816	ESTs	12.60

	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.30
	420077	AW512260	Hs.87767	ESTs	12.24
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	12.22
5	441610	AW576148	Hs.148376	ESTs	12.20
	451009	AA013140	Hs.115707	ESTs	12.18
	433764	AW753676	Hs.39982	ESTs	12.16
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	12.04
	443912	R37257	Hs.184780	ESTs	11.92
	419526	AI821895	Hs.193481	ESTs	11.91
10	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	11.87
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.86
	414422	AA147224	Hs.71814	ESTs	11.76
	450203	AF097994	Hs.301528	L-kynurenin/alpha-aminoadipate aminotra	11.68
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.60
15	440901	AA909358	Hs.128612	ESTs	11.60
	448045	AJ297436	Hs.20166	prostate stem cell antigen	11.51
	433887	AW204232	Hs.279522	ESTs	11.50
	434980	AW770553	Hs.293640	sterol O-acyltransferase (acyl-Coenzyme	11.38
	425905	AB032959	Hs.161700	novel C3HC4 type Zinc finger (ring finger)	11.33
20	434680	T11738	Hs.127574	ESTs	11.32
	449650	AF055575	Hs.297647	calcium channel, voltage-dependent, L type	11.18
	431173	AW971198	Hs.294068	ESTs	11.16
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	11.16
	410037	AB020725	Hs.58009	KIAA0918 protein	11.14
25	417708	N74392	Hs.50495	ESTs	11.14
	458332	AI000341	Hs.220491	ESTs	11.12
	420381	D50640	Hs.301782	phosphodiesterase 3B, cGMP-inhibited	11.10
	425665	AK001050	Hs.159066	hypothetical protein FLJ10188	11.08
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.08
30	428728	NM_016625	Hs.191381	hypothetical protein	11.04
	407021	U52077		gb.Human mariner1 transposase gene, comp	11.02
	410733	D84284	Hs.66052	CD38 antigen (p45)	11.02
	401714				10.90
	434485	AI623511	Hs.118567	ESTs	10.89
35	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	10.87
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	10.85
	453628	AW243307	Hs.170187	hypothetical protein	10.72
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	10.67
	417687	AI828596	Hs.250691	ESTs	10.64
40	434666	AF151103	Hs.112259	T cell receptor gamma locus	10.53
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	10.50
	428819	AL135623	Hs.193914	KIAA0575 gene product	10.48
	413409	AI638418	Hs.21745	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	10.44
	428775	AA434579	Hs.143691	ESTs	10.21
45	436556	AI364997	Hs.7572	ESTs	10.20
	441690	R81733	Hs.33106	ESTs	10.14
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	10.10
	421991	NM_014918	Hs.110488	KIAA0990 protein	10.04
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	10.02
50	452039	AI922988	Hs.172510	ESTs	10.00
	433043	W57554	Hs.125019	ESTs	9.98
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.97
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	9.96
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	9.88
55	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	9.84
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	9.82
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	9.75
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	9.70
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	9.70
60	421470	R27496	Hs.1378	annexin A3	9.64
	406554				9.60
	401424				9.58
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	9.56
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	9.54
65	439024	R96696	Hs.35598	ESTs	9.51
	431548	AI834273	Hs.9711	novel protein	9.48
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	9.45
	446271	D82484	Hs.100469	ESTs	9.42
	448692	AW013907	Hs.224276	methylcrotonoyl-Coenzyme A carboxylase 2	9.26

	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	9.24
	435980	AF274571	Hs.129142	deoxyribonuclease II beta	9.24
	421246	AW582962	Hs.300961	CGI-47 protein	9.20
5	427304	AA761526	Hs.163853	ESTs	9.16
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	9.16
	413627	BE182082	Hs.246973	ESTs	9.14
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	9.10
	437718	AI927288	Hs.196779	ESTs	9.07
10	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	9.06
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.05
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	9.04
	410001	AB041036	Hs.57771	kallikrein 11	9.03
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	9.03
15	441791	AW372449	Hs.175982	hypothetical protein FLJ21159	9.02
	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	9.02
	414269	AA298489		olfactory receptor, family 51, subfamily	8.99
	442081	AA401863	Hs.22380	ESTs	8.98
	420092	AA814043	Hs.88045	ESTs	8.85
20	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	8.80
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	8.80
	454141	AW138413	Hs.182356	ATP-binding cassette, sub-family C (CFTR	8.80
	418278	AI088489	Hs.83937	hypothetical protein	8.78
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.76
25	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	8.75
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	8.74
	415245	N59650	Hs.27252	ESTs	8.72
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	8.70
	404571				8.66
30	418033	W68180	Hs.259855	elongation factor-2 kinase	8.64
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	8.56
	405876				8.54
	448807	AI571940	Hs.7549	ESTs	8.52
	445372	N36417	Hs.144928	ESTs	8.48
35	425171	AW732240	Hs.300615	ESTs	8.44
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	8.36
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	8.31
	433172	AB037841	Hs.102652	hypothetical protein ASH1	8.30
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	8.27
40	412719	AW016610	Hs.129911	ESTs	8.24
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	8.22
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.22
	427674	NM_003528	Hs.2178	H2B histone family, member Q	8.20
	432101	AI918950	Hs.11092	EphA3	8.17
45	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	8.15
	404915				8.08
	440106	AA864968	Hs.127699	KIAA1603 protein	8.07
	442861	AA243837	Hs.57787	ESTs	8.06
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	8.06
50	443250	AI041530	Hs.132107	ESTs	8.06
	437267	AW511443	Hs.258110	ESTs	8.04
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILI	8.02
	422219	AW978073		regulator of mitotic spindle assembly 1	8.00
	453049	BE537217	Hs.30343	ESTs	8.00
55	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	7.98
	408554	AA836381	Hs.7323	nuclear receptor co-repressor/HDAC3 comp	7.94
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	7.94
	430107	AA465293	Hs.105069	ESTs	7.94
	433404	T32982	Hs.102720	ESTs	7.93
60	450813	AI739625	Hs.203376	ESTs	7.90
	416239	AL038450	Hs.48948	ESTs	7.85
	448212	AI475858		gb:tc87d07.x1 NCLCGAP_CLL1 Homo sapiens	7.82
	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	7.82
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	7.80
	458191	AI420611	Hs.127832	ESTs	7.80
65	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	7.78
	457498	AI732230	Hs.191737	ESTs	7.78
	407225	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	7.76
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	7.74
	433805	AA706910	Hs.112742	ESTs	7.74

	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-	7.72
	446028	R44714	Hs.106795	Homo sapiens cDNA FLJ13136 fis, clone NT	7.72
	418555	AJ417215	Hs.87159	hypothetical protein FLJ12577	7.70
5	447499	AW262580	Hs.147674	protocadherin beta 16	7.70
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	7.68
	416857	AA188775	Hs.292453	ESTs	7.68
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	7.66
	425480	AB023198	Hs.158135	KIAA0981 protein	7.66
10	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.64
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.64
	446307	T50083	Hs.9094	ESTs	7.63
	429220	AW207206	Hs.136319	ESTs	7.59
	420345	AW295230	Hs.25231	ESTs	7.54
	429208	AA447990	Hs.190478	ESTs	7.54
15	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	7.53
	440995	T57773	Hs.10263	ESTs	7.53
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.52
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	7.49
20	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	7.46
	434217	AW014795	Hs.23349	ESTs	7.44
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	7.42
	448519	AW175665	Hs.244334	Homo sapiens prostein mRNA, complete cds	7.42
	446791	AI632278	Hs.34981	ESTs	7.40
25	419743	AW408762	Hs.127478	Homo sapiens clone 24416 mRNA sequence	7.39
	445855	BE247129	Hs.145569	ESTs	7.36
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.35
	419131	AA406293	Hs.301622	ESTs	7.34
	400294	N95796	Hs.179809	Homo sapiens prostein mRNA, complete cds	7.33
30	441736	AW292779	Hs.169799	ESTs	7.28
	427701	AA411101	Hs.221750	nuclear autoantigenic sperm protein (his	7.24
	457733	AW974812	Hs.291971	ESTs	7.24
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	7.22
	441201	AW118822	Hs.128757	ESTs	7.21
35	419953	BE267154	Hs.125752	ESTs	7.20
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	7.20
	425018	BE245277	Hs.154196	E4F transcription factor 1	7.20
	424560	AA158727	Hs.150555	protein predicted by clone 23733	7.18
	435380	AA679001	Hs.192221	ESTs	7.14
40	420658	AW965215	Hs.130707	ESTs	7.12
	408291	AB023191	Hs.44131	KIAA0974 protein	7.10
	409110	AA191493	Hs.48778	niban protein	7.10
	414485	W27026	Hs.182625	VAMP (vesicle-associated membrane protei	7.10
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.10
45	450832	AW970602	Hs.105421	ESTs	7.10
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	7.08
	412446	AI768015	Hs.92127	ESTs	7.07
	412953	Z45794	Hs.238809	ESTs	7.06
	418051	AW192535	Hs.19479	ESTs	7.06
50	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.04
	446999	AA151520	Hs.279525	hypothetical protein MGC4485	7.04
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.04
	441111	AI806867	Hs.126594	ESTs	7.01
	451027	AW519204	Hs.40808	ESTs	7.00
55	408432	AW195262	Hs.285336	gb:mn67b05.x1 NCL_CGAP_CML1 Homo sapiens	7.00
	432223	AA333283	Hs.12017	Homo sapiens, clone IMAGE:3460280, mRNA	7.00
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	6.99
	414212	AA138569	Hs.295940	KIAA0187 gene product	6.98
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	6.98
	449685	AW296669	Hs.66095	ESTs	6.97
60	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	6.96
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.94
	449655	AI021987	Hs.59970	ESTs	6.92
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	6.90
65	434163	AW974720	Hs.25206	group XII secreted phospholipase A2	6.89
	415809	Z32789	Hs.46601	ESTs	6.86
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	6.85
	417958	AA767382	Hs.193417	ESTs	6.84
	427408	AA583206	Hs.2156	RAR-related orphan receptor A	6.79
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	6.74

	410718	AI920783	Hs.191435	ESTs	6.74
	432363	AA534489		gb:nl76g11.s1 NCL_CGAP_Co3 Homo sapiens	6.74
	436521	AW203986	Hs.213003	ESTs	6.73
5	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	6.73
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	6.72
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.70
	420714	BE172704	Hs.222746	KIAA1610 protein	6.70
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	6.67
	421896	N62293	Hs.45107	ESTs	6.66
10	411078	AI222020	Hs.182364	CocooCrisp	6.66
	452465	AA610211	Hs.34244	ESTs	6.66
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	6.66
	444618	AV653785	Hs.300171	ELL-RELATED RNA POLYMERASE II, ELONGATIO	6.64
	450164	AI239923	Hs.30098	ESTs	6.63
15	431060	AF039307	Hs.249171	homeo box A11	6.62
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	6.62
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	6.62
	444670	H58373	Hs.37494	hypothetical protein MGC5370	6.62
	444489	AI151010	Hs.157774	ESTs	6.60
20	445685	AW779829	Hs.263436	gb:hn88a05.x1 NCL_CGAP_Kid11 Homo sapien	6.60
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	6.59
	452221	C21322	Hs.11577	hypothetical protein FLJ22242	6.59
	431510	AA580082	Hs.112264	ESTs	6.56
	415874	AF091622	Hs.78893	KIAA0244 protein	6.54
25	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	6.54
	452768	AW069459	Hs.61539	ESTs	6.54
	401451				6.52
	416289	W26333		ESTs	6.52
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	6.51
30	409089	NM_014781	Hs.50421	KIAA0203 gene product	6.50
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	6.50
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.49
	418833	AW974899	Hs.292776	ESTs	6.48
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.46
35	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	6.46
	443058	AW451642	Hs.16732	ESTs	6.46
	418584	AA631143	Hs.179809	Homo sapiens prostein mRNA, complete cds	6.44
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	6.44
	423600	AI633559	Hs.29076	ESTs	6.44
40	404253				6.42
	433610	AA806822	Hs.112547	ESTs	6.42
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.41
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.40
	408608	N79738	Hs.136102	KIAA0853 protein	6.40
45	421452	AI925946	Hs.104530	fetal hypothetical protein	6.40
	433285	AW975944	Hs.237396	ESTs	6.40
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	6.40
	446189	H85224	Hs.214013	ESTs	6.40
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	6.38
50	416467	H57585	Hs.37467	ESTs	6.36
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.34
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	6.34
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	6.32
	425843	BE313280	Hs.159627	death associated protein 3	6.32
55	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	6.32
	428194	AA765603	Hs.180877	H3 histone, family 3B (H3.3B)	6.30
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	439366	AF100143	Hs.6540	fibroblast growth factor 13	6.30
	452789	AW081626	Hs.242561	ESTs	6.30
60	416836	D54745	Hs.80247	cholecystokinin	6.30
	438962	AW377314	Hs.5364	DKFZP564I052 protein	6.29
	433383	AF034837	Hs.192731	double-stranded RNA specific adenosine d	6.29
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	6.26
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.25
65	440293	AI004193	Hs.22123	ESTs	6.24
	453745	AA952989	Hs.63908	hypothetical protein MGC14726	6.24
	426595	AW971980	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	6.24
	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	6.24
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.22

	426320	W47595	Hs.169300	transforming growth factor, beta 2	6.22
	423349	AF010258	Hs.127428	homeo box A9	6.20
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	6.18
	424800	AL035588	Hs.153203	MyoD family inhibitor	6.18
5	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	6.16
	438796	W67821	Hs.109590	genethonin 1	6.16
	425451	AF242769	Hs.157461	mesenchymal stem cell protein DSC54	6.14
	451663	AI872360	Hs.209293	ESTs	6.14
	413623	AA825721	Hs.246973	ESTs	6.12
10	452232	AW020603	Hs.271698	radial spoke protein 3	6.12
	453390	AA862496	Hs.28482	ESTs	6.12
	435542	AA687376	Hs.269533	ESTs	6.12
	420424	AB033036	Hs.97594	KIAA1210 protein	6.11
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	6.10
15	409734	BE161664	Hs.56155	hypothetical protein	6.10
	432686	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fis, clone NT	6.10
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	6.10
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.10
	438849	W28948	Hs.10762	ESTs	6.08
20	452726	AF188527	Hs.61661	ESTs, Weakly similar to AF174605 1 F-box	6.08
	445895	D29954	Hs.13421	KIAA0056 protein	6.08
	440774	AI420611	Hs.127832	ESTs	6.07
	422583	AA410506	Hs.118578	KIAA0874 protein	6.06
	427500	AW970017	Hs.293948	ESTs, Weakly similar to S65657 alpha-1C-	6.04
25	443646	AI085198	Hs.298699	ESTs	6.04
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	6.02
	417845	AL117461	Hs.82719	Homo sapiens mRNA: cDNA DKFZp586F1822 (f	6.02
	430273	AI311127	Hs.125522	ESTs	6.02
	434792	AA649253	Hs.132458	ESTs	6.01
30	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	6.01
	420026	AI831180	Hs.166676	ESTs	6.00
	437782	AI370876	Hs.123163	exportin 1 (CRM1, yeast, homolog)	6.00
	447359	NM_012093	Hs.18268	adenylate kinase 5	6.00
	447713	AI420733	Hs.207083	ESTs	6.00
35	451073	AI758905	Hs.206063	ESTs	6.00
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	6.00
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.97
	441222	AI277237	Hs.44208	hypothetical protein FLJ23153	5.96
	447732	AI758398	Hs.161318	ESTs	5.96
40	437756	AA767537	Hs.197096	ESTs	5.95
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.94
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	5.94
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.93
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	5.92
45	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.92
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	5.91
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	5.91
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	5.91
	450480	X82125	Hs.25040	zinc finger protein 239	5.90
50	408446	AW450669	Hs.45068	hypothetical protein DKFZp434I143	5.88
	421039	NM_003478	Hs.101299	cullin 5	5.88
	451684	AF216751	Hs.26813	CDA14	5.88
	436063	AK000028	Hs.250867	ribosomal protein S24	5.86
	410507	AA355288	Hs.271408	transitional epithelia response protein	5.86
55	420179	N74530	Hs.21168	ESTs	5.84
	453878	AW964440	Hs.19025	DC32	5.84
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	5.83
	435867	AA954229	Hs.114052	ESTs	5.82
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	5.82
60	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA P	5.81
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	5.80
	437980	R50393	Hs.278436	KIAA1474 protein	5.80
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	5.79
	400301	X03635	Hs.1657	estrogen receptor 1	5.78
65	446261	AA313893	Hs.13399	hypothetical protein FLJ12615 similar to	5.78
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.77
	427258	AA400091	Hs.39421	ESTs	5.76
	419108	AA389724	Hs.191264	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.76
	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	5.76

	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	5.75
	434408	AI031771	Hs.132586	ESTs	5.74
	415077	L41607	Hs.934	glucosaminyl (N-acetyl) transferase 2, I	5.74
	432435	BE218886	Hs.282070	ESTs	5.74
5	433313	W20128	Hs.296039	ESTs	5.73
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	5.73
	412991	AW949013		gb:QV4-FT0005-110500-201-e12 FT0005 Homo	5.72
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.72
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.72
10	446867	AB007891	Hs.16349	KIAA0431 protein	5.72
	437866	AA156781	Hs.83992	metallothionein 1E (functional)	5.72
	410232	AW372451	Hs.61184	CGI-79 protein	5.70
	414452	AA454038	Hs.29032	ESTs	5.70
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.70
15	428730	AA625947	Hs.25750	ESTs	5.70
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (5.70
	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	5.70
	450616	AL133067	Hs.25214	hypothetical protein	5.70
	443774	AL117428	Hs.9740	DKFZP434A236 protein	5.69
20	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	5.69
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	5.68
	416653	AA768553	Hs.77496	metallothionein 1E (functional)	5.67
	452679	Z42387	Hs.4299	transmembrane, prostate androgen induced	5.66
	450244	AA007534	Hs.125062	ESTs	5.66
25	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	5.65
	450325	AI935962	Hs.26289	ESTs	5.65
	439671	AW162840	Hs.6641	kinesin family member 5C	5.64
	452387	AI680772	Hs.4316	trinucleotide repeat containing 12	5.64
	413992	W26276	Hs.136075	RNA, U2 small nuclear	5.63
30	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	5.63
	417791	AW965339	Hs.111471	ESTs	5.62
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.60
	415123	D60925		ESTs	5.60
35	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	5.60
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	5.60
	440738	AI004650	Hs.225674	WD repeat domain 9	5.60
	443830	AI142095	Hs.143273	ESTs	5.60
	449603	AI655662	Hs.197698	ESTs	5.60
	414342	AA742181	Hs.75912	KIAA0257 protein	5.59
40	422634	NM_016010	Hs.118821	CGI-62 protein	5.56
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.55
	400268				5.55
	452055	AI377431	Hs.293772	hypothetical protein MGC10858	5.54
	437073	AI885608	Hs.94122	ESTs	5.54
45	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	5.53
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	5.52
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.52
	439569	AW602166	Hs.222399	CEGP1 protein	5.51
	441102	AA973905	Hs.16003	intermediate filament protein syncollin	5.50
50	448310	AI480316		gb:tm26h09.x1 Soares_NFL_T_GBC_S1 Homo s	5.50
	413173	BE076928	Hs.70980	ESTs	5.48
	436246	AW450963	Hs.119991	ESTs	5.48
	449300	AI656959	Hs.222165	ESTs	5.48
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	5.48
55	451403	AA885569	Hs.15727	Homo sapiens cDNA FLJ14511 fis, clone NT	5.46
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	5.44
	429126	AW172356	Hs.99083	ESTs	5.44
	431316	AA502663	Hs.145037	ESTs	5.44
	439192	AW970536	Hs.105413	ESTs	5.44
60	431938	AA938471	Hs.115242	specific granule protein (28 kDa); cyste	5.44
	451552	AA047233	Hs.33810	ESTs	5.43
	416991	N36389	Hs.295091	KIAA0226 gene product	5.42
	427638	AA406411	Hs.208341	ESTs, Weakly similar to KIAA0989 protein	5.42
	427718	AI798680	Hs.25933	ESTs	5.42
65	438710	AA833907	Hs.178724	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.42
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	5.40
	431263	AW129203	Hs.13743	ESTs	5.40
	421264	AL039123	Hs.103042	microtubule-associated protein 1B	5.38
	421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	5.37

	408460	AA054726	Hs.285574	ESTs	5.36
	409091	AW970386	Hs.269423	ESTs	5.36
	421987	AI133161	Hs.286131	CGI-101 protein	5.36
5	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.36
	441217	AI922183	Hs.213246	ESTs	5.36
	426006	R49031	Hs.22627	ESTs	5.35
	422806	BE314767	Hs.1581	glutathione S-transferase theta 2	5.34
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	5.32
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	5.32
10	421129	BE439899	Hs.89271	ESTs	5.31
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	5.31
	410150	AW382942	Hs.6774	ESTs	5.30
	423952	AW877787	Hs.136102	KIAA0853 protein	5.30
15	452822	X85689	Hs.288617	hypothetical protein FLJ22621	5.30
	447752	M73700	Hs.347	lactotransferrin	5.29
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	5.29
	431359	AW993522	Hs.292934	ESTs	5.27
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.27
20	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	5.27
	454014	AW016670	Hs.233275	ESTs	5.27
	419714	AA758751	Hs.98216	ESTs	5.26
	428845	AL157579	Hs.153610	KIAA0751 gene product	5.26
	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	5.24
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	5.24
25	407182	AA312551	Hs.230157	ESTs	5.22
	420111	AA255652		gb:zs21h11.1 NCL_CGAP_GCB1 Homo sapiens	5.22
	426058	AI821625	Hs.191602	ESTs	5.22
	459551	AI472808		gb:ij70e07.x1 Soares_NSF_F8_9W_OT_PA_P_S	5.22
30	432524	AI458020	Hs.293287	ESTs	5.22
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	5.22
	410870	U81599	Hs.66731	homeo box B13	5.22
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	5.22
	409757	NM_001898	Hs.123114	cystatin SN	5.21
35	441124	T97717	Hs.119563	ESTs	5.21
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.21
	436401	AI087958	Hs.29088	ESTs	5.20
	437113	AA744693		gb:ny26c10.s1 NCL_CGAP_GCB1 Homo sapiens	5.20
	450947	AI745400	Hs.204662	ESTs	5.20
40	453279	AW893940	Hs.59698	ESTs	5.20
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.19
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.19
	412198	AA937111	Hs.69165	ESTs	5.18
	422646	H87863	Hs.151380	ESTs, Weakly similar to T16584 hypotheti	5.18
45	438986	AF085888	Hs.269307	ESTs	5.18
	453954	AW118336	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	5.18
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	5.18
	434029	AA621763	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	5.16
	459294	AW977286	Hs.169531	RBP1-like protein	5.16
50	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	5.16
	424692	AA429834	Hs.151791	KIAA0092 gene product	5.15
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.15
	419872	AI422951	Hs.146162	ESTs	5.15
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	5.14
55	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	5.14
	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypotheti	5.14
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	5.14
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	5.13
	426372	AK000684	Hs.183887	hypothetical protein FLJ22104	5.12
60	434401	AI864131	Hs.71119	Putative prostate cancer tumor suppresso	5.12
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	5.11
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.10
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	5.10
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	5.10
65	427958	AA418000	Hs.98280	potassium intermediate/small conductance	5.09
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	5.08
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.08
	412863	AA121673	Hs.59757	zinc finger protein 281	5.06
	420807	AA280627	Hs.57846	ESTs	5.06
	430568	AA769221	Hs.270847	delta-tubulin	5.06

	433687	AA743991		gbny57g01.s1 NCI_CGAP_Pr18 Homo sapiens	5.06
	438375	AW015940	Hs.232234	ESTs	5.06
	418092	R45154	Hs.106604	ESTs	5.06
5	418576	AW968159	Hs.289104	Alu-binding protein with zinc finger dom	5.05
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.04
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	5.04
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	5.04
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	5.04
	439662	H97552	Hs.269060	ESTs	5.04
10	439743	AL389956	Hs.283858	Homo sapiens mRNA full length insert cDN	5.04
	417511	AL049176	Hs.82223	chordin-like	5.02
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	5.02
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.02
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	5.02
15	429975	AI167145	Hs.165538	ESTs	5.02
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	5.02
	438571	AW020775	Hs.56022	ESTs	5.02
	450223	AA418204	Hs.241493	natural killer-tumor recognition sequenc	5.02
	408267	AW380525	Hs.267705	tubulin-specific chaperone e	5.01
20	417730	Z44761		gb:HSC28F061 normalized infant brain cDN	5.00
	425465	L18964	Hs.1904	protein kinase C, iota	5.00
	430599	NM_004855	Hs.247118	phosphatidylinositol glycan, class B	5.00
	450961	AW978813	Hs.250867	metallothionein 1E (functional)	5.00
25	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	5.00
	420380	AA640891	Hs.102406	ESTs	4.99
	424947	R77952	Hs.239625	ESTs, Weakly similar to alternatively sp	4.99
	424653	BE269247	Hs.170226	gb:601185486F1 NIH_MGC_8 Homo sapiens cD	4.98
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.97
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	4.97
30	446279	AA490770	Hs.182382	ESTs	4.96
	433377	AI752713	Hs.43845	ESTs	4.96
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	4.96
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.94
35	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	4.94
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.94
	421689	N87820	Hs.106826	KIAA1696 protein	4.93
	445808	AV655234	Hs.298083	ESTs, Moderately similar to PC4259 ferri	4.92
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	4.92
40	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	4.92
	436039	AW023323	Hs.121070	ESTs	4.92
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	4.91
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	4.91
	403047				4.91
45	436899	AA764852	Hs.291567	ESTs	4.90
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.90
	427617	D42063	Hs.179825	RAN binding protein 2	4.88
	428604	AK000713	Hs.193736	hypothetical protein FLJ20706	4.88
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	4.88
50	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	4.86
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	4.86
	412652	AI801777	Hs.6774	ESTs	4.86
	432473	AI202703	Hs.152414	ESTs	4.86
	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	4.86
55	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.85
	418866	T65754	Hs.100489	gb:yc11c07.s1 Stratagene lung (937210) H	4.85
	407596	R86913		gb:yq30f05.r1 Soares fetal liver spleen	4.84
	456516	BE172704	Hs.222746	KIAA1610 protein	4.84
	426501	AW043782	Hs.293616	ESTs	4.84
60	448730	AB032983	Hs.21894	KIAA1157 protein	4.84
	458339	AW976853	Hs.172843	ESTs	4.83
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.82
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	4.82
	424103	NM_001918	Hs.139410	dihydroipoamide branched chain transacy	4.82
65	449535	W15267	Hs.23672	low density lipoprotein receptor-related	4.82
	422048	NM_012445	Hs.288126	spodin 2, extracellular matrix protein	4.82
	416737	AF154335	Hs.79691	LIM domain protein	4.82
	419972	AL041465	Hs.294038	golgin-67	4.81
	420235	AA256756	Hs.31178	ESTs	4.81
	423412	AF109300	Hs.147924	prostate cancer associated protein 5	4.80

	429598	AA811257	Hs.269710	ESTs	4.80
	457114	AI821625	Hs.191602	ESTs	4.80
	421828	AW891965	Hs.289109	histone deacetylase 3	4.79
5	424602	AK002055	Hs.301129	hypothetical protein FLJ11193	4.78
	428364	AA426565	Hs.160541	ESTs, Moderately similar to ALU1_HUMAN A	4.78
	452335	AW188944	Hs.61272	ESTs	4.78
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	4.77
	421040	AA715026	Hs.135280	ESTs	4.76
10	421518	AI056392	Hs.208819	ESTs	4.76
	452560	BE077084		ESTs	4.76
	409752	AW963990		gb:EST376063 MAGE resequences, MAGH Homo	4.75
	439703	AF086538	Hs.196245	ESTs	4.75
	418836	AI655499	Hs.161712	ESTs	4.74
	450642	R39773	Hs.7130	copine IV	4.74
15	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	4.74
	411440	AW749402		gb:QV4-BT0383-281299-061-c06 BT0383 Homo	4.74
	450649	NM_001429	Hs.297722	E1A binding protein p300	4.74
	408738	NM_014785	Hs.47313	KIAA0258 gene product	4.73
20	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.72
	411624	BE145964		KIAA0594 protein	4.72
	439360	AA448488	Hs.55346	ribosomal protein L44	4.72
	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	4.72
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	4.72
25	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	4.72
	453800	BE300741	Hs.288416	hypothetical protein FLJ13340	4.72
	457528	AW973791	Hs.292784	ESTs	4.72
	416795	AI497778	Hs.168053	HBV pX associated protein-8	4.71
	407302	R74206	Hs.268755	ESTs, Weakly similar to I78885 serine/th	4.71
	404721				4.70
30	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	4.70
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	4.70
	435256	AF193766	Hs.13872	cytokine-like protein C17	4.70
	438295	AI394151	Hs.37932	ESTs	4.70
35	442655	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypotheti	4.70
	415788	AW628686	Hs.78851	KIAA0217 protein	4.69
	442760	BE075297	Hs.10067	ESTs, Weakly similar to A43932 mucin 2 p	4.69
	432432	AA541323	Hs.115831	ESTs	4.68
	454398	AA463437	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.68
40	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	4.67
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	4.67
	419706	C04649	Hs.77899	tropomyosin 1 (alpha)	4.66
	412088	AI689496	Hs.108932	ESTs	4.65
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.64
45	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	4.64
	448207	AI475490	Hs.170577	ESTs	4.64
	408374	AW025430	Hs.155591	forkhead box F1	4.64
	447162	BE328091	Hs.157396	ESTs, Weakly similar to A46010 X-linked	4.64
	451900	AB023199	Hs.27207	KIAA0982 protein	4.63
50	421437	AW821252	Hs.104336	hypothetical protein	4.63
	418624	AI734080	Hs.104211	ESTs	4.63
	426172	AA371307	Hs.125056	ESTs	4.62
	439831	AW136488	Hs.25545	ESTs	4.61
	452994	AW962597	Hs.31305	KIAA1547 protein	4.61
55	457726	AI217477	Hs.194591	ESTs	4.60
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	4.60
	403764				4.58
	410659	AI080175	Hs.68826	ESTs	4.58
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	4.58
60	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	4.58
	433234	AB040928	Hs.65366	KIAA1495 protein	4.57
	424983	AI742434	Hs.169911	ESTs	4.56
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	4.56
	438447	AI082883	Hs.167593	hypothetical protein FLJ13409; KIAA1711	4.55
65	434715	BE005346	Hs.116410	ESTs	4.55
	447673	AI823987	Hs.182285	ESTs	4.54
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	4.54
	436645	AW023424	Hs.156520	ESTs	4.54
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	4.53
	450377	AB033091	Hs.24936	KIAA1265 protein	4.53

	433644	AW342028	Hs.256112	gb:hb75d03.x1 NCI_CGAP_Ut2 Homo sapiens	4.53
	408321	AW405882	Hs.44205	cortistatin	4.53
	439225	AA192669	Hs.45032	ESTs	4.52
	440348	AW015802	Hs.47023	ESTs	4.52
5	446351	AW444551	Hs.258532	x 001 protein	4.52
	451212	AW902672	Hs.287334	ESTs	4.52
	430294	AI538226	Hs.135184	guanine nucleotide binding protein 4	4.52
	435005	U80743	Hs.4316	trinucleotide repeat containing 12	4.52
	448072	AI459306	Hs.24908	ESTs	4.50
10	403721				4.50
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	4.50
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	4.49
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.48
	439735	AI635386	Hs.142846	hypothetical protein	4.48
15	435663	AI023707	Hs.134273	ESTs	4.48
	424036	AA770688	Hs.81946	H2A histone family, member L	4.48
	426386	AA748850	Hs.174877	bladder cancer overexpressed protein	4.48
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	4.47
	444269	AI590346	Hs.146220	ESTs	4.47
20	430187	AI799909	Hs.158989	ESTs	4.46
	427761	AA412205	Hs.140996	ESTs	4.46
	430261	AA305127	Hs.237225	hypothetical protein HT023	4.46
	444169	AV648170	Hs.58756	ESTs	4.44
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.44
25	412903	BE007967	Hs.155795	ESTs	4.44
	417048	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	4.44
	442710	AI015631	Hs.23210	ESTs	4.44
	457413	AA743462	Hs.165337	ESTs	4.44
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	4.42
30	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.42
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	4.42
	431724	AA514535	Hs.283704	ESTs	4.41
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	4.40
	440801	AA906366	Hs.190535	ESTs	4.40
35	452959	AI933416	Hs.189674	ESTs	4.40
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	4.40
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.40
	447270	AC002551	Hs.331	general transcription factor IIIC, polyp	4.38
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	4.38
40	447078	AW885727	Hs.301570	ESTs	4.38
	424242	AA337476		hypothetical protein MGC13102	4.37
	408170	AW204516	Hs.31835	ESTs	4.36
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	4.36
	420021	AA252848	Hs.293557	ESTs	4.36
45	448694	AI659790	Hs.253302	ESTs	4.36
	453867	AI929383	Hs.108196	hypothetical protein DKFZp434N185	4.36
	458712	AI347502	Hs.173066	hypothetical protein FLJ20761	4.36
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	4.35
	434423	NM_006769	Hs.3844	LIM domain only 4	4.35
50	423427	AL137612	Hs.285848	KIAA1454 protein	4.34
	415715	F30364		ESTs	4.33
	404561				4.32
	422969	AA782536	Hs.122647	N-myristoyltransferase 2	4.32
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	4.32
55	443977	AL120986	Hs.150627	ESTs, Weakly similar to I38022 hypotheti	4.32
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.32
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.31
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	4.30
	421476	AW953805	Hs.21887	ESTs	4.30
60	425178	H16097	Hs.161027	ESTs	4.30
	439262	AA832333	Hs.124399	ESTs	4.30
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	4.30
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.29
	437114	AA836641	Hs.163085	ESTs	4.28
65	420195	N44348	Hs.300794	Homo sapiens cDNA FLJ11177 fis, clone PL	4.28
	418330	BE408405	Hs.94722	ESTs	4.27
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	4.26
	437065	AL036450	Hs.103238	ESTs	4.26
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.24

	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	4.24
	423740	Y07701	Hs.132243	aminopeptidase puromycin sensitive	4.24
	442023	AI187878	Hs.144549	ESTs	4.24
5	426764	AA732524	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN IIII	4.23
	454058	AI273419	Hs.135146	hypothetical protein FLJ13984	4.23
	456511	AA282330	Hs.145668	ESTs	4.22
	448330	AL036449	Hs.207163	ESTs	4.22
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	4.21
10	432621	AI298501	Hs.12807	ESTs, Weakly similar to T46428 hypotheti	4.20
	445707	AI248720	Hs.114390	ESTs	4.20
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	4.20
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	4.20
	440749	W22335	Hs.7392	hypothetical protein MGC3199	4.20
15	442787	W93048	Hs.227203	hypothetical protein MGC2747	4.20
	443414	R54594	Hs.25209	ESTs	4.20
	443556	AA256769	Hs.94949	methylmalonyl-CoA epimerase	4.20
	444170	AW613879	Hs.102408	ESTs	4.20
	446751	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21	4.20
20	421041	N36914	Hs.14691	ESTs, Moderately similar to I38022 hypot	4.19
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	4.19
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f	4.18
	410294	AB014515	Hs.288891	KIAA0615 gene product	4.18
	433607	AA602004	Hs.23260	ESTs	4.18
25	435552	AI668636	Hs.193480	ESTs, Moderately similar to ALU6_HUMAN A	4.18
	447124	AW976438	Hs.17428	RBP1-like protein	4.18
	453308	AW959731	Hs.32538	ESTs	4.17
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	4.16
	430473	AW130690	Hs.299842	ESTs	4.16
30	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	4.16
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.16
	443857	AI089292	Hs.287621	hypothetical protein FLJ14069	4.15
	446711	AF169692	Hs.12450	protocadherin 9	4.15
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	4.14
	405403				4.14
35	407378	AA299264		ESTs, Moderately similar to I38022 hypot	4.14
	408986	AW298602	Hs.197687	ESTs	4.14
	418727	AA227609	Hs.94834	ESTs	4.14
	434400	AI478211	Hs.186896	Homo sapiens cDNA FLJ11417 fis, clone HE	4.14
40	438578	AA811244	Hs.164168	ESTs	4.14
	450459	AI697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	4.14
	429887	AW366286	Hs.145696	splicing factor (CC1.3)	4.13
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	4.13
	450316	W84446	Hs.17850	hypothetical protein MGC4643	4.12
45	417531	NM_003157	Hs.1087	serine/threonine kinase 2	4.12
	431592	R69016	Hs.293871	hypothetical protein MGC10895s	4.12
	432463	AA548518	Hs.186733	ESTs	4.12
	433613	AA836126	Hs.5669	ESTs	4.12
	434739	AA804487	Hs.144130	ESTs	4.12
50	438259	AW205969	Hs.131808	ESTs	4.12
	425810	AI923627	Hs.31903	ESTs	4.10
	432672	AW973775	Hs.130760	myosin phosphatase, target subunit 2	4.10
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	4.10
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.09
55	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	4.09
	412045	AA099802	Hs.4299	transmembrane, prostate androgen induced	4.09
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	4.08
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	4.08
	445459	AI478629	Hs.158465	likely ortholog of mouse putative IKK re	4.08
60	438938	H46212	Hs.137221	ESTs	4.07
	454119	BE549773	Hs.40510	uncoupling protein 4	4.06
	411000	N40449	Hs.201619	ESTs, Weakly similar to S38383 SEB4B pro	4.06
	418928	AA232658	Hs.87070	UDP-glucose:glycoprotein glucosyltransfe	4.06
	424432	AB037821	Hs.146858	protocadherin 10	4.06
65	449673	AA002064	Hs.18920	ESTs	4.06
	429299	AI620463	Hs.99197	hypothetical protein MGC13102	4.06
	422174	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (fr	4.05
	455497	AA112573	Hs.285691	Homo sapiens protein mRNA, complete cds	4.05
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	4.04
	402791				4.04

	428792	AL044854	Hs.172329	KIAA0576 protein	4.04
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.04
	442768	AL048534	Hs.48458	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.04
	447568	AF155655	Hs.18885	CGI-116 protein	4.04
5	428342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	4.04
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	4.02
	453857	AL080235	Hs.35661	DKFZP586E1621 protein	4.02
	428249	AA130914	Hs.183291	zinc finger protein 268	4.02
10	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	4.02
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	4.02
	451746	M86178		ESTs	4.02
	452211	AI985513	Hs.233420	ESTs	4.02
	453046	AA284040	Hs.219441	ESTs, Highly similar to CA5B_HUMAN CARBO	4.02
	456038	AA203285	Hs.294141	ESTs, Weakly similar to alternatively sp	4.02
15	452449	AW068658	Hs.20943	ESTs	4.02
	407204	RA1933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.01
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	4.01
	438520	AA706319	Hs.98416	ESTs	4.01
	443292	AK000213	Hs.9196	hypothetical protein	4.01
20	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	4.00
	403797				4.00
	418347	AA216419	Hs.269295	gb:nc16e03.s1 NCL_CGAP_Pr1 Homo sapiens	4.00
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	4.00
25	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.00
	425176	AW015644	Hs.301430	TEA domain family member 1 (SV40 transcr	4.00
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	4.00
	453773	AL133761		gb:DKFZp761C1413_r1 761 (synonym: hamy2)	4.00
	434384	AA631910	Hs.162849	ESTs	3.99
30	422471	AA311027	Hs.271894	ESTs, Weakly similar to I38022 hypotheti	3.99
	427386	AW836261	Hs.177486	ESTs	3.98
	433394	AI907753	Hs.93810	cerebral cavernous malformations 1	3.98
	441269	AW015206	Hs.178784	ESTs	3.97
	419629	AB020695	Hs.91662	KIAA0888 protein	3.96
35	435008	AF150262	Hs.162898	ESTs	3.96
	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	3.96
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.96
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.95
	430456	AA314998	Hs.241503	hypothetical protein	3.95
40	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.95
	409960	BE261944	Hs.153028	hexokinase 1	3.95
	455309	AW894017		gb:RC4-NN0027-150400-012-g04 NN0027 Homo	3.95
	450295	AI766732	Hs.201194	ESTs	3.94
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.94
45	410908	AA121686	Hs.10592	ESTs	3.94
	447145	AA761073	Hs.192943	TRAF family member-associated NFKB activ	3.94
	449318	AW236021	Hs.108788	Homo sapiens, Similar to RIKEN cDNA 5730	3.94
	449869	W57990	Hs.60059	Homo sapiens cDNA FLJ11478 fis, clone HE	3.94
	411887	AW182924	Hs.128790	ESTs	3.93
50	437531	AI400752	Hs.112259	T cell receptor gamma locus	3.93
	452238	F01811	Hs.187931	ESTs	3.93
	410486	AW235094	Hs.193424	zinc finger protein	3.92
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	3.92
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.92
55	427043	AA397679	Hs.298460	ESTs	3.92
	440404	AI015881	Hs.125616	mitochondrial ribosomal protein S5	3.92
	452762	AW501435	Hs.171409	v-akt murine thymoma viral oncogene homo	3.92
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.92
	423583	AL122055	Hs.129836	KIAA1028 protein	3.92
60	408001	AA046458	Hs.95296	ESTs	3.92
	419197	N48921	Hs.27441	KIAA1615 protein	3.91
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.91
	401747				3.91
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.91
65	432205	AI806583	Hs.125291	ESTs	3.91
	447857	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	3.91
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.91
	408928	AL137163	Hs.57549	hypothetical protein dJ47384	3.90
	411598	BE336654	Hs.70937	H3 histone family, member A	3.90
	424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	3.90

	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	3.90
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	3.89
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.89
	401045				3.89
5	433023	AW864793	Hs.34161	thrombospondin 1	3.89
	452160	BE378541	Hs.279815	cysteine sulfinic acid decarboxylase-rel	3.89
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.89
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.88
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.88
10	422660	AW297582	Hs.237062	hypothetical protein FLJ22548 similar to	3.88
	431930	AB035301	Hs.272211	cadherin 7, type 2	3.88
	453047	AW023798	Hs.286025	ESTs	3.88
	433891	AA613792		gbno97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.88
	401785				3.88
15	431088	AA491824	Hs.196881	ESTs	3.88
	451952	AL120173	Hs.301663	ESTs	3.87
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.87
	452277	AL049013	Hs.28783	KIAA1223 protein	3.87
	438279	AA805166	Hs.165165	HIV-1 rev binding protein 2	3.86
20	458229	AJ929602	Hs.177	phosphatidylinositol glycan, class H	3.86
	406414				3.86
	417193	AJ922189	Hs.288390	hypothetical protein FLJ22795	3.85
	413174	AA723564	Hs.191343	ESTs	3.85
25	433332	AJ367347	Hs.127809	Homo sapiens clone TCCCTA00151 mRNA sequ	3.85
	411089	AA456454	Hs.118637	cell division cycle 2-like 1 (PITSLRE pr	3.85
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.84
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	3.84
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF I [3.84
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.83
30	451468	AW503398	Hs.210047	ESTs, Moderately similar to I38022 hypot	3.83
	434804	AA649530		gb.ms44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.83
	401819				3.82
	424179	F30712		Homo sapiens, clone IMAGE:4285740, mRNA	3.82
35	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	3.82
	426472	BE246138	Hs.30853	ESTs	3.82
	426625	T78300	Hs.171409	serologically defined colon cancer antig	3.82
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.82
	427756	AJ376540	Hs.15574	ESTs	3.82
	444701	AJ916512	Hs.198394	ESTs	3.82
40	423052	M28214	Hs.123072	RAB3B, member RAS oncogene family	3.82
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	3.82
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.82
	433586	T85301		gb.yd78d06.s1 Soares fetal liver spleen	3.81
45	438527	AJ969251	Hs.143237	RAB7, member RAS oncogene family-like 1	3.81
	410297	AA148710	Hs.159441	lumican	3.81
	429898	AW117322	Hs.42366	ESTs	3.81
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.80
	418423	D26488	Hs.90315	KIAA0007 protein	3.80
50	429643	AA455889	Hs.187548	FYVE-finger-containing Rab5 effector pro	3.80
	431499	NM_001514	Hs.258561	general transcription factor IIB	3.80
	445060	AA830811	Hs.88808	ESTs	3.80
	449419	R34910	Hs.119172	ESTs	3.80
	450584	AA040403	Hs.60371	ESTs	3.80
55	426137	AL040683	Hs.167031	DKFZP566D133 protein	3.79
	420185	AL044056	Hs.158047	ESTs	3.79
	410076	T05387	Hs.7991	ESTs	3.78
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.78
	417318	AW953937	Hs.12891	ESTs	3.78
60	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.78
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.77
	410503	AW975746	Hs.188662	KIAA1702 protein	3.77
	434170	AA626509	Hs.122329	ESTs	3.77
	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (I	3.77
65	425268	AI807883	Hs.156932	Homo sapiens cDNA FLJ20653 fis, clone KA	3.76
	431696	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	3.76
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	3.76
	430291	AV660345	Hs.238126	CGI-49 protein	3.76
	448779	BE042877	Hs.177135	ESTs	3.76
	452682	AA456193	Hs.155606	progesterone membrane binding protein	3.75

5	452598	AJ831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.75
	439498	AA908731	Hs.58297	CLLL9 protein	3.75
	440258	AI741633	Hs.125350	ESTs	3.74
	456848	AL121087	Hs.296406	KIAA0685 gene product	3.74
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosyl	3.74
10	420653	AI224532	Hs.88550	ESTs	3.74
	431637	AI879330	Hs.265960	hypothetical protein FLJ10563	3.74
	440411	N30256	Hs.156971	hypothetical protein DKFZp434G1415	3.74
	405917				3.74
	419440	AB020689	Hs.90419	KIAA0882 protein	3.74
15	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.73
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.73
	430144	AI732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.72
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	3.72
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	3.72
20	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	3.72
	456228	BE503227	Hs.134759	ESTs	3.72
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.72
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	3.72
	433544	AI793211	Hs.165372	ESTs, Moderately similar to ALU1_HUMAN A	3.71
25	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.71
	449897	AW819842	Hs.24135	transmembrane protein vezatin; hypotheti	3.71
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.70
	423065	R96158	Hs.194606	Homo sapiens, clone MGC:5406, mRNA, comp	3.70
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (I	3.70
30	437777	AA768098	Hs.189079	ESTs	3.70
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.70
	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.70
	446965	BE242873	Hs.16677	WD repeat domain 15	3.70
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.70
35	433852	AI378329	Hs.126629	ESTs	3.70
	433142	AL120697	Hs.110640	ESTs	3.69
	419994	AA282881	Hs.190057	ESTs	3.69
	412628	AI972402	Hs.173902	hypothetical protein MGC2648	3.69
	431416	AA532718	Hs.178604	ESTs	3.69
40	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.68
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.68
	447397	BE247676	Hs.18442	E-1 enzyme	3.68
	405718				3.68
	425217	AU076696	Hs.155174	CDC5 (cell division cycle 5, S. pombe, h	3.68
45	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.68
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	3.68
	421734	AI318824	Hs.107444	Homo sapiens cDNA FLJ20562 fis, clone KA	3.67
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	3.67
	439884	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.66
50	402408				3.66
	426327	W03242	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	3.66
	427119	AW880562	Hs.114574	ESTs	3.66
	427356	AW023482	Hs.97849	ESTs	3.66
	452946	X95425	Hs.31092	EphA5	3.66
55	419078	M93119	Hs.89584	insulinoma-associated 1	3.66
	416295	AI064824	Hs.193385	ESTs	3.65
	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	3.65
	447500	AI381900	Hs.159212	ESTs	3.65
	453127	AI696671	Hs.294110	ESTs	3.65
60	423396	AI382555	Hs.127950	bromodomain-containing 1	3.65
	419346	AI830417		polybromo 1	3.64
	441540	C01367	Hs.127128	ESTs	3.64
	446501	AI302616	Hs.150819	ESTs	3.64
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	3.63
65	446320	AF126245	Hs.14791	acyl-Coenzyme A dehydrogenase family, me	3.63
	435706	W31254	Hs.7045	GL004 protein	3.63
	400110				3.62
	410313	R10305	Hs.185683	ESTs	3.62
	414713	BE465243	Hs.12664	ESTs	3.62
	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-	3.62
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.62
	451797	AW663858	Hs.56120	small inducible cytokine subfamily E, me	3.62
	451294	AI457338	Hs.29894	ESTs	3.62

	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.62
	404939				3.62
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.62
5	435846	AA700870	Hs.14304	ESTs	3.61
	432833	N51075	Hs.47191	ESTs	3.61
	427276	AA400269	Hs.49598	ESTs	3.61
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.60
	403137				3.60
	404165				3.60
10	409571	AA504249	Hs.187585	ESTs	3.60
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.60
	412924	BE018422	Hs.75258	H2A histone family, member Y	3.60
	434228	Z42047	Hs.263978	Homo sapiens PRO2751 mRNA, complete cds	3.60
	436797	AA731491	Hs.178518	hypothetical protein MGC14879	3.60
15	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.60
	437444	H46008	Hs.31518	ESTs	3.60
	404210				3.59
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.59
	437587	AI591222	Hs.122421	Human DNA sequence from clone RP1-187J11	3.58
20	423147	AA987927	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.57
	452226	AA024898	Hs.296002	ESTs	3.56
	443775	AF291664	Hs.204732	matrix metalloproteinase 26	3.56
	452501	AB037791	Hs.29716	hypothetical protein FLJ10980	3.56
	428647	AA830050	Hs.124344	ESTs	3.56
25	422443	NM_014707	Hs.116753	histone deacetylase 7B	3.55
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.55
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	3.55
	420230	AL034344	Hs.298020	forkhead box C1	3.55
	418428	Y12490	Hs.85092	thyroid hormone receptor interactor 11	3.54
30	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	3.54
	444929	AI685841	Hs.161354	ESTs	3.54
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.54
	424369	R87622	Hs.26714	KIAA1831 protein	3.54
	433002	AF048730	Hs.279906	cyclin T1	3.53
35	435425	H16263	Hs.31416	ESTs	3.53
	415621	AI648602	Hs.131189	ESTs	3.53
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.53
	405793				3.52
	409770	AW499536		gb:U1-HF-BR0p-aj-c-12-0-U1.r1 NIH_MGC_5	3.52
40	425305	AA363025	Hs.155572	Human clone Z3801 mRNA sequence	3.52
	428939	AW236550	Hs.131914	ESTs	3.52
	438388	AA806349	Hs.44698	ESTs	3.52
	443703	AV646177	Hs.213021	ESTs	3.52
	457940	AL360159	Hs.30445	Homo sapiens TRlpartite motif protein ps	3.52
45	402444				3.52
	409643	AW450866	Hs.257359	ESTs	3.51
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	3.51
	432745	AI821826	Hs.269507	gb:m78f05.x5 NCI_CGAP_Pr3 Homo sapiens	3.51
50	414222	AL135173	Hs.878	sorbitol dehydrogenase	3.51
	430061	AB037817	Hs.230188	KIAA1396 protein	3.51
	421491	H99999	Hs.42736	ESTs	3.50
	422384	AA224077	Hs.42438	Sm protein F	3.50
	434565	T52172		ESTs	3.50
	438379	N23018	Hs.171391	C-terminal binding protein 2	3.50
55	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDN	3.50
	447311	R37010	Hs.33417	Homo sapiens cDNA: FLJ22806 fis, clone K	3.50
	447805	AW627932	Hs.19614	gemin4	3.50
	454265	H03556	Hs.300949	ESTs, Weakly similar to thyroid hormone	3.50
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.50
60	448804	AW512213	Hs.42500	ADP-ribosylation factor-like 5	3.50
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	3.49
	434075	AW003416	Hs.160604	ESTs	3.49
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.49
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.48
65	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	3.48
	420271	AI954365	Hs.42892	ESTs	3.48
	443684	AI681307	Hs.166674	ESTs	3.48
	444168	AW379879		gb:RC1-HT0256-081199-011-f01 HT0256 Homo	3.48
	446074	AA079799	Hs.29263	hypothetical protein FLJ11896	3.48

	452582	AL137407	Hs.29911	Homo sapiens mRNA; cDNA DKFZp434M232 (fr	3.48
	431542	H63010	Hs.5740	ESTs	3.48
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.48
5	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	3.47
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.47
	413435	X51405	Hs.75360	carboxypeptidase E	3.46
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.46
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.46
10	425312	AA354940	Hs.145958	ESTs	3.46
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	3.46
	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	3.45
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.45
	408739	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.45
15	436024	AI800041	Hs.190555	ESTs	3.45
	408418	AW963897	Hs.44743	KIAA1435 protein	3.45
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.44
	418626	AW299508	Hs.135230	ESTs	3.44
	420560	AW207748	Hs.59115	ESTs	3.44
20	420686	AI950339	Hs.40782	ESTs	3.44
	428870	AA436831	Hs.36049	ESTs	3.44
	436754	AI061288	Hs.133437	ESTs	3.44
	437960	AI669586	Hs.222194	ESTs	3.44
	452300	AW628045	Hs.28896	Homo sapiens mRNA full length insert cDN	3.44
25	421887	AW161450	Hs.109201	CGI-86 protein	3.44

TABLE 5A shows the accession numbers for those primekeys lacking a unigeneID in Tables 5, 6, and 7. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number	
		Gene cluster number	Genbank accession numbers
	Pkey	CAT number	Accession
15	407596	1003489_1	R86913 R86901 H25352 R01370 H43764 AW044451 W21298
	408432	1058667_1	AW195262 R27868 AW811262
	409752	115301_1	AW963990 AA078196 AW749482 AA077468 BE151571 AA376917
	409770	1154048_1	AW499536 AW499553 AW502138 AW499537 AW502136 AW501743
	411440	124577_1	AW749402 AW749403 Z45743 R03376 AA093358
20	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571
			AW848009 AW848067 AW848069 AW848905 AW848214
	411624	1252166_1	BE145964 BE146286 AW854564
	412991	134248_1	AW949013 AA126111
	414269	143133_1	AA298469 AA137165
25	415123	1523390_1	D60925 D60828 D80787
	415715	1548818_1	F30364 F36559 T15435
	416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
	416289	1586037_1	W26333 R05358 H44682
	417730	1695795_1	Z44761 R25801 R11926 R35604
30	418636	177402_1	AW749855 AA225995 AW750208 AW750206
	419346	184129_1	AI830417 AA236612
	419536	185688_1	AA603305 AA244095 AA244183
	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	422219	213547_1	AW978073 AW978072 AA807550 AA306567
35	424179	236389_1	F30712 F35665 AW263888 AI904014 AI904018 AA336927 AA336502
	424242	237181_1	AA337476 AW966227 AA450376 AW960222 AA381051
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	429163	300543_1	AA884766 AW974271 AA592975 AA447312
	432189	342819_1	AA527941 AI810608 AI620180 AA635266
40	432340	345248_1	AA534222 AA632632 T81234
	432363	345469_1	AA534489 AW970240 AW970323
	432966	356839_1	AA650114 AW974148 AA572946
	433586	370470_1	T85301 AW517087 AA601054 BE073959
	433641	37186_1	AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547
45			AI680833 AI633818 N29986 U87592 U87593 U87590 U87591 S46404 U87587 AA463992 AW206802 AI970376
			AI583718 AI672574 N25695 AW665466 AI818326 AA126128 AI480345 AW013827 AA248638 AI214968
			AA204735 AA207155 AA206262 AA204833 AW003247 AW496808 AI080480 AI631703 AI651023 AI867418
			AW818140 AA502500 AI206199 AI671282 AI352545 BE501030 AI652535 BE465762 AA206331 AW451866
			AA471088 AA206342 AA204834 AA206100 AW021661 AA332922 N66048 AA703396 H92278 AW139734
50			H92683 U87589 U87595 H69001 U87594 BE466420 AI624817 BE466611 AI206344 AA574397 AA348354
			AI493192
	433687	373061_1	AA743991 AA604852 AW272737
	433891	376239_1	AA613792 AW182329 T05304 AW858385
	434415	385931_1	BE177494 AW276909 AA632849
55	434565	38898_1	T52172 AF147324 T52248
	434804	393481_1	AA649530 AA659316 H64973
	437113	433234_1	AA744693 AW750059
	444168	593829_1	AW379879 AI126285 H12014
	448212	755099_1	AI475858 AW969013
	448310	757918_1	AI480316 AW847535
	451746	883303_1	M86178 AI813822 D56993

5 452560 922216_1 BE077084 AW139963 AW863127 AW806209 AW806204 AW806205 AW806206 AW806211 AW806212
AW806207 AW806208 AW806210 AI907497
452712 928309_1 AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
453773 980699_1 AL133761 AL133767
455276 1272541_1 BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610
BE176362
455309 1278153_1 AW894017 AW893956 AW894032

TABLE 5B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Tables 5, 6, and 7. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
15				
	Pkey	Ref	Strand	Nt_position
20	401045	8117619	Plus	90044-90184,91111-91345
	401424	8176894	Plus	24223-24428
	401451	6634068	Minus	119926-121272
	401714	6715702	Plus	96484-96681
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
25	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401819	7467933	Minus	28217-28486
	402408	9796239	Minus	110326-110491
	402444	9796614	Plus	28391-28517
	402791	6137008	Minus	51036-51207
30	403047	3540153	Minus	59793-59968
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403721	7528046	Minus	156647-157366
	403764	7717105	Minus	118692-118853
	403797	8099896	Minus	123065-125008
35	404165	9926489	Minus	69025-69128
	404210	5006246	Plus	169926-170121
	404253	9367202	Minus	55675-56055
	404561	9795980	Minus	69039-70100
	404571	7249169	Minus	112450-112648
40	404721	9856648	Minus	173763-174294
	404915	7341766	Minus	100915-101087
	404939	6862697	Plus	175318-175476
	405403	6850244	Minus	37491-37670,40951-41031
	405685	4508129	Minus	37956-38097
45	405718	9795467	Plus	113080-113266
	405793	1405887	Minus	89197-89453
	405876	6758747	Plus	39694-40031
	405917	7712162	Minus	106829-107213
	406414	9256407	Plus	49593-49850
50	406554	7711566	Plus	106956-107121

TABLE 6:286 GENES ENCODING EXTRACELLULAR OR CELL SURFACE PROTEINS UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

5 Table 6 shows 286 genes up-regulated in prostate cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 5 and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. egf, 7tm domains).

	Pkey:		Unique Eos probaset identifier number		
	ExAccn:		Exemplar Accession number, Genbank accession number		
	UnigenelD:		Unigene number		
	Unigene Title:		Unigene gene title		
	R1:		Ratio of tumor to normal tissue		
10	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	48.28
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	45.24
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.48
15	420154	AI093155	Hs.95420	JM27 protein	41.12
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	31.80
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	24.91
	425075	AA506324	Hs.1852	acid phosphatase, prostate	24.23
	424846	AU077324	Hs.1832	neuropeptide Y	23.57
20	405685				20.90
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	19.72
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	19.56
	452792	AB037765	Hs.30652	KIAA1344 protein	17.39
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	17.00
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	16.82
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	16.60
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	16.28
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.54
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	15.40
30	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	14.76
	418601	AA279490	Hs.86368	calmegin	14.56
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	14.55
	416182	NM_004354	Hs.79069	cyclin G2	12.94
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	12.79
35	445413	AA151342	Hs.12677	CGI-147 protein	12.64
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	12.22
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	12.04
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.86
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	11.68
40	448045	AJ297436	Hs.20166	prostate stem cell antigen	11.51
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	11.18
	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	11.10
	425665	AK001050	Hs.159066	hypothetical protein FLJ10188	11.08
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.08
45	428728	NM_016625	Hs.191381	hypothetical protein	11.04
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.02
	410733	D84284	Hs.66052	CD38 antigen (p45)	11.02
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	10.85
	428819	AL135623	Hs.193914	KIAA0575 gene product	10.48
50	421991	NM_014918	Hs.110488	KIAA0990 protein	10.04
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	9.75
	421470	R27496	Hs.1378	annexin A3	9.64
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	9.45
	435980	AF274571	Hs.129142	deoxyribonuclease II beta	9.24
55	421246	AW582962	Hs.102897	CGI-47 protein	9.20
	410001	AB041036	Hs.57771	kallikrein 11	9.03
	441791	AW372449	Hs.175982	hypothetical protein FLJ21159	9.02

	404571				8.66
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	8.56
	419968	X04430	Hs.93913	Interleukin 6 (interferon, beta 2)	8.36
	433172	AB037841	Hs.102652	hypothetical protein ASH1	8.30
5	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	8.27
	427674	NM_003528	Hs.2178	H2B histone family, member Q	8.20
	404915				8.08
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	8.06
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	8.02
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	7.98
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	7.68
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.64
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.64
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.52
15	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	7.49
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	7.35
	441736	AW292779	Hs.169799	ESTs	7.28
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	7.20
	425018	BE245277	Hs.154196	E4F transcription factor 1	7.20
20	424560	AA158727	Hs.150555	protein predicted by clone 23733	7.18
	409110	AA191493	Hs.48778	niban protein	7.10
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.04
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	6.98
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	6.85
25	427408	AA583206	Hs.2156	RAR-related orphan receptor A	6.79
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	6.73
	415874	AF091622	Hs.78893	KIAA0244 protein	6.54
	401451				6.52
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	6.51
30	409089	NM_014781	Hs.50421	KIAA0203 gene product	6.50
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.49
	404253				6.42
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.41
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	6.38
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	439366	AF100143	Hs.6540	fibroblast growth factor 13	6.30
	416836	D54745	Hs.80247	cholecystokinin	6.30
	433383	AF034837	Hs.192731	double-stranded RNA specific adenosine d	6.29
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.25
40	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.22
	423349	AF010258	Hs.127428	homeo box A9	6.20
	424800	AL035588	Hs.153203	MyoD family inhibitor	6.18
	425451	AF242769	Hs.157461	mesenchymal stem cell protein DSC54	6.14
	447359	NM_012093	Hs.18268	adenylate kinase 5	6.00
45	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.97
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.94
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	5.94
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	5.92
	450480	X82125	Hs.25040	zinc finger protein 239	5.90
50	451684	AF216751	Hs.26813	CDA14	5.88
	400301	X03635	Hs.1657	estrogen receptor 1	5.78
	415077	L41607	Hs.934	glucosaminyl (N-acetyl) transferase 2, I	5.74
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.72
	446867	AB007891	Hs.16349	KIAA0431 protein	5.72
55	410232	AW372451	Hs.61184	CGI-79 protein	5.70
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.70
	450616	AL133067	Hs.302689	hypothetical protein	5.70
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	5.65
	439671	AW162840	Hs.6641	kinesin family member 5C	5.64
60	410196	AI938442	Hs.59838	hypothetical protein FLJ10808	5.60
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	5.60
	440738	AI004650	Hs.225674	WD repeat domain 9	5.60
	414342	AA742181	Hs.75912	KIAA0257 protein	5.59
	422634	NM_016010	Hs.118821	CGI-62 protein	5.56
65	400268				5.55
	439569	AW602166	Hs.222399	CEGP1 protein	5.51
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	5.48
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	5.44
	427638	AA406411	Hs.208341	ESTs, Weakly similar to KIAA0989 protein	5.42

5	421264	AL039123	Hs.103042	microtubule-associated protein 1B	5.38
	421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	5.37
	421987	AI133161	Hs.286131	CGI-101 protein	5.36
	422806	BE314767	Hs.1581	glutathione S-transferase theta 2	5.34
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	5.32
10	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (I	5.32
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	5.31
	447752	M73700	Hs.105938	lactotransferrin	5.29
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	5.22
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.21
15	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	5.18
	459294	AW977286	Hs.17428	RBP1-like protein	5.16
	424692	AA429834	Hs.151791	KIAA0092 gene product	5.15
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	5.11
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.10
20	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	5.10
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	5.10
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	5.09
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	5.08
	418576	AW968159	Hs.289104	Alu-binding protein with zinc finger dom	5.05
25	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.04
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	5.04
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.02
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	5.02
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	5.02
30	430599	NM_004855	Hs.247118	phosphatidylinositol glycan, class B	5.00
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	5.00
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.97
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	4.97
	421689	N87820	Hs.106826	KIAA1696 protein	4.93
35	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	4.92
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	4.91
	403047				4.91
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.90
	427617	D42063	Hs.199179	RAN binding protein 2	4.88
40	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	4.88
	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	4.86
	407596	R86913		gb:yq30f05.r1 Soares fetal liver spleen	4.84
	456516	BE172704	Hs.222746	KIAA1610 protein	4.84
	458339	AW976853	Hs.172843	ESTs	4.83
45	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.82
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	4.82
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.82
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	4.78
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	4.77
50	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	4.74
	450649	NM_001429	Hs.25272	E1A binding protein p300	4.74
	411624	BE145964	Hs.103283	KIAA0594 protein	4.72
	404721				4.70
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	4.70
55	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.64
	408374	AW025430	Hs.155591	forkhead box F1	4.64
	451900	AB023199	Hs.27207	KIAA0982 protein	4.63
	421437	AW821252	Hs.104336	hypothetical protein	4.63
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	4.60
60	403764				4.58
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	4.53
	403721				4.50
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	4.49
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.48
65	439735	AI635386	Hs.142846	hypothetical protein	4.48
	430261	AA305127	Hs.237225	hypothetical protein HT023	4.46
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.44
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	4.42
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	4.42
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.40
	447270	AC002551	Hs.331	general transcription factor IIIC, polyp	4.38
	434423	NM_006769	Hs.3844	LIM domain only 4	4.35
	404561				4.32

5	422969	AA782536	Hs.122647	N-myristoyltransferase 2	4.32
	423685	BE350494	Hs.49753	uvcal autoantigen with coiled coil domain	4.32
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.32
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.31
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	4.30
10	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	4.24
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	4.21
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	4.20
	410294	AB014515	Hs.323712	KIAA0615 gene product	4.18
	447124	AW976438	Hs.17428	RBP1-like protein	4.18
15	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.16
	443857	AI089292	Hs.287621	hypothetical protein FLJ14069	4.15
	446711	AF169692	Hs.12450	protocadherin 9	4.15
	405403				4.14
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	4.13
20	417531	NM_003157	Hs.1087	serine/threonine kinase 2	4.12
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	4.10
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.09
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	4.08
	445459	AI478629	Hs.158465	likely ortholog of mouse putative IKK re	4.08
25	402791				4.04
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.04
	447568	AF155655	Hs.18885	CGI-116 protein	4.04
	452211	AI985513	Hs.233420	ESTs	4.02
	443292	AK000213	Hs.9196	hypothetical protein	4.01
30	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.00
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.95
	430456	AA314998	Hs.241503	hypothetical protein	3.95
	437531	AI400752	Hs.112259	T cell receptor gamma locus	3.93
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.91
35	410011	AB020641	Hs.57856	PFTAIR protein kinase 1	3.91
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.91
	409928	AL137163	Hs.57549	hypothetical protein DJ473B4	3.90
	411598	BE336654	Hs.70937	H3 histone family, member A	3.90
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	3.90
40	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.89
	401045				3.89
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.89
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.88
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.88
45	431930	AB035301	Hs.272211	cadherin 7, type 2	3.88
	453047	AW023798	Hs.286025	ESTs	3.88
	401785				3.88
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.86
	406414				3.86
50	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.84
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.83
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	3.82
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.82
	423052	M28214	Hs.123072	RAB3B, member RAS oncogene family	3.82
55	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.82
	419423	D26488	Hs.90315	KIAA0007 protein	3.80
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.80
	431499	NM_001514	Hs.258561	general transcription factor IIB	3.80
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPp8-	3.78
60	430291	AV660345	Hs.238126	CGI-49 protein	3.76
	431637	AI879330	Hs.265960	hypothetical protein FLJ10563	3.74
	440411	N30256	Hs.151093	hypothetical protein DKFZp434G1415	3.74
	405917				3.74
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.73
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.73
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	3.72
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.70
	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.70
	446965	BE242873	Hs.16677	WD repeat domain 15	3.70
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.70
	433852	AI378329	Hs.126629	ESTs	3.70
	447397	BE247676	Hs.18442	E-1 enzyme	3.68
	405718				3.68

	425217	AU076696	Hs.155174	CDC5 (cell division cycle 5, S. pombe, h	3.68
	421734	AI318624	Hs.107444	Homo sapiens cDNA FLJ20562 lis, clone KA	3.67
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	3.67
	402408				3.66
5	452946	X95425	Hs.31092	EphA5	3.66
	419078	M93119	Hs.89584	insulinoma-associated 1	3.66
	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	3.65
	423396	AI382555	Hs.127950	bromodomain-containing 1	3.65
	446320	AF126245	Hs.14791	acyl-Coenzyme A dehydrogenase family, me	3.63
10	404939				3.62
	403137				3.60
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.60
	404210				3.59
	443775	AF291664	Hs.204732	matrix metalloproteinase 26	3.56
15	452501	AB037791	Hs.29716	hypothetical protein FLJ10980	3.56
	422443	NM_014707	Hs.116753	histone deacetylase 7B	3.55
	420230	AL034344	Hs.284186	forkhead box C1	3.55
	418428	Y12490	Hs.85092	thyroid hormone receptor interactor 11	3.54
	433002	AF048730	Hs.279906	cyclin T1	3.53
20	405793				3.52
	457940	AL360159	Hs.306517	Homo sapiens TRlpartite motif protein ps	3.52
	402444				3.52
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isolo	3.51
	414222	AL135173	Hs.878	sorbitol dehydrogenase	3.51
25	422384	AA224077	Hs.42438	Sm protein F	3.50
	447805	AW627932	Hs.19614	gemin4	3.50
	454265	H03556	Hs.300949	ESTs, Weakly similar to thyroid hormone	3.50
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	3.48
	413435	X51405	Hs.75360	carboxypeptidase E	3.46
30	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.46
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.45
	408418	AW963897	Hs.44743	KIAA1435 protein	3.45
	421887	AW161450	Hs.109201	CGI-86 protein	3.44

Table 7: 42 GENES ENCODING SMALL MOLECULE TARGETS UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

5 Table 7 shows 42 genes up-regulated in prostate cancer compared to normal adult tissues that are likely to be small molecule targets. These were selected as for Table 5 and the predicted protein contained a structural domain that is indicative of a drugable structure (e.g. protease, kinase, phosphatase, receptor). The functional domain is indicated for each gene.

10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 15 R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain	R1
20	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	trypsin	31.80
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	trypsin	24.91
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	Androgen_recep,hormone_rec,zf-C4	19.72
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	DPPIV_N_term,Peptidase_S9	16.28
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	7tm_1	15.40
25	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	Peptidase_M3	14.81
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	7tm_1	12.04
	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	PDEase	11.10
	407021	U52077		gb:Human mariner1 transposase gene, comp	SET,Transposase_1	11.02
	401424				arginase	9.58
30	410001	AB041036	Hs.57771	kallikrein 11	trypsin	9.03
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	Peptidase_M10	8.76
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	ABC_tran,ABC_membrane	7.64
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	Hydrolase	7.20
	431892	NM_002742	Hs.2891	protein kinase C, mu	pkinase,DAG_PE-bind,PH	6.49
35	447359	NM_012093	Hs.18268	adenylate kinase 5	adenylatekinase	6.00
	400301	X03635	Hs.1657	estrogen receptor 1	Oest_recep,zf-C4,hormone_rec	5.78
	421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	E1-E2_ATPase,Hydrolase	5.37
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	ABC_tran	5.31
	447752	M73700	Hs.105938	lactotransferrin	transferrin,7tm_1	5.29
40	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	E1-E2_ATPase,Hydrolase,HMA	5.08
	403047				trypsin	4.91
	427617	D42063	Hs.199179	RAN binding protein 2	Ran_BP1,zf-RanBP,TPR,pro_isomerase	4.88
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	lipoxygenase,PLAT	4.82
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	ldl_recept_b,ldl_recept_a,EGF	4.82
45	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	T4_deiodinase	4.32
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	Peptidase_M1	4.24
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	pkinase	4.21
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	AAA,Viral_helicase1	4.20
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	pkinase	4.12
50	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	7tm_1	3.91
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	pkinase	3.91
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	ldl_receptLa	3.82
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	Y_phosphatase,Band_41,PDZ	3.70
	447397	BE247676	Hs.18442	E-1 enzyme	Hydrolase	3.68
55	452946	X95425	Hs.31092	EphA5	EPH_bdb,fn3,pkinase,SAM	3.66
	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	7tm_2	3.65
	443775	AF291664	Hs.204732	matrix metalloproteinase 26	Peptidase_M10	3.56
	457940	AL360159	Hs.306517	Homo sapiens TRIPartite motif protein ps	SPRY,7tm_1	3.52
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isolo	A_deaminase	3.51
60	413435	X51405	Hs.75360	carboxypeptidase E	Zn_carbOpept	3.46
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	lipase	3.46

TABLE 8: 136 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Table 8 shows 136 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2. The "average" normal prostate level was set to the mean amongst 4 normal prostate tissues. The "average" prostate cancer level was set to the 85th percentile amongst 73 tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of normal prostate to prostate cancer			
Pkey	ExAccn	UnigeneID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	57.69
425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	19.70
426752	X69490	Hs.172004	titin	15.25
442082	R41823	Hs.7413	ESTs; calyntenin-2	10.05
407245	X90568	Hs.172004	titin	9.38
422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp58611518 (I	9.05
420813	X51501	Hs.99949	prolactin-induced protein	8.18
411987	AA375975	Hs.183380	*ESTs, Moderately similar to ALU7_HUMAN	7.45
404567				5.62
416030	H15261	Hs.21948	ESTs	5.51
444892	A1620617	Hs.148565	ESTs	5.27
444573	AW043590	Hs.225023	ESTs	5.20
428068	AW016437	Hs.233462	ESTs	5.08
437440	AA846804	Hs.123694	ESTs	4.95
404113				4.75
452279	AA286844	Hs.61260	hypothetical protein FLJ13164	4.75
421058	AW297967	Hs.188181	ESTs	4.63
445592	AV654382	Hs.17947	*ESTs, Weakly similar to K02F3.10 [C.ele	4.53
405163				4.49
405227				4.45
454059	NM_003154	Hs.37048	statherin	4.45
450152	A1138635	Hs.22968	ESTs	4.40
407013	U35637		*gb:Human nebulin mRNA, partial cds"	4.03
403612				4.02
440089	AA864468	Hs.135646	ESTs	4.00
408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	3.98
436726	AA324975	Hs.128993	*ESTs, Weakly similar to KIAA0465 protei	3.95
459367	BE148877		*gb:CM4-HT0244-111199-040-h12 HT0244 Hom	3.95
427318	AF186081	Hs.175783	zinc transporter	3.92
411762	AW860972		*gb:QVO-CT0387-180300-167-h07 CT0387 Hom	3.85
418668	AW407987	Hs.87150	Human clone A9A2BR11 (CAC)n/(GTG)n repea	3.75
458311	AF069478		*gb:AF069478 Homo sapiens astrocytoma li	3.61
403649				3.60
419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.58
412519	AA196241	Hs.73980	*troponin T1, skeletal, slow"	3.51
414206	AW276887	Hs.46609	ESTs	3.45
427419	NM_000200	Hs.177888	histatin 3	3.37
420777	AA280223	Hs.130865	ESTs	3.35
428134	AA421773	Hs.161008	ESTs	3.31
450218	R02018	Hs.168640	*Ank, mouse, homolog of	3.30
433474	A1192195	Hs.147174	*EST, Highly similar to ubiquitin-protei	3.30
418833	AW974899	Hs.292776	ESTs	3.26
400440	X83957	Hs.83870	nebulin	3.16

	413778	AA090235	Hs.75535	*myosin, light polypeptide 2, regulatory	3.06
	423151	AW838068		*gb:QV3-LT0048-010300-109-f02 LT0048 Hom	3.05
	445060	AA830811	Hs.88808	ESTs	2.98
	457065	AI476318	Hs.192480	ESTs	2.95
5	432456	H00093		*gb:ph8f12u_19/1TV Outward Alu-primed hn	2.92
	405678				2.85
	406707	S73840	Hs.931	*myosin, heavy polypeptide 2, skeletal m	2.81
	444105	AW189097	Hs.166597	ESTs	2.78
10	433968	AL157518	Hs.90421	PRO2463 protein	2.73
	438522	AA809431	Hs.258886	ESTs	2.73
	436562	H71937	Hs.169756	*complement component 1, s subcomponent	2.68
	412417	AA102268	Hs.42175	ESTs	2.67
	455590	BE072259		*gb:QV4-BT0536-271299-059-g04 BT0536 Hom	2.65
	415380	F07953	Hs.16085	putative G-protein coupled receptor	2.65
15	428729	AL162331	Hs.191436	hypothetical protein FLJ10619	2.64
	408537	AW207734		*gb:Ul-H-BI2-age-h-01-0-Uls1 NCI_CGAP_S	2.63
	424706	AA741336	Hs.152108	transcriptional unit N143	2.63
	413212	BE072092		*gb:PM4-BT0532-160200-003-b11 BT0532 Hom	2.63
20	406704	M21665	Hs.929	*myosin, heavy polypeptide 7, cardiac mu	2.62
	437507	AA758538	Hs.246882	ESTs	2.60
	410384	AI933794	Hs.42745	ESTs	2.58
	408074	R20723	Hs.124764	ESTs	2.58
	436653	AA829828	Hs.292402	ESTs	2.52
25	458090	AI282149	Hs.56213	*ESTs, Highly similar to FXD3_HUMAN FORK	2.51
	432003	AI689154	Hs.122972	ESTs	2.50
	436915	AA737400	Hs.142230	ESTs	2.50
	410028	AW576454	Hs.258553	ESTs	2.46
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.45
30	422046	AI638562		*gb:ts50a10.x1 NCI_CGAP_Ut1 Homo sapiens	2.44
	451122	AA015767	Hs.193587	ESTs	2.40
	422646	H87863	Hs.151380	ESTs	2.36
	451237	AW600293		*gb:EST00049 pGEM-T library Homo sapiens	2.36
	400001			AFFX control: BioB-3	2.36
35	415835	Z45365		*gb:HSC2NF061 normalized infant brain cD	2.36
	439706	AW872527	Hs.59761	ESTs	2.36
	423341	AW242394	Hs.252495	ESTs	2.36
	436486	AA742221	Hs.120633	ESTs	2.35
	407449	AJ002784		gb:Homo sapiens mRNA; fetal brain cDNA 5	2.33
40	430573	AA744550	Hs.136345	ESTs	2.32
	401974				2.31
	443356	AL044498	Hs.133262	*ESTs, Weakly similar to PH0217 reverse	2.31
	430751	NM_012471	Hs.247868	transient receptor potential channel 5	2.25
	439128	AI949371	Hs.153089	ESTs	2.25
45	448765	R15337	Hs.21958	*Homo sapiens cDNA FLJ10532 fis, clone N	2.25
	451130	AI762250	Hs.211347	ESTs	2.24
	405420				2.23
	455029	AW851258		*gb:IL3-CT0220-160200-066-H06 CT0220 Hom	2.23
	438224	AA933999		*gb:con91f04.s1 Soares_NFL_T_GBC_S1 Homo	2.23
50	407764	BE008347		*gb:CMO-BN0154-080400-325-h04 BN0154 Hom	2.23
	413549	BE252470		*gb:601108292F1 NIH_MGC_16 Homo sapiens	2.23
	437010	AA741368	Hs.291434	ESTs	2.23
	435111	AI914279	Hs.213740	ESTs	2.22
	403375				2.21
55	455060	AW853441		*gb:RC1-CT0252-030100-023-g09 CT0252 Hom	2.21
	409792	AW854153		*gb:RC3-CT0254-060400-029-d03 CT0254 Hom	2.20
	421154	AA284333	Hs.287631	*Homo sapiens cDNA FLJ14269 fis, clone P	2.19
	401963				2.18
	435034	AF168711	Hs.159397	x 010 protein	2.18
60	448998	AW998989	Hs.105749	KIAA0553 protein	2.18
	436816	AW297599	Hs.255667	ESTs	2.17
	442252	AI733395	Hs.129124	ESTs	2.17
	419310	AA236233	Hs.188716	ESTs	2.16
	418579	H91800	Hs.124156	ESTs	2.16
	423315	R54109	Hs.26096	ESTs	2.16
65	432744	AA988835	Hs.38664	ESTs	2.15
	424492	AI133482	Hs.165210	ESTs	2.15
	424770	AA425562		*gb:zw46e05.r1 Soares_total_fetus_Nb2HF8	2.15
	437101	AA744518	Hs.120610	ESTs	2.15
	428793	AC004957	Hs.298975	*ESTs, Highly similar to collapsin-2-lik	2.15

	415708	H56475	"gb:yt87d11.r1 Soares_pineal_gland_N3HPG	2.13
	459619			2.12
	427506	AK000134	Hs.179100 hypothetical protein FLJ20127	2.12
	452508	AA804174	Hs.184354 ESTs	2.10
5	410881	AW809157	"gb:RCO-ST0118-041099-031-c07_1 ST0118 Homo sapiens cDNA, mRNA sequence"	2.10
	403087			2.10
	403869			2.10
	445028	D81194	Hs.282499 ESTs	2.10
10	447884	H29505	"gb:ym60d10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone 5', mRNA sequence"	2.10
	414575	H11257	Hs.295233 ESTs	2.09
	420351	BE218221	Hs.190044 ESTs	2.08
	426998	BE274360	"gb:601121068F1 NIH_MGC_20 Homo sapiens cDNA clone 5', mRNA sequence"	2.08
	405455			2.08
15	423843	AA332652	"gb:EST36627 Embryo, 8 week I Homo sapiens cDNA 5' end similar to similar to monoamine oxidase B, mRNA sequence"	2.08
	406135			2.07
	427048	BE246180	Hs.121385 ESTs	2.07
	403493			2.05
20	444514	AI682905	Hs.270431 "ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]"	2.05
	435884	AA701443	Hs.192868 ESTs	2.05
	419629	AB020695	Hs.91662 KIAA0888 protein	2.03
	405900			2.03
25	457350	AW974438	Hs.194136 "ESTs, Moderately similar to AF091457 1 zinc finger protein RIN ZF [R.norvegicus]"	2.02
	400007		AFFX control: BioDn-5	2.01
	406978	M64358	"gb:Human rhom-3 gene, exon."	2.00

TABLE 8A shows the accession numbers for those primekeys lacking a unigeneID in Table 8. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
<hr/>			
15	Pkey	CAT number	Accessions
	407764	1014849_1	BE008347 BE008320 BE083307 BE083311 AW075968
	408537	1064753_1	AW207734 D60164 D81150 D81078 D61356 AW996804
	409792	1154677_1	AW854153 AW500210 BE145772 AW501310
20	410881	1225682_1	AW809157 AW812181 AW812175 AW812172 AW812161 AW812165
	411762	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860988 AW860925 AW860922 AW860986 AW860984 AW860989
	413212	1353792_1	BE072092 BE072106 BE072086 BE072098 BE072103
	413549	1375933_2	BE252470 BE147573
	415708	1548209_1	H56475 F29401 F34552
25	415835	1558511_1	Z45365 R25905 H05203 T77496
	422046	210744_1	AI638562 T16929 H13401 F07773 R55836
	423151	225415_1	AW838068 AW837986 AW838067 AA322487 AW837936
	423843	232510_1	AA332652 AA331633 AW999369 AW902993 BE170475 AA378845 AW964175 A475221
	424770	243504_1	AA425562 AI880208 AA346646 N22655 AW811775 AW811786
30	426998	274259_1	BE274360
	432456	347718_2	H00093 H00079 H00070 H00054 H00049 H00063 AW905306 AW905241 AW905410 AW905307 AW905411 AW905240
	AW905210		AW905352 AW905304 AW905239 AW905242 AW905243 H00087
	438224	452656_1	AA933999 AA781181
35	447884	740749_1	H29505 R18575 Z43580 T48738 AI435454 BE004683
	451237	863269_1	AW600293 AI767468
	455029	1249374_1	AW851258 AW851435 AW851106 AW851421
	455060	1251259_1	AW853441 BE145228 BE145218 BE145162 BE145283
	455590	1335127_1	BE072259 BE072230 BE007911
40	458311	543550_1	AF069478 AF069479 AF069480

TABLE 8B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in table 8. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5				
10	Pkey:	Unique number corresponding to an Eos probe set		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
15	Pkey	Ref	Strand	Nt_position
	401963	3126783	Plus	51382-51521
	401974	3126777	Plus	85330-85683
	403087	8954241	Plus	169511-169795
20	403375	9255944	Minus	92554-92795
	403493	7341425	Plus	157568-159084
	403612	8469060	Minus	94723-94859
	403649	8705159	Minus	27141-27247
	403869	7280046	Minus	34379-34583
25	404113	9588571	Minus	13446-13646
	404567	7249169	Minus	101320-101501
	405163	9966267	Minus	161171-161299
	405227	6731245	Minus	22550-22802
	405420	7211837	Minus	13428-13582
30	405455	7656675	Plus	134112-134671
	405678	4079670	Plus	151821-152027
	405900	6758795	Minus	71181-71535
	406135	9164918	Minus	65489-65715

TABLE 9: 1001 GENES SIGNIFICANTLY UP-REGULATED IN NORMAL PROSTATE COMPARED TO PROSTATE CANCER

Table 9 shows 1001 genes significantly up-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 8.14. The "average" normal prostate level was set to the mean amongst 4 normal prostate tissues. The "average" prostate cancer level was set to the 85th percentile amongst 73 tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

15	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of prostate cancer to normal prostate			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
20	451002	AA013299	Hs.8018	ESTs, Weakly similar to ALU3_HUMAN ALU S	1684.00
	435596	AA689465	Hs.188999	ESTs	738.00
	443576	AI078027	Hs.169338	ESTs	246.86
	434247	AA928116	Hs.272065	ESTs	245.20
25	400452	AK000185	gb:Homo sapiens cDNA FLJ20178 fis, clone		222.00
	405932				221.33
	427906	AA864330	Hs.166520	ESTs	212.00
	443685	AI686550	Hs.174481	ESTs	163.20
	451554	AI474866	Hs.193237	ESTs	149.45
30	418323	NM_002118	Hs.1162	major histocompatibility complex, class	126.11
	429480	M36860	Hs.9295	elastin (supravalvular aortic stenosis,	123.27
	426025	AW138330	Hs.233778	ESTs	120.00
	418917	X02994	Hs.1217	adenosine deaminase	106.75
	404407				105.71
35	442027	AI652926	Hs.128395	ESTs	100.53
	433704	AA608684	Hs.121705	ESTs, Moderately similar to ALUC_HUMAN I	94.00
	453758	U83527	gb:HSU83527 Human fetal brain (M.Lovett)		89.18
	415354	F06495	gb:HSC1AB051 normalized infant brain cDN		87.73
	424239	M67439	Hs.143526	dopamine receptor D5	86.82
40	444143	AW747996	Hs.160999	ESTs	86.43
	401672				77.26
	430590	AW383947	Hs.246381	CD68 antigen	68.47
	411972	BE074959	gb:PM0-BT0582-310100-001-f08 BT0582 Homo		68.00
	448992	AI766053	Hs.188346	ESTs	61.26
45	408828	BE540279	gb:601059857F1 NIH_MGC_10 Homo sapiens c		57.71
	409653	AW451693	Hs.220826	ESTs	56.40
	402864				54.67
	422673	N59027	gb:yv59d11.r1 Soares fetal liver spleen		54.00
50	422568	AA372275	Hs.279800	Homo sapiens cDNA FLJ11383 fis, clone HE	54.00
	438907	R32704	Hs.301298	ESTs	52.96
	405172				52.96
	444897	AW137088	Hs.144857	ESTs	52.32
	458019	AW592931	Hs.256298	ESTs	51.63
	405275	AB028989	Hs.88500	mitogen-activated protein kinase 8 inter	50.98
55	457815	AA703679	Hs.106999	ESTs, Weakly similar to SYT5_HUMAN SYNAP	49.60
	424385	AA339666	gb:EST44776 Fetal brain I Homo sapiens c		48.90
	407172	T54095	gb:ya92c05.s1 Stratagene placenta (93722		47.98
	428202	AA424163	Hs.156895	ESTs	46.83
	435672	AI700148	Hs.283626	ESTs	43.57
60	420283	AA485224	Hs.57734	G protein-coupled receptor kinase-intera	43.00
	417016	AA837098	Hs.269933	ESTs	42.70
	438854	AF074994	Hs.24240	ESTs	42.67

	406134			42.43	
	457319	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypotheti	42.31
	409314	AA070266		gb:zm69d04.r1 Stratagene neuroepithelium	42.25
	401124				41.61
5	429316	AI371157	Hs.178538	ESTs	40.00
	420317	AB006628	Hs.96485	KIAA0290 protein	39.64
	457586	AW062439		gb:MR0-CT0060-120899-001-f08 CT0060 Homo	39.60
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi]	38.73
	430269	BE221682	Hs.178364	ESTs	38.06
10	439602	W79114	Hs.58558	ESTs	36.69
	433686	AA604799	Hs.136528	ESTs, Moderately similar to ALU1_HUMAN A	36.29
	417993	AW963705	Hs.295806	ESTs, Weakly similar to ALU7_HUMAN ALU S	36.18
	428214	AA936282	Hs.120397	ESTs	36.10
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	36.08
15	426264	BE314852	Hs.168694	hypothetical protein FLJ10257	36.00
	415911	H08796	Hs.124952	ESTs	36.00
	457502	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	35.23
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	35.20
	401468				34.89
20	458561	AI220150	Hs.211195	ESTs	34.60
	433601	BE350738	Hs.123993	ESTs, Weakly similar to T00366 hypotheti	33.24
	454977	AW848032		gb:IL3-CT0214-231299-053-D11 CT0214 Homo	32.96
	402828				32.93
	414522	AW518944	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone L	31.76
25	402842				31.68
	421245	AA285363		gb:HTH280 HTCCL1 Homo sapiens cDNA 5'/3'	31.59
	401631	F05183	Hs.1799	CD1D antigen, d polypeptide	31.26
	408057	AW139565		gb:UL-H-BI1-aea-d-04-0-UI.s1 NCI_CGAP_Su	31.24
	408069	H81795		gb:ys68a10.r1 Soares retina N2b4HR Homo	31.20
30	438694	T87479	Hs.291797	ESTs	31.09
	449156	AF103907	Hs.171353	prostate cancer antigen 3	29.78
	428796	AU076734	Hs.193665	solute carrier family 28 (sodium-coupled	29.76
	452549	AI907039		gb:PM-BT134-020499-566 BT134 Homo sapien	29.59
	410129	BE244074	Hs.285531	regulator of Fas-induced apoptosis	29.53
35	414464	AI870175	Hs.13957	ESTs	29.47
	412326	R07566	Hs.73817	Small inducible cytokine A3 (homologous	29.22
	459081	W07808		gb:zb03a12.r1 Soares_fetal_lung_NbHL19W	29.20
	448702	AW102670	Hs.122464	ESTs	29.13
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	28.74
40	443412	W84893	Hs.9305	angiotensin receptor-like 1	28.61
	457324	AB028990	Hs.243901	KIAA1067 protein	28.24
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	28.18
	457140	AI279960	Hs.178140	ESTs	28.12
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	28.06
45	457669	AW104257	Hs.123426	ESTs, Weakly similar to putative serine/	27.61
	412429	AV650262	Hs.75765	GRO2 oncogene	27.36
	405495				27.33
	406516				27.25
	407997	AW135429	Hs.243577	ESTs	26.96
50	442115	AW452332	Hs.257554	ESTs	26.36
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	26.34
	402838				26.32
	449846	AI979284	Hs.200552	ESTs	26.21
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	26.20
55	439792	NM_014856	Hs.6684	KIAA0476 gene product	25.91
	450096	AI682088	Hs.223368	ESTs	25.60
	424196	AL133660	Hs.142926	Homo sapiens mRNA; cDNA DKFZp434M0927 (f	25.57
	414246	BE391090	Hs.280278	EST	25.57
	420848	NM_005188	Hs.99980	Cas-Br-M (murine) ecotropic retroviral t	25.48
60	424778	AA251048	Hs.153042	lymphocyte antigen 9	25.42
	409126	AA063426		gb:zf70c08.s1 Soares_pineal_gland_N3HPG	25.25
	443936	AW083491	Hs.31196	ESTs	25.22
	419392	W28573		gb:51110 Human retina cDNA randomly prim	25.01
	411201	T74588	Hs.8509	ESTs, Weakly similar to CO3_HUMAN COMPLE	24.85
65	422940	BE077458		gb:RC1-BT0606-090500-015-b04 BT0606 Homo	24.76
	437571	AA760894	Hs.153023	ESTs	24.74
	433973	AI014723	Hs.131770	ESTs	24.57
	422416	BE019557	Hs.11900	Human DNA sequence from clone RP4-583P15	24.53
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	24.49

	443668	U25758	Hs.134584	ESTs	24.49
	424800	AL035588	Hs.153203	MyoD family inhibitor	24.10
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	24.04
	430565	AL122081	Hs.244343	cadherin related 23	24.00
5	433694	AI208611	Hs.12066	Homo sapiens cDNA FLJ11720 fis, clone HE	23.89
	451045	AA215672		gb:zr96e09.s1 NCI_CGAP_GCB1 Homo sapiens	23.83
	408583	AW449674	Hs.47359	ESTs	23.73
	444040	AF204231	Hs.182982	golgin-67	23.62
	414182	AA136301		gb:zk93g04.s1 Soares_pregnant_uterus_NbH	23.39
10	418678	NM_001327	Hs.167379	cancer/testis antigen	23.20
	408380	AF123050	Hs.44532	diubiquitin	22.68
	456076	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly	22.65
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	22.38
	444917	R68651	Hs.144997	ESTs	22.26
15	444381	BE387335	Hs.283713	ESTs	22.08
	415788	AW628686	Hs.78851	KIAA0217 protein	22.04
	410896	AW809637		gb:MR4-ST0124-261099-015-b07 ST0124 Homo	22.00
	412978	AI431708	Hs.820	homeo box C6	21.95
	458418	AV653846	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	21.94
20	454791	BE071874		gb:RC2-BT0522-120200-014-a06 BT0522 Homo	21.84
	408748	J05500	Hs.47431	spectrin, beta, erythrocytic (includes s	21.26
	416011	H14487		gb:ym18c10.r1 Soares infant brain 1NIB H	21.24
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	21.14
	447047	AI623698	Hs.246306	Homo sapiens cDNA: FLJ23529 fis, clone L	21.11
25	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	21.10
	409841	AW502139		gb:UH-HF-BR0p-ajr-e-05-0-UI.r1 NIH_MGC_5	21.07
	405685				20.90
	457359	AI983207	Hs.192481	ESTs, Weakly similar to SYPH_HUMAN SYNAP	20.84
30	423067	AA321355	Hs.285401	ESTs	20.74
	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3 (G	20.73
	401201				20.73
	458278	W28912	Hs.129019	ESTs	20.68
	439097	H66948		gb:yr86d10.r1 Soares fetal liver spleen	20.67
35	414875	H42679	Hs.77522	major histocompatibility complex, class	20.66
	400926				20.66
	451355	NM_004197	Hs.444	serine/threonine kinase 19	20.64
	446982	AW500221	Hs.43616	Homo sapiens mRNA for FLJ00029 protein,	20.61
	417105	X60992	Hs.81226	CD6 antigen	20.61
	405777				20.51
40	424123	AW966158	Hs.58582	Homo sapiens cDNA FLJ12702 fis, clone NT	20.20
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	20.10
	443271	BE568568	Hs.195704	ESTs	19.98
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	19.98
	418819	AA228776	Hs.191721	ESTs	19.94
45	457595	AA584854		gb:nc09h11.s1 NCI_CGAP_Phe1 Homo sapiens	19.90
	404426				19.84
	412571	U43143	Hs.74049	fms-related tyrosine kinase 4	19.79
	431457	NM_012211	Hs.256297	integrin, alpha 11	19.62
50	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	19.57
	418994	AA296520	Hs.89546	Selectin E (endothelial adhesion molecu	19.56
	437158	AW090198	Hs.4779	KIAA1150 protein	19.52
	437866	AA156781	Hs.83992	ESTs	19.44
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	19.34
55	433057	X15675	Hs.296832	Human pTR7 mRNA for repetitive sequence	19.22
	421730	AW449808	Hs.164036	glucosamine (N-acetyl)-6-sulfatase (Sanf	19.21
	456557	AA284477	Hs.96618	ESTs	18.77
	440806	AI247422	Hs.129966	ESTs	18.76
	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	18.65
60	416155	AI807264	Hs.205442	ESTs, Weakly similar to AF117610 1 inner	18.64
	437820	AA769062	Hs.16029	ESTs, Weakly similar to alternatively sp	18.62
	450923	AW043951	Hs.38449	ESTs	18.59
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	18.58
	424537	AI673027	Hs.143271	ESTs	18.55
65	447742	AF113925	Hs.19405	caspase recruitment domain 4	18.52
	415251	RA2863	Hs.7124	ESTs	18.47
	440770	AA912815	Hs.222078	ESTs	18.40
	407711	AI085846	Hs.25522	ESTs	18.32
	427157	U51166	Hs.173824	thymine-DNA glycosylase	18.28
	409847	AW501751	Hs.279733	ESTs	18.15

	417240	N57568	Hs.176028	EST	18.13
	435732	AF229178	Hs.123136	leucine rich repeat and death domain con	18.12
	436896	AW977385	Hs.278615	ESTs	18.12
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	17.90
5	429490	AJ971131	Hs.293684	ESTs, Weakly similar to alternatively sp	17.82
	429984	AL050102	Hs.227209	DKFZP586F1019 protein	17.82
	449214	AI889114	Hs.195663	ESTs	17.75
	433867	AK000596	Hs.3618	hippocalcin-like 1	17.72
10	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	17.71
	401515				17.67
	444045	AI097439	Hs.135548	ESTs	17.58
	442754	AL045825	Hs.210197	ESTs	17.55
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	17.54
	432415	T16971	Hs.289014	ESTs	17.50
15	427829	AI188225	Hs.127462	ESTs	17.50
	432516	R08003	Hs.188013	ESTs	17.44
	435259	AA152106	Hs.4859	cyclin L ania-6a	17.36
	414989	T81668		gb:yd29c04.r1 Soares fetal liver spleen	17.31
20	444880	AW118683	Hs.154150	ESTs	17.30
	417651	R06874	Hs.268628	ESTs	17.27
	453457	AL037103	Hs.270599	ESTs, Weakly similar to unnamed protein	17.22
	424246	AW452533	Hs.143604	Kaiso	17.22
	419078	M93119	Hs.89584	insulinoma-associated 1	17.18
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	17.14
25	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	17.14
	455254	AW877015		gb:QV2-PT0010-250300-096-f12 PT0010 Homo	17.14
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	17.12
	426678	H08170	Hs.113755	ESTs	17.12
	426403	NM_000361	Hs.2030	thrombomodulin	17.01
30	425905	AB032959	Hs.161700	KIAA1133 protein	17.00
	438867	AW451157	Hs.181157	ESTs	16.98
	420940	AA830664	Hs.143974	ESTs	16.94
	459234	AJ940425		gb:CM0-CT0052-150799-024-c04 CT0052 Homo	16.92
	404756				16.91
35	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	16.90
	420568	F09247	Hs.167399	protocadherin alpha 5	16.88
	443559	AJ076765	Hs.269899	ESTs	16.80
	438703	AJ803373	Hs.31599	ESTs	16.78
	411424	AW845985		gb:RC2-CT0163-200999-002-H08 CT0163 Homo	16.70
40	402895				16.69
	422538	NM_006441	Hs.118131	5,10-methenyltetrahydrofolate synthetase	16.68
	447108	AW449602	Hs.217953	ESTs, Moderately similar to NK-TUMOR REC	16.65
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	16.54
	438567	AW451955	Hs.153065	ESTs	16.52
45	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	16.50
	410721	R23534	Hs.2730	heterogeneous nuclear ribonucleoprotein	16.50
	437133	AB018319	Hs.5460	KIAA0776 protein	16.40
	408182	AA047854		gb:zf49g04.r1 Soares retina N2b4HR Homo	16.32
	417315	AI080042	Hs.180450	ribosomal protein S24	16.30
50	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	16.28
	439882	AA847856	Hs.124565	ESTs	16.20
	418277	AW135221	Hs.130812	ESTs	16.09
	410688	AW796342		gb:PM2-UM0027-230200-002-h02 UM0027 Homo	16.04
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	16.04
55	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	16.02
	447033	AJ357412	Hs.157601	EST - not in UniGene	16.02
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	15.94
	408599	AA055800	Hs.222933	ESTs	15.93
	446012	AV656098	Hs.172382	hypothetical protein FLJ20001	15.86
60	409671	AA076769		gb:7B02B10 Chromosome 7 Fetal Brain cDNA	15.85
	405934				15.84
	426108	AA622037	Hs.166468	programmed cell death 5	15.84
	416208	AW291168	Hs.41285	ESTs	15.48
	410708	AA534370	Hs.154088	Homo sapiens cDNA: FLJ22756 fis, clone K	15.42
65	447342	AI199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAM1	15.38
	454563	AW807530		gb:CM0-ST0081-130999-054-d02 ST0081 Homo	15.37
	411507	AW850140		gb:IL3-CT0219-261099-023-D11 CT0219 Homo	15.36
	438170	AJ916685	Hs.194601	ESTs	15.29
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	15.26

	406638	M13861	gb:Human T-cell receptor active beta-cha	15.26
	446686	AW138043	Hs.156307 ESTs	15.25
	434485	AI623511	Hs.118567 ESTs	15.24
	441188	AW292830	Hs.255609 ESTs	15.22
5	444172	BE147740	Hs.104558 ESTs	15.22
	409521	BE244854	Hs.159578 Homo sapiens mRNA for FLJ00020 protein,	15.16
	420748	AA279956	Hs.88672 ESTs	15.14
	422583	AA410506	Hs.118578 H.sapiens mRNA for ribosomal protein L18	15.14
	424240	AB023185	Hs.143535 calcium/calmodulin-dependent protein kin	15.12
10	451118	AI862096	Hs.60640 ESTs	15.12
	437495	BE177778	gb:RC1-HT0598-310300-012-f07 HT0598 Homo	15.12
	445467	AI239832	Hs.15617 ESTs, Weakly similar to ALU4_HUMAN ALU S	15.06
	418305	AW006783	Hs.6686 ESTs	15.03
	402812			15.02
15	436851	AA732480	Hs.293581 ESTs	15.00
	400991			15.00
	415752	BE314524	Hs.78776 Human putative transmembrane protein (nm	14.96
	429900	AA460421	Hs.30875 ESTs	14.90
	403683			14.84
20	430315	NM_004293	Hs.239147 guanine deaminase	14.80
	451952	AL120173	Hs.301663 ESTs	14.72
	424687	J05070	Hs.151738 matrix metalloproteinase 9 (gelatinase B	14.69
	447229	BE617135	gb:601441677F1 NIH_MGC_65 Homo sapiens c	14.67
	425818	AB021225	Hs.159581 matrix metalloproteinase 17 (membrane-in	14.65
25	448553	AI638449	Hs.173031 ESTs	14.63
	431089	BE041395	Hs.283676 ESTs, Weakly similar to unknown protein	14.60
	459145	AI903354	gb:RC-BT029-100199-117 BT029 Homo sapien	14.55
	449650	AF055575	Hs.297647 ESTs, Moderately similar to calcium chan	14.54
	400952			14.46
30	445885	AI734009	Hs.127699 EST cluster (not in UniGene)	14.44
	407938	AA905097	Hs.85050 phospholamban	14.42
	431676	AI685464	Hs.292638 ESTs	14.40
	437210	AA311443	Hs.293563 Homo sapiens mRNA; cDNA DKFZp586E2317 (f	14.36
	451900	AB023199	Hs.27207 KIAA0982 protein	14.36
35	445800	AA126419	Hs.301632 ESTs	14.32
	412368	AW945992	Hs.181125 immunoglobulin lambda locus	14.31
	409055	AW304028	Hs.300578 ESTs	14.23
	408763	W57550	Hs.301526 Homo sapiens cDNA FLJ13181 fis, clone NT	14.22
40	446734	AL049278	Hs.16074 Homo sapiens mRNA; cDNA DKFZp5641153 (lr	14.22
	413551	BE242639	Hs.75425 ubiquitin associated protein	14.22
	421913	AI934365	Hs.109439 osteoglycin (osteoinductive factor, mime	14.22
	452712	AW838616	gb:RC5-LT0054-140200-013-D01 LT0054 Homo	14.22
	451468	AW503398	Hs.210047 ESTs	14.16
	406038	Y14443	Hs.88219 zinc finger protein 200	14.14
45	424909	S78187	Hs.153752 cell division cycle 25B	14.07
	434078	AW880709	Hs.283683 EST	14.07
	415254	AI815831	Hs.184378 ESTs	14.05
	418196	AI745649	Hs.26549 ESTs, Weakly similar to T00066 hypotheti	14.02
	410020	T86315	Hs.728 ribonuclease, RNase A family, 2 (liver,	13.98
50	411352	NM_002890	Hs.758 RAS p21 protein activator (GTPase activa	13.98
	429848	AF145439	Hs.225946 chemokine (C-C motif) receptor 9	13.95
	413729	BE159999	gb:QV1-HT0412-270300-123-d10 HT0412 Homo	13.90
	400125			13.88
	420319	AW406289	Hs.96593 hypothetical protein	13.85
55	448272	AI479094	Hs.170786 ESTs	13.80
	422695	AA315158	gb:EST186956 HCC cell line (maltastasis t	13.80
	424565	AW102723	Hs.75295 guanylate cyclase 1, soluble, alpha 3	13.78
	458048	H30340	Hs.173705 Homo sapiens cDNA: FLJ22050 fis, clone H	13.78
	408894	AI935400	Hs.217286 ESTs	13.76
60	454093	AW860158	gb:RC0-CT0379-290100-032-b04 CT0379 Homo	13.75
	410889	X91662	Hs.66744 twist (Drosophila) homolog (acrocephalos	13.74
	457751	AI908238	gb:IL-BT166-180399-010 BT166 Homo sapien	13.72
	455131	AW857913	gb:RC0-CT0323-231199-031-b05 CT0323 Homo	13.69
	408364	AW015238	Hs.128453 ESTs	13.67
65	425907	AA365752	Hs.155965 ESTs	13.62
	402359			13.60
	401044			13.53
	409877	AW502498	Hs.157150 ESTs, Weakly similar to zinc finger prot	13.53
	423690	AA328648	Hs.23804 ESTs	13.49

	430685	AI690234	Hs.191666	ESTs, Weakly similar to reverse transcri	13.47
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	13.46
	447858	AW080339	Hs.211911	ESTs	13.44
	435716	AI573283	Hs.38458	ESTs	13.44
5	439120	H56389	gb:yt87c03.r1	Soares_pineal_gland_N3HPG	13.43
	402788				13.40
	451591	AA886446	Hs.146278	ESTs	13.40
	405411				13.38
10	426558	AW188574	Hs.24218	ESTs	13.34
	453506	AA132818	Hs.110407	ESTs, Weakly similar to coded for by C.	13.33
	416445	ALO43004	Hs.300678	Human serine/threonine kinase mRNA, part	13.32
	457084	AI074149	Hs.150905	ESTs, Weakly similar to chondroitin 4-su	13.32
	403838				13.32
15	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	13.30
	434318	AW207552	Hs.116328	ESTs, Weakly similar to dJ134E15.1 [H.sa	13.28
	435193	N41359	Hs.218107	ESTs	13.28
	414756	AW451101	Hs.159489	ESTs, Moderately similar to hexokinase I	13.27
	420626	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	13.26
	420052	AA418850	Hs.44410	ESTs	13.25
20	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	13.25
	403851				13.24
	422647	W07492	Hs.157101	ESTs	13.21
	433598	AI762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN A	13.21
	409065	AB033113	Hs.50187	KIAA1287 protein	13.20
25	435063	R21966	Hs.57734	G protein-coupled receptor kinase-intera	13.19
	439367	BE386844	Hs.248746	ESTs	13.17
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	13.16
	420569	AA278362	Hs.289062	Homo sapiens cDNA FLJ12334 fis, clone MA	13.14
	447883	BE262802	Hs.4909	dickkopf (Xenopus laevis) homolog 3	13.07
30	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	13.06
	414789	AA155859	Hs.79708	ESTs	13.05
	451418	BE387790	Hs.26369	ESTs	13.04
	443494	T99719	Hs.270404	Homo sapiens cDNA: FLJ22389 fis, clone H	13.03
35	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	13.02
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	13.00
	407122	H20276	Hs.31742	ESTs	13.00
	456491	AL137466	Hs.97277	Homo sapiens mRNA; cDNA DKFZp434H1322 (I	12.99
	448172	N75276	Hs.135904	ESTs	12.98
	452144	AA032197	Hs.102558	ESTs	12.96
40	418953	BE267154	Hs.125752	ESTs	12.96
	416182	NM_004354	Hs.79069	cyclin G2	12.94
	451154	AA015879	Hs.33536	ESTs	12.93
	412257	AW903830		gb:CM4-NN1037-250400-155-h04 NN1037 Homo	12.93
45	449784	AW161319	Hs.12915	ESTs	12.92
	432695	D63480	Hs.278634	KIAA0146 protein	12.92
	454105	NM_001259	Hs.38481	cyclin-dependent kinase 6	12.92
	439093	AA534163	Hs.5476	serine protease inhibitor, Kazal type, 5	12.90
	416098	H41324	Hs.31581	ESTs, Moderately similar to ST1B_HUMAN S	12.88
	424897	D63216	Hs.153684	frizzled-related protein	12.88
50	414604	AU076649	Hs.76556	growth arrest and DNA-damage-inducible 3	12.88
	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cds	12.84
	452560	BE077084		gb:RC5-BT0603-220200-013-C07 BT0603 Homo	12.84
	413869	NM_000878	Hs.75596	Interleukin 2 receptor, beta	12.80
55	452359	BE167229	Hs.29206	Homo sapiens clone 24659 mRNA sequence	12.80
	435886	BE265839	Hs.12126	hepatocellular carcinoma-associated anti	12.78
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	12.78
	412226	W26786		gb:15d7 Human retina cDNA randomly prime	12.77
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.76
60	447769	AW873704	Hs.48764	ESTs	12.76
	414478	AI306389	Hs.76240	adenylate kinase 1	12.76
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	12.68
	450704	H85157	Hs.40696	ESTs	12.66
	405856				12.66
65	412935	BE267045	Hs.75064	tubulin-specific chaperone c	12.65
	402802				12.62
	452588	AA889120	Hs.110637	Homeo box A10	12.62
	419978	NM_001454	Hs.93974	forkhead box J1	12.62
	403137				12.60
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	12.57

	448076	AJ133123	Hs.20196	adenylate cyclase 9	12.56
	450462	F07097	Hs.300828	Homo sapiens mRNA full length insert cDN	12.54
	405236				12.52
5	409292	AA071051		gb:zm58e05.s1 Stratagene fibroblast (937	12.47
	421540	AA767669	Hs.10242	ESTs	12.47
	425840	AW978731	Hs.301824	ESTs	12.44
	443181	AI039201	Hs.54548	ESTs	12.42
	452436	BE077546	Hs.31447	ESTs	12.42
10	455183	AW984111		gb:RCO-HN0007-160300-011-f09 HN0007 Homo	12.40
	432887	AI926047	Hs.162859	ESTs	12.37
	410494	M36564	Hs.64016	protein S (alpha)	12.36
	439024	R96696	Hs.35598	ESTs	12.36
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	12.36
	432892	AL042615	Hs.15995	ESTs	12.35
15	418982	AJ348838	Hs.13073	ESTs	12.35
	414516	AJ307802	Hs.279551	ESTs	12.34
	440134	BE410734		gb:601301619F1 NIH_MGC_21 Homo sapiens c	12.29
	443873	AL048542	Hs.16291	ESTs	12.28
	401286				12.26
20	454020	AW962845	Hs.256527	ESTs	12.24
	420077	AW512260	Hs.87767	ESTs	12.24
	443837	AI984625	Hs.9884	spindle pole body protein	12.24
	407519	X64979		gb:H.sapiens mRNA HTPCRX01 for olfactory	12.23
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (12.22
25	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	12.20
	405325				12.20
	451009	AA013140	Hs.115707	ESTs	12.18
	423066	Y18264	Hs.120171	ESTs	12.17
	439556	AI623752	Hs.163603	ESTs	12.16
30	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	12.15
	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	12.14
	453542	AW836724	Hs.33190	Homo sapiens mRNA expressed only in plac	12.11
	440106	AA864968	Hs.127699	ESTs	12.10
35	417605	AF006609	Hs.82294	regulator of G-protein signalling 3	12.10
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	12.04
	420061	AW024937	Hs.29410	ESTs	12.02
	458727	AI022813	Hs.92679	Homo sapiens clone CDABP0014 mRNA sequen	11.96
	445407	AI222658	Hs.221889	ESTs, Weakly similar to la costa (D.mela	11.95
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (Isofo	11.94
40	414129	AI990287	Hs.270798	ESTs	11.93
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	11.92
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	11.92
	443912	R37257	Hs.184780	ESTs	11.92
45	424606	AA343936		gb:EST49786 Gall bladder 1 Homo sapiens	11.90
	434217	AW014795	Hs.23349	ESTs	11.90
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	11.90
	422423	AF283777	Hs.116481	CD72 antigen	11.89
	409398	AW386461		gb:PM4-PT0019-121299-004-F02 PT0019 Homo	11.89
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	11.82
50	446180	AI074413	Hs.14220	hypothetical protein FLJ20450	11.80
	414341	D80004	Hs.75909	KIAA0182 protein	11.80
	406538				11.79
	433253	AW450502	Hs.24218	ESTs	11.79
	447397	BE247676	Hs.18442	E-1 enzyme	11.78
55	451684	AF216751	Hs.26813	CDA14	11.76
	416862	R23765	Hs.23575	ESTs	11.74
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.72
	428826	AL048842	Hs.194019	attractin	11.72
60	433037	NM_014158	Hs.279938	HSPC067 protein	11.72
	447476	BE293466	Hs.20880	ESTs	11.72
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	11.72
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	11.72
	401680	NM_005578	Hs.180398	LIM domain-containing preferred transloc	11.69
	422576	BE548555	Hs.118554	CGI-83 protein	11.68
65	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	11.68
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	11.67
	425917	W28517	Hs.117167	Homo sapiens cDNA: FLJ23067 fis, clone L	11.66
	418693	AI750878	Hs.87409	thrombospondin 1	11.64
	400557				11.62

	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	11.60
	419047	AW952771	Hs.90043	ESTs	11.59
	420441	AJ986160	Hs.88446	ESTs	11.59
	400885				11.57
5	409853	AW502327		gb:UH-HF-BR0p-aka-a-07-0-UI.r1 NIH_MGC_5	11.56
	400802				11.56
	434540	NM_016045	Hs.5184	TH1 drosophila homolog	11.55
	431449	M55994	Hs.256278	tumor necrosis factor receptor superfamily	11.55
10	425928	S55736	Hs.238852	ESTs, Weakly similar to hypothetical pro	11.54
	434701	AA460479	Hs.4096	KIAA0742 protein	11.53
	434228	Z42047	Hs.283978	ESTs; KIAA0738 gene product	11.52
	420729	AW964897	Hs.290825	ESTs	11.52
	428328	AA426080	Hs.98489	ESTs	11.50
	433887	AW204232	Hs.279522	ESTs	11.50
15	414812	X72755	Hs.77367	monokine induced by gamma interferon	11.46
	457718	F18572	Hs.22978	ESTs	11.44
	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	11.42
	459029	AA131376	Hs.285203	fibroblast growth factor 12	11.42
	456267	AI127958	Hs.83393	cystatin E/M	11.39
20	433285	AW975944	Hs.237396	ESTs	11.38
	449186	AW291876	Hs.196986	ESTs	11.37
	447861	AI434593	Hs.164294	ESTs	11.37
	456023	R00028		gb:ye70a06.s1 Soares fetal liver spleen	11.36
	439444	AI277652	Hs.54578	ESTs	11.31
25	401163				11.31
	430886	L36149	Hs.248116	chemokine (C motif) XC receptor 1	11.28
	450784	AW246803	Hs.47289	ESTs	11.28
	452391	AL044829	Hs.29331	carnitine palmitoyltransferase I, muscle	11.27
	449625	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	11.26
30	456827	AA075687	Hs.147176	epidermal growth factor receptor substra	11.24
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	11.24
	432093	H28383		gb:yf52c03.r1 Soares breast 3NbHBst Homo	11.24
	407335	AA631047	Hs.158761	Homo sapiens cDNA FLJ13054 fis, clone NT	11.23
	442501	AA315267	Hs.23128	ESTs	11.22
35	429746	AJ237672	Hs.214142	5,10-methylenetetrahydrofolate reductase	11.21
	422858	R35398		gb:yg64g10.r1 Soares infant brain 1NIB H	11.20
	415156	X84908	Hs.78060	phosphorylase kinase, beta	11.20
	446713	AV660122	Hs.282675	ESTs	11.20
	452221	C21322	Hs.11577	ESTs	11.20
40	418261	W78902	Hs.293297	ESTs	11.17
	433332	AJ367347	Hs.127809	ESTs	11.16
	434539	AW748078	Hs.214410	ESTs	11.16
	413471	BE142098		gb:CM4-HT0137-220999-017-d11 HT0137 Homo	11.14
	410037	AB020725	Hs.58009	KIAA0918 protein	11.14
45	405601				11.13
	458332	AI000341	Hs.220491	ESTs	11.12
	427654	AA410183	Hs.137475	ESTs	11.12
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	11.10
	431475	AI567669	Hs.287316	ESTs	11.10
50	425710	AF030880	Hs.159275	solute carrier family, member 4	11.08
	413748	AW104057	Hs.19193	ESTs	11.07
	409208	Y00093	Hs.51077	integrin, alpha X (antigen CD11C (p150),	11.07
	457278	W92745	Hs.193324	ESTs	11.03
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.02
55	445701	AF055581	Hs.13131	lymphocyte adaptor protein	11.02
	408338	AW867079		gb:MR1-SN0033-120400-002-c10 SN0033 Homo	10.95
	401030	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	10.95
	437891	AW006969	Hs.6311	hypothetical protein FLJ20859	10.94
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	10.94
60	421562	AA530994	Hs.105803	ghrelin precursor	10.92
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.92
	400132				10.92
	436420	AA443966	Hs.31595	ESTs	10.90
	424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	10.88
65	433264	D85782	Hs.3229	cysteine dioxygenase, type I	10.88
	429842	AI366213	Hs.173422	KIAA1605 protein	10.87
	412405	AW948126		gb:RCO-MT0013-280300-031-a12 MT0013 Homo	10.85
	400615				10.80
	425018	BE245277	Hs.154196	E4F transcription factor 1	10.80

	456011	BE243628		gb:TCBAP1D1053 Pediatric pre-B cell acut	10.79
	455982	BE176862		gb:RC4-HT0587-170300-012-a04 HT0587 Homo	10.74
	450418	BE218418	Hs.201802	ESTs	10.73
5	412490	AW803564	Hs.288850	ESTs	10.72
	436962	AW377314	Hs.5364	DKFZP5641052 protein	10.70
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.70
	449967	RA0978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	10.70
	449590	AA694070	Hs.268835	ESTs	10.68
10	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.68
	426530	U24578	Hs.170250	complement component 4A	10.66
	428600	AW863261	Hs.15036	ESTs, Highly similar to AF161358 1 HSPCO	10.64
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	10.64
	451593	AF151879	Hs.26706	CGI-121 protein	10.62
	438893	AF075031	Hs.29327	ESTs	10.62
15	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	10.61
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	10.58
	406513	AA715328	Hs.291205	ESTs	10.57
	407826	AA128423	Hs.40300	calpain 3, (p94)	10.57
	419550	D50918	Hs.90998	KIAA0128 protein; septin 2	10.56
20	428522	R10184	Hs.191987	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.56
	459526	AI142350	Hs.146735	EST	10.55
	411448	AA178955	Hs.271439	ESTs	10.54
	410102	AW248508	Hs.279727	ESTs;	10.52
	406577				10.52
25	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	10.51
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	10.50
	400880				10.48
	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	10.48
30	434715	BE005346	Hs.116410	ESTs	10.46
	406851	AA609784	Hs.180255	major histocompatibility complex, class	10.44
	413409	AI638418	Hs.21745	ESTs	10.44
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	10.44
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 lis, clone L	10.44
35	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	10.44
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	10.44
	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.42
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	10.41
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, lol	10.41
40	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chai	10.40
	458873	AW150717	Hs.296176	STAT induced STAT inhibitor 3	10.38
	415082	AA160000	Hs.137396	ESTs	10.37
	429124	AW505086	Hs.196914	minor histocompatibility antigen HA-1	10.36
	417187	AB011151	Hs.81505	KIAA0579 protein	10.34
45	426827	AW067805	Hs.172665	methyleneetetrahydrofolate dehydrogenase	10.34
	424280	NM_000030	Hs.271366	alanine-glyoxylate aminotransferase homo	10.33
	446099	T93096	Hs.17126	ESTs	10.32
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	10.31
	409995	AW960597	Hs.30164	ESTs	10.30
50	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	10.30
	406394	AA172106	Hs.110950	Rag C protein	10.30
	406189				10.29
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	10.26
	401598	AA172106	Hs.110950	Rag C protein	10.26
55	456995	T89832	Hs.170278	ESTs	10.26
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	10.24
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	10.24
	401384				10.23
	456226	D13168	Hs.82002	endothelin receptor type B	10.22
60	426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-cis and 9-cis	10.21
	423032	AI684746	Hs.119274	ESTs	10.20
	436556	AI364997	Hs.7572	ESTs	10.20
	418400	BE243026	Hs.301989	KIAA0246 protein	10.19
	437401	AA757196	Hs.121190	ESTs	10.19
	403690				10.17
65	423790	BE152393		gb:CM2-HT0323-171199-033-a08 HT0323 Homo	10.16
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	10.16
	434967	AW975009	Hs.292274	ESTs	10.16
	432827	Z68128	Hs.3109	Rho GTPase activating protein 4	10.16
	432660	AI288430	Hs.64004	ESTs	10.14

	452234	AW084176	Hs.223296	ESTs	10.14
	445629	AI245701		gb:qk31f05.x1 NCI_CGAP_Kid3 Homo sapiens	10.13
	457236	AA626142	Hs.179991	ESTs, Weakly similar to KPCE_HUMAN PROTE	10.13
	444605	AI174603	Hs.254105	enolase 1, (alpha)	10.12
5	450313	AI038989	Hs.24809	hypothetical protein FLJ10826	10.12
	407482	NM_006056			10.12
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	10.11
	441201	AW118822	Hs.128757	ESTs	10.10
	435157	AW014605	Hs.179872	ESTs	10.10
10	417308	H60720	Hs.81892	KIAA0101 gene product	10.09
	442582	AI204266	Hs.179303	ESTs	10.05
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.04
	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar t	10.04
	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	10.04
15	423698	AA329796	Hs.1098	DKFZp434J1813 protein	10.02
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	10.00
	414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD)	10.00
	421832	NM_016098	Hs.108725	HSPC040 protein	10.00
20	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	10.00
	452039	AI922988	Hs.172510	ESTs	10.00
	434673	AW137442	Hs.136965	ESTs	10.00
	427978	AA418280	Hs.180040	Homo sapiens cDNA: FLJ22439 fis, clone H	10.00
	457803	BE501815	Hs.198011	ESTs	9.99
	428279	AA425310	Hs.155766	ESTs	9.98
25	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	9.98
	417049	N72394	Hs.44862	ESTs	9.96
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a 1	9.96
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	9.96
	443678	AW009605	Hs.231923	ESTs	9.96
30	447567	AW474513	Hs.224397	ESTs, Weakly similar to B48013 proline-r	9.94
	414709	AA704703	Hs.77031	Sp2 transcription factor	9.94
	434596	T59538		gb:yb65g12.s1 Stratagene ovary (937217)	9.94
	427630	BE276115	Hs.144980	ESTs, Weakly similar to CA13_HUMAN COLLA	9.93
35	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (9.92
	423349	AF010258	Hs.127428	homeo box A9	9.92
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	9.92
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	9.90
	417986	AA481003	Hs.97128	ESTs	9.90
	425174	D87450	Hs.154978	KIAA0261 protein	9.90
40	438171	AW976507	Hs.293515	ESTs	9.90
	421984	AW972187	Hs.110443	hypothetical protein FLJ22215	9.89
	408597	NM_005291	Hs.46453	G protein-coupled receptor 17	9.88
	413907	AI097570	Hs.71222	ESTs	9.87
	451296	AW801383	Hs.118578	H.sapiens mRNA for ribosomal protein L18	9.86
45	433409	AI278802	Hs.25661	ESTs	9.85
	450360	AW117416	Hs.245484	ESTs	9.85
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	9.84
	449824	AI962552	Hs.226765	ESTs	9.84
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	9.82
50	431066	AF026273	Hs.249175	interleukin-1 receptor-associated kinase	9.82
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	9.80
	443371	AI792888	Hs.145489	ESTs	9.80
	437159	AL050072		gb:Homo sapiens mRNA; cDNA DKFZp566E1346	9.75
55	425242	D13635	Hs.155287	KIAA0010 gene product	9.74
	447498	N67619	Hs.43687	ESTs	9.74
	426759	AI590401	Hs.21213	ESTs	9.73
	435129	AI381659	Hs.267086	ESTs	9.72
	437672	AW748265	Hs.5741	flavohepatoxin b5+b5R	9.72
	438209	AL120659	Hs.6111	KIAA0307 gene product	9.72
60	438440	AA807228	Hs.225161	ESTs	9.72
	449720	AA311152	Hs.288708	ESTs; Weakly similar to KIAA0226 [H.sapi	9.72
	414291	AI289619	Hs.13040	ESTs	9.72
	436206	AK001451	Hs.265561	CD2-associated protein	9.70
	446896	T15767	Hs.22452	Homo sapiens cDNA: FLJ21084 fis, clone C	9.70
65	412667	AW977540	Hs.269254	ESTs	9.70
	423301	S67580	Hs.1645	cytochrome P450, subfamily IVA, polypept	9.67
	440757	AW118645	Hs.160004	ESTs	9.67
	441412	AI393657	Hs.159750	ESTs	9.66
	421044	AF061871	Hs.101302	collagen, type XII, alpha 1	9.66

	414726	BE466863	Hs.280099	ESTs	9.66
	418485	R91679	Hs.124981	ESTs	9.66
	433480	X02422	Hs.181125	immunoglobulin lambda locus	9.65
	441530	AI248301	Hs.127112	ESTs	9.65
5	433533	D53304	Hs.653394	ESTs	9.65
	421470	R27496	Hs.1378	annexin A3	9.64
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	9.64
	429324	AA488101	Hs.199245	inactivation escape 1	9.62
	450244	AA007534	Hs.125062	ESTs	9.62
10	407660	AW063190	Hs.279101	ESTs	9.61
	406554				9.60
	426404	AA377607	Hs.273138	ESTs	9.58
	447045	AW392394	Hs.278569	KIAA0064 gene product	9.58
	449894	AK001578	Hs.24129	hypothetical protein FLJ10716	9.58
15	448376	AI494332	Hs.196963	ESTs	9.58
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (lr	9.56
	446572	AV659151	Hs.282961	ESTs	9.56
	459245	BE242623	Hs.31939	manic fringe (Drosophila) homolog	9.55
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	9.54
20	414697	BE266134	Hs.76927	translocase of outer mitochondrial membr	9.54
	410846	AW807057		gb:MR4-ST0062-031199-018-b03 ST0062 Homo	9.52
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	9.52
	427308	D26067	Hs.174905	KIAA0033 protein	9.52
	415995	NM_004573	Hs.994	phospholipase C, beta 2	9.51
25	434846	AW295389	Hs.119768	ESTs	9.51
	414342	AA742181	Hs.75912	Homo sapiens cDNA: FLJ22199 fis, clone H	9.50
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	9.50
	443123	AA094538	Hs.6588	ESTs	9.50
	439312	AA833902	Hs.270745	ESTs	9.48
30	449375	R07114	Hs.271224	ESTs	9.48
	436357	AJ132085		gb:Homo sapiens mRNA for axonemal dynein	9.44
	458723	AW137726	Hs.244352	ESTs, Moderately similar to laminin alph	9.44
	457526	AW450584	Hs.192131	ESTs, Weakly similar to RIBB [H.sapiens]	9.43
	404741				9.43
35	422409	NM_005428	Hs.116237	vav 1 oncogene	9.43
	403708				9.42
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	9.42
	417380	T06809		gb:EST04698 Fetal brain, Stratagene (cat	9.42
40	422501	AA354690	Hs.144967	ESTs	9.42
	426197	AA004410	Hs.167835	acyl-Coenzyme A oxidase 1, palmitoyl	9.42
	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	9.42
	412110	AW893569		gb:RCO-NN0021-040400-021-c10 NN0021 Homo	9.41
	414158	AA361623	Hs.288775	Homo sapiens cDNA FLJ13900 fis, clone TH	9.41
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	9.40
45	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	9.40
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	9.40
	426959	BE262745		gb:601153869F1 NIH_MGC_19 Homo sapiens c	9.39
	417519	AI689987	Hs.177669	ESTs, Weakly similar to RMS1_HUMAN REGUL	9.39
	457181	BE514362	Hs.296422	FK506-binding protein 3 (25kD)	9.39
50	402835				9.38
	404632				9.38
	446566	H95741	Hs.17914	Homo sapiens cDNA: FLJ22801 fis, clone K	9.37
	455369	AW903533		gb:CM1-NN1031-060400-178-d05 NN1031 Homo	9.37
55	444001	AI095087	Hs.152299	ESTs, Moderately similar to ALU5_HUMAN A	9.36
	458191	AI420611	Hs.127832	ESTs	9.36
	431374	BE258532	Hs.251871	CTP synthase	9.34
	429327	AA283981	Hs.199248	prostaglandin E receptor 4 (subtype EP4)	9.33
	407061	X97748		gb:H.sapiens PTX3 gene promotor region.	9.33
	416967	BE616731	Hs.80645	interferon regulatory factor 1	9.33
60	423013	AW875443	Hs.22209	secreted modular calcium-binding protein	9.33
	439461	AA693960	Hs.103158	ESTs	9.33
	418830	BE513731	Hs.88959	Human DNA sequence from clone 967N21 on	9.32
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MASP-2 [H.sa	9.32
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	9.32
65	452859	AI300555	Hs.288158	Homo sapiens cDNA: FLJ23591 fis, clone L	9.32
	403237				9.32
	415000	AW025529	Hs.239812	ESTs, Weakly similar to CALM_HUMAN CALMO	9.31
	417951	AW976410	Hs.289069	Homo sapiens cDNA: FLJ21016 fis, clone C	9.30
	419066	Z98492	Hs.6975	PRO1073 protein	9.30

	448443	AW167128	Hs.231934	ESTs	9.30
	405125				9.30
	409768	AW499566		gb:U1-HF-BR0p-aj-h-03-0-U1.r1 NIH_MGC_5	9.28
5	453708	AI191811	Hs.54629	ESTs	9.28
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	9.27
	410055	AJ250839	Hs.58241	gene for serine/threonine protein kinase	9.26
	448692	AW013907	Hs.224276	ESTs, Moderately similar to predicted us	9.26
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	9.25
	422497	D29642	Hs.1528	KIAA0053 gene product	9.25
10	414140	AA281279	Hs.23317	ESTs	9.24
	435980	AF274571	Hs.129142	ESTs; Weakly similar to DEOXYRIBONUCLEAS	9.24
	458530	BE395035	Hs.199889	ESTs, Weakly similar to KIAA0874 protein	9.24
	402585				9.24
	420819	AA280700		gb:zs95h11.s1 NCL_CGAP_GCB1 Homo sapiens	9.23
15	444755	AA431791	Hs.183001	ESTs	9.22
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	9.22
	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-4	9.20
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	9.19
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	9.18
20	434267	AI206589	Hs.116243	ESTs	9.17
	409213	U61412	Hs.51133	PTK6 protein tyrosine kinase 6	9.17
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	9.16
	451736	AW080356	Hs.293684	ESTs, Weakly similar to alternatively sp	9.15
	413627	BE182082	Hs.246973	ESTs	9.14
25	416134	AA528402	Hs.74861	activated RNA polymerase II transcriptio	9.14
	449251	AW151660	Hs.31444	ESTs	9.14
	452813	U54727	Hs.191445	ESTs	9.14
	443622	AI911527	Hs.11805	ESTs	9.14
30	413260	BE075281		gb:PM1-BT0585-290200-005-d07 BT0585 Homo	9.12
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	9.12
	446442	BE221533	Hs.257858	ESTs	9.12
	438540	AA810021	Hs.136906	ESTs	9.12
	426251	M24283	Hs.168383	Inter cellular adhesion molecule 1 (CD54)	9.11
	410290	AA402307	Hs.73818	ubiquinol-cytochrome c reductase hinge p	9.10
35	437398	AA913736	Hs.126715	ESTs	9.10
	421559	NM_014720	Hs.105751	Sta20-related serine/threonine kinase	9.10
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	9.10
	430799	C19035	Hs.164259	ESTs	9.09
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	9.08
40	453942	AW190920	Hs.19928	ESTs	9.08
	425844	T68073	Hs.158628	serine (or cysteine) proteinase inhibito	9.08
	434658	AI624436	Hs.194488	ESTs	9.07
	453999	BE328153	Hs.240087	ESTs	9.06
	436490	R71543	Hs.18713	ESTs	9.05
45	409192	AA065131	Hs.233439	ESTs, Weakly similar to ALU7_HUMAN ALU S	9.05
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	9.04
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	9.04
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	9.04
	432012	AW301344	Hs.195969	ESTs	9.04
50	422520	AU076730	Hs.117977	kinesin 2 (60-70kD)	9.02
	418650	BE386750	Hs.86978	prolyl endopeptidase	9.02
	423008	M81590	Hs.123016	5-hydroxytryptamine (serotonin) receptor	9.02
	436476	AA326108	Hs.53631	ESTs	9.02
	448206	BE622585	Hs.3731	ESTs	9.02
55	431574	AW572659	Hs.261373	adenosine A2b receptor pseudogene	9.01
	443453	R99876	Hs.269882	ESTs	9.01
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	9.01
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.00
	449810	AB008681	Hs.23994	activin A receptor, type IIB	9.00
60	406780	AA902386	Hs.286	ribosomal protein L4	8.99
	429169	AW341130	Hs.197757	ESTs, Moderately similar to FGFE_HUMAN F	8.99
	421326	AF051428	Hs.103504	estrogen receptor 2 (ER beta)	8.97
	425491	AA883316	Hs.255221	ESTs	8.96
	425516	BE000707	Hs.29567	ESTs	8.96
65	439773	AI051313	Hs.143315	ESTs	8.96
	443247	BE614387	Hs.47378	ESTs	8.96
	456623	AI084125	Hs.108106	transcription factor	8.95
	438707	L08239	Hs.5326	porcupine	8.95
	402240				8.85

	444152	AI125694	Hs.149305	Homo sapiens cDNA FLJ14264 fis, clone PL	8.95
	409842	AW501756		gb:U1-HF-BR0p-ajm-c-09-0-ULr1 NIH_MGC_5	8.94
	416277	W78765	Hs.73580	ESTs	8.94
	456697	AI908006	Hs.111334	ferritin, light polypeptide	8.94
5	410762	AF226053	Hs.66170	HSKM-B protein	8.92
	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	8.92
	442320	AI287817	Hs.129636	ESTs	8.92
	449673	AA002064	Hs.18920	ESTs	8.91
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	8.90
10	437916	BE566249	Hs.20999	Homo sapiens cDNA: FLJ23142 fis, clone L	8.90
	442732	AA257161	Hs.8658	hypothetical protein DKFZp434E0321	8.89
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	8.89
	411499	AW849282		gb:IL3-CT0215-020300-090-E06 CT0215 Homo	8.89
	431154	AW971228	Hs.290259	ESTs	8.89
15	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	8.88
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	8.87
	406422				8.87
	422926	NM_016102	Hs.121748	ring finger protein 16	8.87
	435220	D50030	Hs.104	HGF activator	8.86
20	418203	X54942	Hs.83758	CDC28 protein kinase 2	8.86
	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	8.85
	439250	H66566	Hs.271711	ESTs	8.85
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	8.84
	450000	AI952797	Hs.10888	Homo sapiens cDNA: FLJ21559 fis, clone C	8.83
25	425657	T89839	Hs.119471	ESTs	8.83
	425694	U51333	Hs.159237	hexokinase 3 (white cell)	8.82
	419972	AL041465	Hs.294038	ESTs, Moderately similar to ALU2_HUMAN A	8.82
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	8.82
	413413	D82520	Hs.301834	Homo sapiens cDNA FLJ10952 fis, clone PL	8.82
30	428807	AA435997	Hs.104930	ESTs	8.82
	415839	R40611	Hs.137565	ESTs	8.81
	419553	N34145	Hs.250614	ESTs	8.80
	420309	AW043637	Hs.21766	ESTs	8.80
35	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	8.80
	447865	AW292577	Hs.94445	ESTs	8.80
	459172	BE063380		gb:PM0-BT0275-291099-002-g10 BT0275 Homo	8.80
	403259				8.78
	411534	AW850473		gb:IL3-CT0219-280100-061-B11 CT0219 Homo	8.78
40	456161	BE264645	Hs.282093	Homo sapiens cDNA: FLJ21918 fis, clone H	8.77
	413654	AA331881	Hs.75454	peroxiredoxin 3	8.76
	401744				8.76
	425348	AL137477	Hs.155912	cadherin-like 24	8.76
	423396	AI382555	Hs.127950	bromodomain-containing 1	8.75
45	450649	NM_001429	Hs.297722	Human DNA sequence from clone RP1-85F18	8.75
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	8.74
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.74
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	8.74
	427596	AA449506	Hs.179765	Homo sapiens mRNA; cDNA DKFZp586H1921 (f	8.73
	432488	AA551010	Hs.216640	ESTs	8.72
50	448980	AL137527	Hs.22703	Homo sapiens mRNA; cDNA DKFZp434P1018 (f	8.72
	429455	AI472111	Hs.292507	ESTs	8.71
	429855	AW385597	Hs.138902	ESTs, Weakly similar to B34087 hypotheti	8.71
	441746	H59955	Hs.127829	ESTs	8.70
55	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	8.70
	413492	D87470	Hs.75400	KIAA0280 protein	8.70
	435706	W31254	Hs.7045	GL004 protein	8.70
	433741	AA609019	Hs.159343	ESTs	8.70
	426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	8.69
	422779	AA317036	Hs.41989	ESTs	8.67
60	449785	AI225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	8.67
	420144	AA811813	Hs.119421	ESTs	8.66
	420235	AA256756	Hs.31178	ESTs	8.66
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.66
65	425762	BE244076	Hs.159578	Homo sapiens mRNA for FLJ00020 protein,	8.65
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombo	8.64
	418033	W68180	Hs.259855	Homo sapiens cDNA FLJ12507 fis, clone NT	8.64
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	8.64
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	8.64
	457277	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	8.63

	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	8.63
	410679	AW795196	Hs.215857	ring finger protein 14	8.63
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	8.62
	401851				8.62
5	401866				8.62
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	8.62
	408242	AA251594	Hs.43913	PIBF1 gene product	8.62
	422250	AW408530	Hs.113823	ClpX (caseinolytic protease X, E. coli)	8.62
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	8.62
10	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.62
	419541	AW749617		gb:RC3-BT0502-130100-012-g07 BT0502 Homo	8.60
	428839	AI767756	Hs.82302	ESTs	8.60
	429328	AA829402	Hs.47939	ESTs	8.60
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	8.60
15	452561	AI692181	Hs.49169	KIAA1634 protein	8.60
	420027	AF009746	Hs.94395	ATP-binding cassette, sub-family D (ALD)	8.60
	435205	X54136	Hs.181125	immunoglobulin lambda locus	8.60
	430900	U91939	Hs.248123	G protein-coupled receptor 25	8.60
	405074				8.59
20	437991	AI479773	Hs.181679	ESTs	8.59
	436346	BE328882	Hs.193096	ESTs, Moderately similar to U119_HUMAN U	8.58
	411079	AA091228		gb:cchn2152.seq.F Human fetal heart, Lam	8.57
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	8.56
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	8.56
25	448019	AW947164	Hs.195641	ESTs	8.56
	449865	AW204272	Hs.199371	ESTs	8.55
	431180	H55883		gb:yq94h03.r1 Soares fetal liver spleen	8.54
	445988	BE007663	Hs.13503	inactivation escape 2	8.54
	405876				8.54
30	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	8.54
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	8.54
	425671	AF193612	Hs.159142	lunatic fringe (Drosophila) homolog	8.54
	452413	AW082633	Hs.212715	ESTs	8.54
	421620	AA446183	Hs.91885	ESTs	8.53
35	444539	AI955765	Hs.146907	ESTs	8.52
	415102	M31899	Hs.77929	excision repair cross-complementing rode	8.51
	405552				8.51
	418068	AW971155	Hs.293902	ESTs, Weakly similar to protyl 4-hydroxy	8.50
	420133	AA426117	Hs.14373	ESTs	8.50
40	438887	R68857	Hs.265499	ESTs	8.50
	446468	AI765890	Hs.16341	ESTs, Moderately similar to !!!! ALU SUB	8.50
	446585	AV659397	Hs.282948	ESTs	8.50
	441896	AW891873		gb:CM3-NT0090-040500-173-b02 NT0090 Homo	8.50
45	437718	AI927288	Hs.196779	ESTs	8.48
	420656	AA279098	Hs.187636	ESTs	8.48
	429303	AW137635	Hs.44238	ESTs	8.48
	450624	AL043983	Hs.125063	Homo sapiens cDNA FLJ13825 fis, clone TH	8.48
	452573	AI907957	Hs.287622	Homo sapiens cDNA FLJ14082 fis, clone HE	8.48
	456341	AA229126	Hs.122647	N-myristoyltransferase 2	8.48
50	423024	AA593731	Hs.75613	CD36 antigen (collagen type I receptor,	8.47
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.46
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	8.46
	400268				8.46
	421828	AW891965	Hs.289109	dimethylarginine dimethylaminohydrolase	8.45
55	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	8.44
	421029	AW057782	Hs.293053	ESTs	8.44
	425171	AW732240	Hs.300615	ESTs	8.44
	459070	AI814302		gb:wj71c12.x1 NCI_CGAP_Lu19 Homo sapiens	8.42
	406006				8.42
60	412643	AW971239	Hs.293982	ESTs	8.42
	424775	AB014540	Hs.153026	SWAP-70 protein	8.42
	446848	AW136083	Hs.195266	ESTs, Weakly similar to S59501 interfero	8.42
	448043	AI458653	Hs.201881	ESTs	8.41
	407183	AA358015		gb:EST66864 Fetal lung III Homo sapiens	8.40
65	412324	AW978439	Hs.69504	ESTs	8.40
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	8.40
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	8.40
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	8.40
	438582	AI521310	Hs.283365	ESTs, Weakly similar to ALU5_HUMAN ALU S	8.40

	447685	AL122043	Hs.19221	hypothetical protein DKFZp566G1424	8.40
	459119	AW844498	Hs.289052	Homo sapiens LENG8 mRNA, variant C, part	8.38
	400817				8.37
5	425265	BE245297		gb:TCBAP1E2482 Pediatric pre-B cell acut	8.37
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	8.36
	439121	BE047779	Hs.44701	ESTs	8.36
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	8.36
	408327	AW182309	Hs.249963	ESTs, Highly similar to dJ1170K4.4 [H.sa	8.35
	403976				8.34
10	448064	AA379036		gb:EST91809 Synovial sarcoma Homo sapien	8.33
	442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fis, clone Y7	8.33
	428032	AW997704	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	8.32
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial ods	8.32
	458677	AW937670	Hs.254379	ESTs	8.32
15	420925	NM_015698	Hs.100391	T54 protein	8.30
	416475	T70298		gb:yd26g02.s1 Soares fetal liver spleen	8.30
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	8.30
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (8.30
	428455	AI732694	Hs.98520	ESTs	8.29
20	435343	AW194962	Hs.199028	ESTs	8.29
	450783	BE266695		gb:601190242F1 NIH_MGC_7 Homo sapiens cD	8.29
	404946				8.28
	422942	AF054839	Hs.122540	tetraspan 2	8.28
	453716	AA037675	Hs.152675	ESTs	8.28
25	437098	AA744488	Hs.132842	ESTs, Moderately similar to ALU1_HUMAN A	8.28
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	8.27
	401930	AF106069	Hs.23168	ubiquitin specific protease 15	8.26
	446554	AA151730	Hs.301789	ESTs, Weakly similar to similar to C.ele	8.26
	426290	AB007918	Hs.169182	KIAA0449 protein	8.25
30	419904	AA974411	Hs.18672	ESTs	8.25
	413886	AW958264	Hs.103832	ESTs, Weakly similar to TRHY_HUMAN TRICH	8.24
	424738	AI963740	Hs.46826	ESTs	8.24
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	8.24
	424534	D87682	Hs.150275	KIAA0241 protein	8.24
35	424429	U63830	Hs.146847	TRAF family member-associated NFKB activ	8.24
	442604	BE263710	Hs.279904	ESTs	8.22
	442992	AI914699	Hs.13297	ESTs	8.22
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	8.22
	457229	BE222450	Hs.266390	ESTs	8.21
40	423730	AA330214		gb:EST33935 Embryo, 12 week II Homo sapi	8.21
	411928	AA888624	Hs.19121	adaptor-related protein complex 2, alpha	8.20
	416051	AA835868	Hs.25253	Homo sapiens cDNA: FLJ20935 fis, clone A	8.20
	417231	R40739	Hs.21326	ESTs	8.20
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.20
45	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	8.20
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	8.19
	417687	AI828596	Hs.250691	ESTs	8.18
	423218	NM_015896	Hs.167380	BLu protein	8.18
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	8.18
50	406964	M21305	Hs.247946	Human alpha satellite and satellite 3 ju	8.18
	402401	U42349	Hs.71119	Putative prostate cancer tumor suppresso	8.18
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	8.18
	427857	AL133017	Hs.2210	thyroid hormone receptor interactor 3	8.17
	401519				8.17
55	447188	H65423	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	8.16
	424704	AI263293	Hs.152096	cytochrome P450, subfamily IIJ (arachido	8.16
	435854	AJ278120	Hs.4996	DKFZP564D166 protein	8.14
	448556	AW885606	Hs.5064	ESTs	8.14
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	8.14
60	453124	AI139058	Hs.23296	ESTs	8.14
	442812	AI018406	Hs.131284	ESTs	8.14
	421129	BE439899	Hs.89271	ESTs	8.14

TABLE 9A shows the accession numbers for those primekeys lacking a unigeneID in Table 9. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT number	Accession
	408057	1035720_-1	AW139565
	408069	103655_1	H81795 Z42291 R20973 AA046920
	408182	104479_1	AA047854 AA057506 AA053841
20	408338	1052148_1	AW867079 AW867086 AW182772
	408828	108463_1	BE540279 AW410659 AA057857 R77693 BE278674
	409126	110159_1	AA063426 AW962323 AW408063 AA063503 AA772927 AW753492 BE175371 AA311147
	409292	111586_1	AA071051 AA070584 AA069938 AA102136 AA074430
	409314	111841_1	AA070266 AA084967 AA126998
25	409385	112523_1	AA071267 T65940 T64515 AA071334
	409398	1126716_1	AW386461 AW876408 AW386672 AW386599 AW876258 AW386619 AW386289 AW876136 AW876203 AW876213 AW876301
			AW876295 AW876349 AW876365 AW876160 AW876369 AW876352 AW876271
	409671	114731_1	AA076769 AA076781 AI087968
	409768	1154035_1	AW499566 AW502378 AW499522 AW502046 AW502671 AW501917 AW501868 AW501721 AW502813
30	409841	1156088_1	AW502139 AW502432 AW502235 AW501683 AW502647
	409842	1156119_1	AW501756 AW502096 AW502465 AW501715
	409853	1156226_1	AW502327 AW502488 AW501829 AW502625 AW502687
	410531	1207200_1	AW752953 H88044 BE156092
	410688	1216101_1	AW796342 AW796356 BE161430
35	410846	1223902_1	AW807057 AW807054 AW807189 AW807193 AW807369 AW807429 AW807364 AW807365 AW807078 AW807256 AW807180
			AW807331
	410896	1226053_1	AW809637 AW809697 AW810554 AW809707 AW809885 AW810000 AW810088 AW809742 AW809816 AW809749 AW809639
			AW809722 AW809836 AW809774 AW810023 AW810013 AW809813 AW809660 AW809728 AW809768 AW809951 AW809657
			AW809954
40	411079	123128_1	AA091228 H71860 H71073
	411424	1245497_1	AW845985 AW845991 AW845982
	411499	1248105_1	AW849292 AW849431 AW849422 AW849428 AW849420 AW849424 AW849427
	411507	1248607_1	AW850140 AW850195 AW850192
	411534	1248827_1	AW850473 AW850471 AW850431 AW850523
45	411972	1268491_1	BE074959 AW880160
	412110	1277844_1	AW893569 AW893571 AW893588 AW893593
	412226	1284289_1	W26786 AW998612 AW902272
	412257	1285376_1	AW903830 BE071916
50	412405	1293012_1	AW948126 AW948139 AW948196 AW948145 AW948162 AW948134 AW948127 AW948124 AW948153 AW948157 AW948125
			AW948131 AW948158 AW948164 AW948151
	413260	1356003_1	BE075281 BE075219 BE075123 BE075119 BE075046
	413471	1371778_1	BE142098 BE142092
	413729	1385114_1	BE159999 BE160056 BE160107 BE160139
	414182	142409_1	AA136301 AI381776 AA136321
55	414989	1511339_1	T81668 C19040 C17569
	415354	1534763_1	F06495 R24336 R13046
	416011	1566439_1	H14487 R50911 Z43216
	416475	1596398_1	T70298 H58072 R02750
	417380	1672461_1	T06809 N75735
60	419392	1843934_-1	W28573
	419541	185724_1	AW749617 R64714 AA244138 AA244137 BE094019
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	420819	196721_1	AA280700 AW975494 AA687385
	421245	200620_1	AA285363 AA285333 AA285359 AA285326 AA285350
65	422673	219674_1	N59027 AA314694 N53937 R08100

	422695	219996_1	AA315158 AW961298 N76067 AW802759 AI858495 W04474
	422858	222209_1	R35398 BE252178 AA318153
	422940	223106_1	BE077458 AA337277 AA319285
5	423730	231462_1	AA330214 AW962519 T54709
	423790	232031_1	BE152393 AA330984 BE073904
	424385	238731_1	AA339666 AW952809 AA349119
	424606	241409_1	AA343936 AA344060 AW963081
	425265	249175_1	BE245297 AA353976 AW505023
10	426959	273830_-1	BE262745
	430676	32168_1	AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812
			AW812041 AW812040 AW812067 BE061583 BE061604 T05808 AJ352469 AA580921 BE141783 BE141782 BE061601
			AW814393 AW885029
	430968	326269_1	AW972830 AA527647 AA489820 AA570362
15	431180	328906_1	H55883 AW971249 AA493900 H55788
	432093	341283_1	H28383 AW972670 H28359 AA525808
	434596	38937_1	T59538 T59589 T59598 T59542 AF147374
	436357	41842_1	AJ132085 Z83805
	437159	43393_1	AL050072 AW900148
20	437495	43765_1	BE177778 BE177779 AL390180 AA359908
	439097	46858_1	H66948 AF085954 H66949
	439120	46879_1	H56389 AF085977 H56173
	440134	48675_1	BE410734 BE560117 BE270054 BE296330 BE267957 AI003007 BE545259
	441896	52842_1	AW891873 AW891897 BE564764
25	445629	645767_1	AI245701 BE272724
	447229	71288_1	BE617135 AW504051 AW504283
	448064	74761_1	AA379036 AA150589 AI696854 BE621316
	450783	84655_1	BE266695 BE265474 N53200 BE267333
	451045	85673_1	AA215672 AI686628 AA013335 H86334 AA017006
30	452549	921802_1	AI907039 AI907081
	452560	922216_1	BE077084 AW139963 AW863127 AW806209 AW806204 AW806205 AW806206 AW806211 AW806212 AW806207 AW806208
			AW806210 AI907497
	452712	928309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
	453758	980026_1	U83527 AL120938 U83522
35	454093	1007366_1	AW860158 AW862385 AW860159 AW862386 AW862341 AW821869 AW821893 AW062660 AW062656
	454563	1224342_1	AW807530 AW807540 AW807537 AW846086 BE141634 AW846089 AW807499 AW807533 AW838499
	454791	1234759_1	BE071874 BE071882 AW820782 AW821007
	454977	1247099_1	AW848032 AW848630 AW848478 AW848623 AW848484 AW848169 AW848830 AW848149 AW848119 AW848893 AW848903
			AW848407
40	455131	1254674_1	AW857913 AW857916 AW857914 AW861627 AW861626 AW861624
	455183	1259023_1	AW984111 AW863918 AW863856
	455254	1266449_1	AW877015 AW877133 AW876978 AW877071 AW876988 AW877069 AW877063 AW877013
	455369	1285173_16	AW903533 AW903516 AW903562 BE085202 BE085215 BE085214 BE085209 BE085172 BE085175 BE085193 BE085211
			BE085199
45	455982	1396849_1	BE176862 BE176876 BE176947 BE176878
	456011	1410860_1	BE243628 BE246081 BE247016 BE241984 BE241534 BE246091 BE245679 BE243620 BE245998 BE242329 BE241417
			BE241457 BE242522 BE241989 BE241464
	456023	1416335_1	R00028 BE247630
	457586	360505_1	AW062439 AW751554 AA579463
50	457595	364225_-1	AA584854
	457751	399422_1	AI908236 AA663731
	459070	883688_1	AI814302 AI814428
	459081	889426_1	W07808 AI822066
	459145	918957_1	AI903354 AI903489 AI903488
	459172	921149_1	BE063380 BE063346 AI906097
55	459234	945240_-1	AI940425

TABLE 9B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 9. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

10

	Pkey	Ref	Strand	Nt_position
15	400452	8113550	Minus	90308-90505
	400557	9801261	Plus	208453-208528,209633-209813
	400615	9908994	Plus	118036-118166,118681-118807
	400802	8567867	Minus	174571-174856
	400817	8569994	Plus	170793-170948
20	400880	9931121	Plus	29235-29336,36363-36580
	400885	9958187	Minus	58242-58733
	400926	7651921	Minus	52033-52158,53956-54120,54957-55052,55420-55480,56452-56666,57221-57718
	400952	7658481	Plus	192667-192826,194387-194876
	400991	8096825	Plus	159197-159320
25	401044	8117619	Plus	73501-73674
	401124	8570296	Minus	124181-124391
	401163	6981820	Plus	5302-5545
	401201	9743387	Minus	138534-138629,139234-139294,140121-140335,142033-142479
	401286	9801342	Minus	147036-147318
30	401384	6850939	Minus	58360-58545
	401468	6433826	Plus	13056-13482
	401515	7630851	Plus	29929-30126
	401519	6649315	Plus	157315-157850
	401672	9838136	Plus	128526-128704,130755-130860
35	401744	2576349	Plus	14595-14751
	401851	7770425	Minus	146443-146664,147794-147971,148351-148480,148980-149111,149801-149949
	401866	8018106	Plus	73126-73623
	402240	7690131	Plus	104382-104527,106136-106372
40	402359	9211204	Minus	40403-41961
	402585	9908890	Minus	174893-175050,183210-183435
	402788	9796102	Plus	98273-101430
	402802	3287156	Minus	53242-53432
	402812	6010110	Plus	25026-25091,25844-25920
	402828	8918414	Plus	69071-69642
45	402835	9187337	Plus	26961-27101
	402838	9369121	Minus	32589-32735,35478-35666
	402842	9369121	Minus	76355-76479
	402895	9967547	Plus	85537-85671,86379-86469
50	402964	9581599	Minus	46624-46784
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403237	7637807	Plus	7271-7527
	403259	7770585	Plus	4693-4857
	403683	7331517	Plus	217175-217446
55	403690	7387384	Minus	78627-79583
	403708	5705981	Minus	134394-134812
	403838	4176355	Plus	19197-19502
	403851	7708872	Plus	22733-23007
	403976	7657840	Plus	24755-24969
60	404407	7329316	Minus	48154-48499
	404426	7407959	Plus	77842-77954
	404632	9796668	Plus	45096-45229
	404741	8574139	Plus	143025-143467
	404756	7706327	Plus	82849-83627
	404946	7382189	Plus	134445-134750
65	405074	7770440	Plus	44340-44559,44790-45059
	405125	8247873	Plus	137113-137814
	405172	9966752	Plus	153027-153262

	405236	7249076	Minus	151699-151915
	405325	6094661	Minus	25818-26380
	405411	3451356	Minus	17503-17778,18021-18290
5	405495	8050952	Minus	72182-72373
	405552	1552506	Plus	45199-45647
	405601	5815493	Minus	147835-147935,149220-149299
	405685	4508129	Minus	37956-38097
	405777	7263187	Minus	104773-105051
10	405856	7653009	Plus	101777-102043
	405876	6758747	Plus	39694-40031
	405932	7767812	Minus	123525-123713
	405934	6758795	Plus	159913-160605
	406006	8247801	Minus	42640-42776
15	406134	9163473	Plus	153291-153452
	406189	7289992	Minus	22007-22234
	406422	9256411	Plus	163003-163311
	406516	7711422	Minus	128375-128449,128560-128784
	406538	7711478	Plus	35196-35367,38229-38476,40080-40216,43522-43840
20	406554	7711566	Plus	106956-107121
	406577	7711730	Plus	11377-11509

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TABLE 11: shows genes, including expression sequence tags that are up-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu01 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

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Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigenelD:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Background subtracted normal prostate : prostate tumor tissue			

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
10	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene homolog B	0.012
	130642	M63438	Hs.156110	Immunoglobulin kappa variable 1D-8	0.015
	133512	X01677	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	0.017
	133436	H44631	Hs.737	Immediate early protein	0.017
	129292	X13810	Hs.1101	POU domain; class 2; transcription factor 2	0.019
15	100610	HG2566-HT4792		Microtubule-Associated Protein Tau, Alt. Splice 3, Exon 8	0.02
	133448	M34516	Hs.170116	immunoglobulin lambda-like polypeptide 3	0.021
	125193	W67577	Hs.84298	CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	0.022
	133456	T49257	Hs.183704	ubiquitin C	0.022
	134546	AA459310	Hs.8518	Homo sapiens mRNA; cDNA DKFZp586L1722 (from clone DKFZp586L1722)	0.023
20	102131	U15085	Hs.1162	major histocompatibility complex; class II; DM beta	0.023
	101375	M13560	Hs.84298	CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	0.023
	100674	HG3033-HT3194		Spliceosomal Protein Sap 62	0.023
	134365	R32377	Hs.82240	synixin 3A	0.024
	132335	D60387	Hs.189885	ESTs	0.027
25	110303	H37901	Hs.32706	ESTs	0.027
	131678	N59162	Hs.30542	ESTs	0.028
	116599	D80046	Hs.250879	ESTs	0.028
	133769	M17733	Hs.75968	thymosin; beta 4; X chromosome	0.029
	107904	AA026648	Hs.61389	ESTs	0.029
30	129427	T80746	Hs.111334	ferritin; light polypeptide	0.03
	105987	AA406631	Hs.110299	mitogen-activated protein kinase kinase 7	0.03
	131466	F03233	Hs.27189	ESTs	0.032
	102859	X00274	Hs.76807	Human HLA-DR alpha-chain mRNA	0.032
	134626	S82198	Hs.8709	caldesmon (serum calcium decreasing factor; elastase IV)	0.032
35	134170	M63138	Hs.79572	cathepsin D (lysosomal aspartyl protease)	0.033
	131713	X57809	Hs.181125	immunoglobulin lambda gene cluster	0.034
	100748	HG3517-HT3711		Alpha-1-Antitrypsin, 5' End	0.034
	118769	N74496		ESTs	0.034
	111734	R25375	Hs.126916	ESTs	0.036
40	109221	AA192755	Hs.85840	ESTs; Weakly similar to stac [H.sapiens]	0.036
	133846	AA480073	Hs.76719	U6 snRNA-associated Sm-like protein	0.036
	135281	AA401575	Hs.97757	ESTs	0.037
	119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 oncogene related	0.037
	100760	HG3576-HT3779		Major Histocompatibility Complex, Class II Beta W52	0.037
45	101426	M19483	Hs.25	ATP synthase; H+ transp. mitochndri F1 complex; beta polypept	0.038
	129568	AA428025	Hs.114360	transforming growth factor beta-stimulated protein TSC-22	0.038
	130900	Z38468	Hs.21036	ESTs; Moderately similar to F25965_3 [H.sapiens]	0.039
	133879	M13829	Hs.77183	v-rat murine sarcoma 3611 viral oncogene homolog 1	0.039
	100627	HG2702-HT2798		Serine/Threonine Kinase (Gb:Z25424)	0.039
50	129424	M55593	Hs.111301	matrix metalloproteinase 2 (gelatinase A; 72kD gelatinase; 72kD type IV collagenase)	0.039
	128652	AA621245	Hs.103147	ESTs; Weakly similar to similar to SP:YR40_BACSU [C.elegans]	0.039
	129979	T72635	Hs.13956	ESTs	0.039
	133468	X03068	Hs.73931	major histocompatibility complex; class II; DQ beta 1	0.04
	102636	U67092		Human ataxia-telangiectasia locus protein (ATM) gene, exons 1a, 1b, 2, 3 and 4, partial cds	0.04
55	129536	M33493	Hs.184504	trypsin; alpha	0.04
	133599	M64788	Hs.75151	RAP1; GTPase activating protein 1	0.041

5	102104	U12139		Human alpha1(XI) collagen (COL11A1) gene, 5' region and exon 1	0.041
	131340	AA478305	Hs.25817	Homo sapiens chromosome 19; cosmid R27216	0.041
	130446	X79510	Hs.155693	protein tyrosine phosphatase; non-receptor type 21	0.042
	101352	L77701	Hs.16297	COX17 (yeast) homolog; cytochrome c oxidase assembly protein	0.042
	122593	AA453310	Hs.128749	alpha-methylacyl-CoA racemase	0.042
10	130181	R39552	Hs.151608	Homo sapiens clone 23622 mRNA sequence	0.042
	134071	Z14093	Hs.78950	branched chain keto acid dehydrogenase E1; alpha polypeptide (maple syrup urine disease)	0.042
	108129	AA053252	Hs.185848	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING	
	130511	L32137	Hs.1584	ENTRY !! [H.sapiens]	0.043
				cartilage oligomeric matrix protein (pseudoachondroplasia; epiphyseal dysplasia 1; multiple)	0.043
15	133336	AA291456	Hs.71190	ESTs	0.043
	132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	0.044
	131880	AA047034	Hs.33818	RecQ protein-like 5	0.044
	130540	U35234	Hs.159534	protein tyrosine phosphatase; receptor type; S	0.044
	133467	AA258595	Hs.73931	major histocompatibility complex; class II; DQ beta 1	0.044
20	101191	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	0.044
	101860	M95610	Hs.37165	collagen; type IX; alpha 2	0.044
	102799	U88898		Human endogenous retroviral H protease/integrase-derived ORF1 mRNA, complete cds, and putative envelope prot mRNA, partial cds	0.044
				ESTs	0.044
	107200	D20350	Hs.5628	lipocalin 1 (protein migrating faster than albumin; tear prealbumin)	0.044
25	101166	L14927	Hs.2099	pim-1 oncogene	0.044
	134289	M54915	Hs.81170	ESTs	0.044
	135329	AA436026	Hs.98858	protein phosphatase 3 (formerly 2B); catalytic subunit; beta isoform (calcineurin A beta)	0.044
	124950	T03786	Hs.151531	aldolase A; fructose-bisphosphate	0.044
				Triosephosphate Isomerase	0.045
30	102919	X12447	Hs.183760	Homo sapiens clones 24718 and 24825 mRNA sequence	0.045
	100574	HG2279-HT2375		Human B-cell receptor associated protein (hBAP) alternatively spliced mRNA, partial 3'UTR	0.045
	131286	AA450092	Hs.25300	ESTs	0.045
	102675	U72512		GRO2 oncogene	0.046
				ESTs	0.046
35	131332	R50487	Hs.25717	ESTs	0.046
	101634	M57731	Hs.75765	ESTs	0.046
	113118	T47906	Hs.220512	ESTs	0.046
	124884	R77276	Hs.120911	ESTs	0.046
	130523	W76097	Hs.214507	ESTs	0.046
40	110244	H26742	Hs.25367	ESTs; Weakly similar to ALR [H.sapiens]	0.046
	131932	AA454980	Hs.25601	chromodomain helicase DNA binding protein 3	0.046
	132509	H09751	Hs.5038	neuropathy target esterase	0.046
	133372	AA291139	Hs.72242	ESTs	0.046
	100817	HG4011-HT4804		Dystrophin-Associated Glycoprotein, 50 Kda, Alt. Splice 2	0.047
45	106746	AA476436	Hs.7991	ESTs	0.047
	135401	L14813	Hs.169271	carboxyl ester lipase-like (bile salt-stimulated lipase-like)	0.047
	130479	R44163	Hs.12457	Homo sapiens clone 23770 mRNA sequence	0.047
	102589	U62015	Hs.8867	cysteine-rich; angiogenic inducer; 61	0.047
	121521	AA412165	Hs.97358	EST	0.048
50	135340	AA425137	Hs.99093	Homo sapiens chromosome 19; cosmid R28379	0.048
	132336	AA342422	Hs.45073	ESTs	0.048
	115368	AA282133	Hs.88960	ESTs; Weakly similar to similar to collagen [C.elegans]	0.048
	101278	L38487	Hs.110849	estrogen-related receptor alpha	0.048
	103284	X80200	Hs.8375	TNF receptor-associated factor 4	0.048
55	100564	HG2239-HT2324		Potassium Channel Protein (GbZ11585)	0.048
	133132	Z40883	Hs.65588	ESTs; Weakly similar to dJ393P12.2 [H.sapiens]	0.048
	121811	AA424535	Hs.98416	ESTs	0.048
	129613	AA279481	Hs.238831	ESTs; Weakly similar to collagen alpha 1(XVIII) chain [M.musculus]	0.049
	132468	S79854	Hs.49322	deiodinase; iodothyronine; type III	0.049
60	120111	W85841	Hs.136031	ESTs	0.049
	103668	Z83741	Hs.248174	H2A histone family; member M	0.049
	130386	F10874	Hs.234249	mitogen-activated protein kinase 8 interacting protein 1	0.049
	104275	C02170	Hs.39387	ESTs; Weakly smlr to weak smlrity to ribosomal prot L14 [C.elegans]	0.049
	106305	AA436146	Hs.12828	ESTs	0.05
65	116431	AA609878	Hs.55289	ESTs; Weakly smlr to 110 KD CELL MEMBRANE GLYCOPROTEIN [H.sapiens]	0.813
	120339	AA206465	Hs.256470	EST	0.05
	114427	AA017063		ESTs; Highly similar to Miz-1 protein [H.sapiens]	0.05
	118821	N79070	Hs.94789	ESTs	0.05
	118979	N93798	Hs.43666	protein tyrosine phosphatase type IVA; member 3	0.05
	107495	W78776	Hs.90375	ESTs	0.051
	120240	Z41732	Hs.66049	ESTs	0.051

5	114331	Z41309	Hs.12400	ESTs	0.051
	130947	R40037	Hs.21506	ESTs	0.052
	129242	W81679	Hs.5174	ribosomal protein S17	0.052
	131413	AA482390	Hs.26510	ESTs; Modly smlr to vacuolar prot sorting homolog r-vps33b [R.norvegicus]	0.052
	112304	R54798	Hs.26239	ESTs	0.052
10	101416	M17254	Hs.45514	v-ets avian erythroblastosis virus E26 oncogene related	0.052
	131201	AA426304	Hs.24174	ESTs	0.052
	101054	K02405	Hs.73933	Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2); complete cds	0.052
	101306	L41143	Hs.232069	T-cell leukemia translocation altered gene	0.053
	129311	T55087		yb45c08.r1 Stratagene fetal spleen (#937205) Homo sapiens cDNA	
15				clone IMAGE:74126 5', mRNA sequence.	0.053
	129942	U95301	Hs.144442	phospholipase A2; group X	0.053
	119210	R93340	Hs.92995	ESTs	0.053
	101046	K01160		Accession not listed in Genbank	0.053
	114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777023 from 7p14-p15	0.053
20	110171	H19964	Hs.31709	ESTs	0.053
	101004	J04101	Hs.248109	v-ets avian erythroblastosis virus E26 oncogene homolog 1	0.053
	129715	N58479	Hs.12126	ESTs; Weakly similar to LR8 [H.sapiens]	0.053
	101581	M34996	Hs.198253	major histocompatibility complex; class II; DQ alpha 1	0.053
	113285	T66830	Hs.182712	ESTs	0.053
25	127537	AA569531	Hs.162859	ESTs	0.054
	100813	HG3995-HT4265		Cpg-Enriched Dna, Clone S19	0.054
	101841	M93107	Hs.76893	3-hydroxybutyrate dehydrogenase (heart; mitochondrial)	0.054
	135053	R77159	Hs.93678	ESTs	0.054
	101419	M17886	Hs.177592	ribosomal protein; large; P1	0.054
30	119724	W69468	Hs.47622	ESTs	0.055
	102673	U72509		Human alternatively spliced B8 (B7) mRNA, partial sequence	0.055
	129877	AA248589	Hs.13094	ESTs; Weakly similar to ORF YGR101w [S.cerevisiae]	0.055
	114788	AA156737	Hs.103904	EST	0.055
	123812	AA620607	Hs.111591	ESTs	0.055
35	117669	N39237	Hs.44977	ESTs	0.055
	123782	AA610111	Hs.162695	EST	0.055
	102395	U41767	Hs.92208	a disintegrin and metalloproteinase domain 15 (metargidin)	0.055
	133795	M12529	Hs.169401	apoptoprotein E	0.055
	123193	AA489228	Hs.136956	ESTs	0.056
40	132595	AA253369	Hs.155742	glyoxylate reductase/hydroxypyruvate reductase	0.056
	104161	AA456471	Hs.7724	KIAA0963 protein	0.056
	115330	AA281145	Hs.88827	ESTs	0.056
	112893	T08000	Hs.194684	bassoon (presynaptic cytomatrix protein)	0.056
	133475	L29217	Hs.73987	CDC-like kinase 3	0.056
45	128699	K03207	Hs.103972	proline-rich protein BstNI subfamily 4	0.056
	102940	X13956	Hs.24998	Hu 12S RNA induced by poly(rI); poly(rC) and Newcastle disease virus	0.056
	131299	AA431464	Hs.25426	ESTs; Weakly similar to unknown [H.sapiens]	0.057
	102495	U51240	Hs.79356	Lysosomal-associated multispanning membrane protein-5	0.057
	129594	R70379	Hs.115396	Human germline IgD chain gene; C-region; C-delta-1 domain	0.057
50	118593	N69020	Hs.207689	EST	0.057
	126702	U54602	Hs.2785	keratin 17	0.057
	124386	N27368	Hs.212414	sema domain; immunoglobulin domain (Ig); short basic domain;	
				secreted; (semaphorin) 3E	0.057
	130538	M20786	Hs.159509	alpha-2-plasmin inhibitor	0.057
55	114299	Z40782	Hs.22920	similar to S68401 (cattle) glucose induced gene	0.057
	115604	AA400378	Hs.48391	ESTs	0.057
	106052	AA416947	Hs.6382	ESTs; Highly similar to KIAA0612 protein [H.sapiens]	0.057
	131730	U05681	Hs.31210	B-cell CLL/lymphoma 3	0.057
	131285	AA479498	Hs.25274	ESTs; Modly smlr to putative seven pass transmembrane prot [H.sapiens]	0.058
60	129705	X78706	Hs.12068	camitine acetyltransferase	0.058
	123175	AA489010	Hs.178400	ESTs	0.058
	103592	Z30644	Hs.123059	chloride channel Kb	0.058
	118198	N59478	Hs.48396	ESTs; Moderately similar to tumor necrosis factor-alpha	
				-induced protein B12 [H.sapiens]	0.058
65	104886	AA053348	Hs.144626	growth differentiation factor 11	0.058
	104250	AF000575	Hs.105928	leukocyte immunoglobulin-like receptor; subfamily B (with TM	
				and ITIM domains); member 3	0.058
	113301	T67452	Hs.13104	EST	0.058
	110441	H50302	Hs.19845	ESTs; Highly smlr to prot phosphatase 2A BR gamma subunit [H.sapiens]	0.058
	125297	Z39215	Hs.159409	ESTs	0.058
	135258	AA292423	Hs.97272	ESTs; Weakly similar to dJ281H8.2 [H.sapiens]	0.058
	130633	T92363	Hs.178703	ESTs	0.058
	112006	R42607	Hs.22241	hypothetical protein	0.058

5	130805	U12194	Hs.170238	sodium channel; voltage-gated; type I; beta polypeptide	0.058
	134907	D80002	Hs.178292	KIAA0180 protein	0.058
	132619	AA404565	Hs.53447	ESTs; Moderately similar to kinesin light chain 1 [M.musculus]	0.058
	135115	N35489	Hs.94653	neurochondrin	0.058
	100531	HG1872-HT1907		Major Histocompatibility Complex, Dg	0.058
10	124530	N62256	Hs.102727	EST	0.058
	119960	W87533	Hs.32699	ESTs; Moderately similar to LIV-1 protein [H.sapiens]	0.058
	132793	AA478999	Hs.56966	KIAA0906 protein	0.058
	101076	L04270	Hs.1116	lymphotoxin beta receptor (TNFR superfamily; member 3	0.058
	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	0.058
15	134458	AA192614	Hs.83577	cysteine and glycine-rich protein 3 (cardiac LIM protein)	0.058
	105904	AA401452	Hs.32060	ESTs	0.059
	132878	AA026793	Hs.58679	ESTs; Weakly similar to 4F2/CD98 light chain [M.musculus]	0.059
	121828	AA425166	Hs.98497	ESTs	0.059
	133418	U76366	Hs.172727	Treacher Collins-Franceschetti syndrome 1	0.059
20	129317	N46244	Hs.110373	ESTs	0.059
	130153	D85815	Hs.15114	ras homolog gene family; member D	0.059
	124403	N31745	Hs.102493	ESTs	0.059
	127683	AA668123	Hs.134170	ESTs	0.059
	129814	W20070	Hs.168625	KIAA0979 protein	0.059
25	131770	D59682	Hs.31833	ESTs	0.06
	117557	N33920	Hs.44532	diubiquitin	0.06
	103522	Y10514		H.sapiens mRNA for CD152 protein	0.06
	120029	W91960	Hs.250640	sequence-specific single-stranded-DNA-binding protein	0.06
	102135	U15460	Hs.41691	activating transcription factor B	0.06
30	123817	AA609183	Hs.181131	ESTs	0.06
	112136	R46100	Hs.9739	ESTs	0.061
	133725	V00563	Hs.179543	immunoglobulin mu	0.061
	102069	U09196	Hs.82520	Hu 1.1 kb mRNA upregitd in retinoic acid treated HL-60 neutrophilic cells	0.061
	106555	AA455000	Hs.16725	ESTs	0.061
35	123269	AA491226	Hs.105280	ESTs; Weakly similar to dJ963K23.2 [H.sapiens]	0.061
	109088	AA166837	Hs.72620	DKFZP434I114 protein	0.061
	129399	AA263028	Hs.111076	malate dehydrogenase 2; NAD (mitochondrial)	0.061
	129375	W79850	Hs.11081	ESTs; Weakly similar to HPBRII-7 protein [H.sapiens]	0.061
	135271	AA397763	Hs.97562	ESTs	0.061
40	129588	W90398	Hs.6147	KIAA1075 protein	0.061
	129364	AA477106	Hs.110757	DNA segment on chromosome 21 (unique) 2056 expressed sequence	0.061
	123427	AA598548	Hs.112471	ESTs	0.061
	105236	AA219179	Hs.19105	translocase of inner mitochondrial membrane 17 (yeast) homolog B	0.061
	101012	J04444	Hs.697	cytochrome c-1	0.062
45	134791	L18983	Hs.89655	protein tyrosine phosphatase; receptor type; N	0.062
	133700	K01396	Hs.75621	protease inhibitor 1 (anti-elastase); alpha-1-antitrypsin	0.062
	123887	AA621065	Hs.112943	ESTs	0.062
	129363	H05704	Hs.110746	H sapiens HCR (a-helix coiled-coil rod homologue) mRNA; complete cds	0.062
	105719	AA291644	Hs.36783	ESTs	0.062
50	124226	H62396	Hs.190266	ESTs	0.062
	117437	N27645		yw5e3.s1 Weizmann Olfactory Epithelium H sapiens cDNA clone	0.062
	132741	AA394133	Hs.55898	IMAGE:255676 3' smir to contains L1.13 L1 repetitive element ; mRNA seq	0.062
	134437	M26041	Hs.198253	ESTs; Highly similar to OASIS protein [M.musculus]	0.062
	107664	AA010594	Hs.5326	major histocompatibility complex; class II; DQ alpha 1	0.062
55	120844	AA349417	Hs.96917	ESTs; Moderately similar to pim-1 protein [H.sapiens]	0.062
	101574	M34182	Hs.158029	ESTs	0.062
	131219	C00476	Hs.24395	protein kinase; cAMP-dependent; catalytic; gamma	0.062
	103495	Y09022	Hs.153591	small inducible cytokine subfamily B (Cys-X-Cys); member 14 (BRAK)	0.062
	129607	AA404594	Hs.11607	Not56 (D. melanogaster)-like protein	0.062
60	106467	AA450040	Hs.154162	ESTs	0.062
	128841	T16358	Hs.106443	ADP-ribosylation factor-like 2	0.062
	100515	HG1723-HT1729		ESTs	0.062
	119332	T54095		Macrophage Scavenger Receptor, Alt. Splice 2	0.062
	134516	AA171939	Hs.23413	ESTs; Weakly similar to fl ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.062
65	135012	X73608	Hs.93029	ESTs	0.062
	103575	Z26256		sparc/osteonectin; cwcv and kazu-like domains proteoglycan (testican)	0.063
	115514	AA297739	Hs.55609	H.sapiens isoform 1 gene for L-type calcium channel, exon 1	0.063
	103996	AA321355		ESTs; Weakly similar to ISOLEUCYL-TRNA SYNTHETASE;	0.063
	110505	H55992	Hs.20495	CYTOPLASMIC [H.sapiens]	0.063
	133912	X62744	Hs.77522	EST2393 Bone marrow Homo sapiens cDNA 5' end, mRNA sequence	0.063
	129581	M33600	Hs.180255	DKFZP434F011 protein	0.063
				major histocompatibility complex; class II; DM alpha	0.063
				major histocompatibility complex; class II; DR beta 1	0.063

5	130139	R38280	Hs.150922	BCS1 (yeast homolog)-like	0.064
	105817	AA397825	Hs.5307	synaptopodin	0.064
	134658	AA410617	Hs.178009	ESTs	0.064
	100306	D50495	Hs.80598	transcription elongation factor A (SII); 2	0.064
	100277	D42053	Hs.75890	site-1 protease (subtilisin-like; sterol-regulated; cleaves sterol regulatory element binding proteins)	0.064
10	133116	D61259	Hs.6529	ESTs	0.064
	134909	AA521488	Hs.90998	KIAA0128 protein	0.064
	130319	X74794	Hs.154443	minichromosome maintenance deficient (S. cerevisiae) 4	0.064
	132057	AA102489	Hs.173484	ESTs	0.064
	108334	AA070473		zm7c8.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:5399 3', mRNA sequence	0.064
15	129763	F10815	Hs.12373	KIAA0422 protein	0.064
	135112	T67464	Hs.94617	ESTs; Weakly similar to predicted using Genefinder [C.elegans]	0.064
	122269	AA436856	Hs.98910	ESTs	0.064
	133082	AA457129	Hs.6455	RuvB (E. coli homolog)-like 2	0.064
	113213	T58607		ya94a02.s1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69290 3', mRNA sequence.	0.065
20	106228	AA429290	Hs.17719	ESTs	0.065
	130192	Y12661	Hs.171014	VGF nerve growth factor inducible	0.065
	104894	AA054087	Hs.18858	phospholipase A2; group IVC (cytosolic; calcium-independent)	0.065
	103508	Y10141		H.sapiens DAT1 gene, partial, VNTR	0.065
	128474	U40671	Hs.100299	ligase III; DNA; ATP-dependent	0.065
25	134012	AA417821	Hs.237924	ESTs; Highly similar to CGI-69 protein [H.sapiens]	0.065
	134536	AA457735	Hs.850	IMP (inosine monophosphate) dehydrogenase 1	0.065
	111714	R23146	Hs.23466	ESTs	0.065
	110521	H57060	Hs.108268	ESTs	0.065
	103282	X80198	Hs.77628	steroidogenic acute regulatory protein related	0.065
30	113921	W80730	Hs.28355	ESTs	0.065
	129331	N93465	Hs.110453	ESTs; Highly similar to CGI-38 protein [H.sapiens]	0.065
	111316	N74597	Hs.180535	ESTs; Weakly similar to mitogen inducible gene mig-2 [H.sapiens]	0.065
	135138	AA036794	Hs.95196	ESTs; Weakly similar to T20B12.3 [C.elegans]	0.065
	107289	T10792	Hs.172098	ESTs	0.065
35	121405	AA406083	Hs.98007	ESTs	0.065
	124965	T16275	Hs.106359	ESTs	0.065
	106595	AA456933	Hs.174481	ESTs	0.066
	100106	AF015910		Homo sapiens unknown protein mRNA, partial cds	0.066
	134715	AA282757	Hs.89040	prepronociceptin	0.066
40	135367	AA480109	Hs.9963	TYRO protein tyrosine kinase binding protein	0.066
	111533	R08548	Hs.251651	EST	0.066
	128509	R53109	Hs.247362	dimethylarginine dimethylaminohydrolase 2	0.066
	101030	J05037	Hs.76751	serine dehydratase	0.066
	102753	U80226		Human gamma-aminobutyric acid transaminase mRNA, partial cds	0.067
45	126991	R31652	Hs.821	biglycan	0.067
	109583	F02322	Hs.26135	ESTs	0.067
	119241	T12559	Hs.221382	ESTs	0.067
	130569	AA156597	Hs.256441	EST; Moderately similar to CGI-136 protein [H.sapiens]	0.067
	112926	T10316	Hs.4302	ESTs	0.067
50	120495	AA256073	Hs.190626	ESTs	0.067
	130931	AA278412	Hs.21346	ESTs; Weakly similar to F42C5.7 gene product [C.elegans]	0.067
	129982	M87789	Hs.140	immunoglobulin gamma 3 (Gm marker)	0.067
	133832	H03387	Hs.241305	estrogen-responsive B box protein	0.067
	110697	H93721	Hs.20798	ESTs	0.067
55	121183	AA400138	Hs.97703	ESTs	0.067
	130953	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	0.067
	102218	U24183	Hs.75160	phosphofructokinase; muscle	0.067
	114181	Z39079	Hs.8021	KIAA1058 protein	0.067
	116581	D51287	Hs.82148	ribosomal protein S12	0.067
60	132498	T87708	Hs.50098	ESTs	0.068
	103788	AA096014	Hs.9527	ESTs; Highly similar to HSPC013 [H.sapiens]	0.068
	102459	U48936		Human amiloride-sensitive epithelial sodium channel gamma subunit mRNA, 5' end, partial cds	0.068
	100373	D79999	Hs.77225	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 1	0.068
	132717	AA203321	Hs.151696	DKFZP727G051 protein	0.068
65	128863	D87462	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	0.068
	115193	AA262029	Hs.88218	ESTs	0.068
	124558	N66046	Hs.141605	ESTs	0.069
	117225	N20392	Hs.42846	ESTs	0.069
	110665	H83380	Hs.32757	ESTs	0.069

5	132805	U70663	Hs.182965	Kruppel-like factor 4 (gut)	0.069
	105778	AA348910	Hs.153299	DOM-3 (C. elegans) homolog Z	0.069
	134770	R72079	Hs.89575	CD79B antigen (immunoglobulin-associated beta)	0.069
	123097	AA485869	Hs.105671	ESTs	0.069
	100750	HG3523-HT4899		Proto-Oncogene C-Myc, Alt. Splice 3, Orf 114	0.069
10	125091	T91518		ye20f05.s1 Stratagene lung (#937210) H sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element; contains MER12 repetitive element; mRNA sequence.	0.069
	100756	HG3565-HT3768		Zinc Finger Protein (Gb:M88357)	0.069
	113483	T87768	Hs.16439	ESTs	0.069
	101119	L09708	Hs.2253	complement component 2	0.069
	102286	U31628	Hs.12503	interleukin 15 receptor; alpha	0.07
15	135349	D83174	Hs.9930	collagen-binding protein 2 (collagen 2)	0.07
	100991	J03764	Hs.82085	plasminogen activator inhibitor; type I	0.07
	133675	AA443720	Hs.7551	ESTs; Weakly similar to T25G3.1 [C.elegans]	0.07
	105422	AA251014	Hs.12210	ESTs	0.07
	102932	X13334	Hs.75627	CD14 antigen	0.07
20	119147	R58878	Hs.65739	ESTs	0.07
	104900	AA055048	Hs.180481	ESTs; Weakly similar to ACROSIN PRECURSOR [H.sapiens]	0.07
	133185	AA481404	Hs.6686	ESTs	0.07
	115496	AA290674	Hs.71819	eukaryotic translation initiation factor 4E binding protein 1	0.07
	121005	AA398332	Hs.97613	ESTs	0.07
25	124869	R69088	Hs.28728	ESTs; Weakly similar to F55A12.9 [C.elegans] =	0.071
	129154	N23673	Hs.108969	mannosidase; alpha; class 2B; member 1	0.071
	112161	R48295		ESTs; Wkly smlr to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.071
	125251	W87486	Hs.141464	ESTs	0.071
	134298	J00116	Hs.81343	collagen; type II; alpha 1 (primary osteoarthritis; spondyloepiphyseal dysplasia; congenital)	0.071
30	119745	W70264	Hs.58093	ESTs	0.071
	131306	AA232686	Hs.25489	ESTs	0.071
	107776	AA018820	Hs.221147	ESTs	0.071
	134271	AA199630	Hs.184456	ESTs; Wkly smlr to !! ALU SUBFAMILY SX WARNING ENTRY !! [H.sapiens]	0.071
	101798	M85220		Accession not listed in Genbank	0.071
35	135402	S76942	Hs.99922	dopamine receptor D4	0.071
	118742	N74052	Hs.50424	EST	0.071
	131867	N64656	Hs.3353	Homo sapiens clone 24940 mRNA sequence	0.071
	102923	X12517	Hs.1063	small nuclear ribonucleoprotein polypeptide C	0.072
	100775	HG371-HT26388		Mucin 1, Epithelial, Alt. Splice 9	0.072
40	111020	N54361	Hs.185726	ESTs	0.072
	134224	X80822	Hs.163593	ribosomal protein L18a	0.072
	124059	F13673	Hs.99769	ESTs	0.072
	133972	AA160743	Hs.78019	Homo sapiens clone 24432 mRNA sequence	0.072
	129681	AA436009	Hs.178186	ESTs; Weakly similar to WASP-family protein [H.sapiens]	0.072
45	103065	X58399	Hs.81221	Human L2-9 transcript of unrearranged immunoglobulin V(H)5 pseudogene	0.072
	124966	T19271	Hs.155560	calnexin	0.072
	112270	R53021	Hs.203358	ESTs	0.072
	116704	F10183	Hs.66140	EST	0.072
	129890	M13699	Hs.111461	ceruloplasmin (ferroxidase)	0.072
50	127345	AA972008	Hs.166253	ESTs; Highly similar to KIAA0476 protein [H.sapiens]	0.072
	112436	R63090	Hs.28391	ESTs	0.072
	114531	AA053033	Hs.203330	ESTs	0.072
	135122	H99080	Hs.94814	ESTs	0.072
	103934	AA281338	Hs.134200	Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186)	0.072
55	109363	AA215369	Hs.185764	ESTs; Weakly similar to hypothetical protein [H.sapiens]	0.072
	112647	R83329	Hs.33403	ESTs	0.073
	127083	Z44079	Hs.91608	otoferlin	0.073
	133027	AA402624	Hs.63236	synuclein; gamma (breast cancer-specific protein 1)	0.073
	122086	AA432121	Hs.250986	EST	0.073
60	110405	H47542	Hs.33962	ESTs	0.073
	128697	AB002344	Hs.103915	KIAA0346 protein	0.073
	112221	R50380	Hs.25670	ESTs	0.073
	100478	HG1067-HT1067		Mucin (Gb:M22406)	0.073
	115598	AA400129	Hs.65735	ESTs	0.073
65	132491	AA227137	Hs.4984	KIAA0828 protein	0.073
	101655	M60299		Human alpha-1 collagen type II gene, exons 1, 2 and 3	0.073
	106018	AA411887	Hs.34737	ESTs	0.073
	129683	W05348	Hs.158196	DKFZP434B103 protein	0.073
	134137	F10045	Hs.78347	KIAA0211 gene product	0.073
	114008	W89128	Hs.19872	ESTs	0.073

5	107653	AA010210	Hs.47041	ESTs	0.073
	104798	AA029462	Hs.17235	ESTs	0.073
	134082	L16991	Hs.79006	deoxythymidylate kinase	0.073
	119180	R80413	Hs.92520	ESTs	0.073
	107741	AA016982	Hs.64341	ESTs	0.073
10	133683	AA335223	Hs.75558	papsinogen 5; group I (papsinogen A)	0.073
	111694	R22035	Hs.23331	ESTs	0.073
	120764	AA338729	Hs.133096	ESTs	0.073
	119389	T88826	Hs.90973	ESTs	0.074
	100929	HG688-HT688		Major Histocompatibility Complex, Class II, Dr Beta 2 (Gb:X65561)	0.074
15	119388	T88798		plasminogen activator inhibitor; type I	0.074
	133019	AF009674	Hs.184434	axin	0.074
	105185	AA191495	Hs.189937	ESTs	0.074
	133413	S72043	Hs.73133	metallothionein 3 (growth inhibitory factor (neurotrophic))	0.074
	101017	J04599	Hs.821	biglycan	0.074
20	132865	K02765	Hs.251972	complement component 3	0.074
	110882	N36001	Hs.17348	ESTs; Wkly smlr to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	0.074
	129197	T90303	Hs.109308	ESTs; Wkly smlr to leucine-rich glioma-inactivated prot precursor [H.sapiens]	0.074
	101184	L19871	Hs.460	activating transcription factor 3	0.075
	134910	AA431320	Hs.9100	ESTs	0.075
25	119411	T96621	Hs.203656	EST	0.075
	102000	U01824	Hs.380	solute carrier family 1 (glial high affinity glutamate transporter); member 2	0.075
	114691	AA121893	Hs.103779	ESTs; Weakly similar to envelope protein [H.sapiens]	0.075
	134179	U53204	Hs.79706	plectin 1; intermediate filament binding protein; 500kD	0.075
	134503	U34880	Hs.84183	diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 1	0.075
30	129719	N66396	Hs.167766	ESTs; Moderately similar to Pro-a2(XI) [H.sapiens]	0.075
	113916	W80464	Hs.31928	ESTs; Wkly smlr to alternatively spliced product using exon 13A [H.sapiens]	0.075
	113897	W73926	Hs.4947	ESTs	0.075
	129697	R00841	Hs.172069	DKFZP434C212 protein	0.075
	112078	R44155	Hs.112218	ESTs	0.075
35	121980	AA429886	Hs.110407	ESTs; Weakly similar to coded for by C. elegans cDNA yk173c12.5 [C.elegans]	0.075
	100698	HG4638-HT5050		Spliceosomal Protein Sap 49	0.075
	121626	AA416974	Hs.98174	ESTs	0.075
	133670	AA243416	Hs.75470	hypothetical protein; expressed in osteoblast	0.075
	131879	AA017161	Hs.33792	ESTs	0.075
40	100254	D38037	Hs.77643	FK506-binding protein 1B (12.6 kD)	0.075
	133194	AA291726	Hs.67201	ESTs	0.075
	106081	AA418394	Hs.25354	ESTs	0.075
	115544	AA351433	Hs.66187	Homo sapiens clone 23700 mRNA sequence	0.076
	119955	W87460	Hs.58989	ESTs	0.076
45	104407	H61361	Hs.102171	immunoglobulin superfamily containing leucine-rich repeat	0.076
	135019	X58431	Hs.98428	Human Hox2.2 gene for a homeobox protein	0.076
	114815	AA161488	Hs.103931	DKFZP434B0335 protein	0.076
	119471	W31352	Hs.55445	ESTs	0.076
	117788	N48292	Hs.46849	ESTs	0.076
50	119406	T95064	Hs.193771	EST	0.076
	130777	R61742	Hs.256554	ESTs	0.076
	130494	L13197	Hs.75874	pregnancy-associated plasma protein A	0.076
	104107	AA424111	Hs.12598	T-cell lymphoma invasion and metastasis 2	0.076
	121483	AA411981	Hs.25274	ESTs; Modly smlr to putative seven pass transmembrane prot [H.sapiens]	0.076
55	104451	M13289	Hs.102119	blue cone pigment	0.076
	118027	N52770	Hs.75968	thymosin; beta 4; X chromosome	0.076
	109419	AA227560	Hs.86987	receptor-interacting serine-threonine kinase 3	0.076
	115783	AA424487	Hs.72289	ESTs; Weakly similar to LIV-1 protein [H.sapiens]	0.076
	110585	H62223	Hs.133526	ESTs; Wkly smlr to !!ALU SUBFAMILY SB1 WARNING ENTRY !!! [H.sapiens]	0.076
60	123165	AA488863	Hs.105216	ESTs; Weakly smlr to !!ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.077
	103966	AA303166	Hs.127270	ESTs	0.077
	109549	F01528	Hs.21192	Homo sapiens clone 25155 mRNA sequence	0.077
	106730	AA465520	Hs.22313	ESTs	0.077
	120310	AA193676	Hs.118926	DKFZP586K0919 protein	0.077
65	104078	AA402801	Hs.222010	ESTs	0.077
	117624	N35978	Hs.82364	ESTs	0.077
	112421	R62441	Hs.23127	ESTs	0.077
	106958	AA497026	Hs.22059	ESTs	0.077
	129984	W92811	Hs.183927	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.077
	122044	AA431456	Hs.98736	EST	0.077
	123280	AA491285	Hs.175144	ESTs	0.077
	115710	AA412535	Hs.55235	sphingomyelin phosphodiesterase 2; neutra	0.077

				I membrane (neutral sphingomyelinase)	0.077
				KIAA0255 gene product	0.077
				Homo sapiens clone 643 unknown mRNA; complete sequence	0.078
				ESTs	0.078
5	134129	D87444	Hs.79305	interferon; gamma-inducible protein 30	0.078
	129321	AA224502	Hs.206501	ESTs	0.078
	130513	AA460257	Hs.15866	KIAA0296 gene product	0.078
	100996	J03909	Hs.14623	ESTs	0.078
	128358	AI095718	Hs.135015	ESTs; Moderately similar to KIAA0544 protein [H.sapiens]	0.078
	128544	R59352	Hs.119273	glycine receptor; beta	0.078
	106040	AA412681	Hs.125139	ESTs	0.078
10	106495	AA452113	Hs.32454	ESTs	0.078
	131833	R40899	Hs.32973	even-skipped homeo box 1 (homolog of Drosophila)	0.078
	119219	R97176	Hs.110783	ESTs; Weakly similar to sphingosine kinase [M.musculus]	0.078
	135415	X60655	Hs.99967	ESTs	0.078
	109457	AA232646	Hs.68061	ESTs	0.078
	117137	H96670	Hs.42221	ESTs	0.078
15	107094	AA609614	Hs.5241	ESTs	0.078
	130165	T90529	Hs.251613	EST	0.078
	124072	H05252	Hs.101637	EST; Weakly similar to hypothetical protein [H.sapiens]	0.078
	126151	AA324743	Hs.40808	ESTs	0.078
	119035	R01779	Hs.7740	ESTs	0.078
20	110157	H18987	Hs.169731	ESTs	0.078
	128515	AA149044	Hs.10086	ESTs; Highly similar to HYPOTHETICAL PROTEIN KIAA0195 [H.sapiens]	0.078
	133069	U94836	Hs.6430	protein with polyglutamine repeat	0.078
	112209	R49844	Hs.24865	ESTs	0.078
	133361	R28279	Hs.71848	Human clone 23548 mRNA sequence	0.078
25	134714	U89922	Hs.890	lymphotoxin beta (TNF superfamily; member 3)	0.078
	129905	T86796	Hs.132875	ESTs; Weakly similar to predicted using Genefinder [C.elegans]	0.079
	120421	AA236166	Hs.132957	ESTs; Weakly similar to chondromodulin-1 precursor [H.sapiens]	0.079
	100885	HG4490-HT4876		Proline-Rich Protein Prb4, Allele	0.079
	102789	U86759	Hs.158336	netrin 2 (chicken)-like	0.079
30	120139	Z39273	Hs.77876	Human DNA from chromosome 19-specific cosmid R30923; genomic sequence	0.079
	135238	U76343	Hs.96970	Human liver GABA transport protein mRNA; 3' end	0.079
	129618	N54845	Hs.173030	ESTs	0.079
	132960	AA609742	Hs.6150	KIAA0521 protein	0.079
	108751	AA127063	Hs.203717	ESTs	0.079
35	134060	D42039	Hs.78871	KIAA0081 protein	0.079
	111338	N79778	Hs.35094	extracellular matrix protein 2; female organ and adipocyte specific	0.079
	112345	R56880	Hs.26563	ESTs	0.079
	126456	W00881		za56d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	0.079
				IMAGE:296547 5', mRNA sequence.	0.079
40	128937	Z39939	Hs.10726	ESTs	0.079
	103485	Y08409	Hs.248415	thyroid hormone responsive SPOT14 (rat) homolog	0.079
	111202	N68280	Hs.107922	ESTs	0.079
	132625	AA429890	Hs.166066	cisplatin resistance associated	0.079
	103434	X98085	Hs.54433	tenascin R (restrictin; janusin)	0.079
45	102616	U65581	Hs.159191	ribosomal protein L3-like	0.079
	102667	U70867	Hs.83974	solute carrier family 21 (prostaglandin transporter); member 2	0.079
	111422	R01127	Hs.19104	ESTs	0.079
	101411	M16938	Hs.820	homeo box C6	0.08
	113267	T65058	Hs.12725	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.08
50	103559	Z19585	Hs.75774	thrombospondin 4	0.08
	131588	AA258613	Hs.29189	KIAA1021 protein	0.08
	107821	AA020991	Hs.172856	ESTs	0.08
	134278	H82839	Hs.81001	ESTs; Weakly similar to DY3.6 [C.elegans]	0.08
	120893	AA369800	Hs.97058	EST; Highly similar to CMP-N-acetylneuraminic acid hydroxylase [H.sapiens]	0.08
55	108786	AA128999		zo8112.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens	0.08
				cDNA clone IMAGE:567119 3', mRNA sequence	0.08
	106890	AA489245	Hs.88500	KIAA1066 protein; JSAP1 homolog (mouse); JIP3 homolog (mouse)	0.08
	119760	W72267	Hs.58219	ESTs	0.08
	132999	Y00787	Hs.624	interleukin 8	0.08
60	129156	AA028195	Hs.108973	dolichyl-phosphate mannosyltransferase polypeptide 2; regulatory subunit	0.08
	121171	AA400008	Hs.161814	ESTs	0.08
	103864	AA207264	Hs.181077	ESTs; Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]	0.08
	128591	AA255537	Hs.102057	ESTs; Weakly similar to O-linked GlcNAc transferase [H.sapiens]	0.08
	122172	AA435753	Hs.161854	EST	0.08
65	112802	R97647	Hs.174855	EST	0.08
	107723	AA015967	Hs.60680	EST	0.08
	113011	T23737	Hs.1600	chaperonin containing TCP1; subunit 5 (epsilon)	0.081
	131279	AA089853	Hs.25197	STIP1 homology and U-Box containing protein 1	0.081
	103190	X70083	Hs.58414	filamin C; gamma (actin-binding protein-280)	0.081

	103956	AA292411	Hs.233348	ESTs	0.081
	112706	R89828	Hs.138493	ESTs	0.081
	126126	M85370		EST01884 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCH10, mRNA sequence.	0.081
5	130094	H43286	Hs.167017	gamma-aminobutyric acid (GABA) B receptor; 1	0.081
	100800	HG3945-HT4215		Phospholipid Transfer Protein	0.081
	108675	AA115240	Hs.61816	ESTs	0.081
	129420	AA234259	Hs.99816	ESTs	0.081
10	129666	M77349	Hs.118787	transforming growth factor; beta-induced; 68kD	0.081
	101645	M59807	Hs.943	natural killer cell transcript 4	0.081
	130536	T17045	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin)	0.081
	107732	AA016181	Hs.59752	ESTs	0.081
	123071	AA482593	Hs.104285	ESTs	0.081
	113537	T90457	Hs.191293	ESTs	0.081
15	101250	L34060	Hs.79133	cadherin 8	0.081
	122521	AA449433	Hs.149227	ESTs; Weakly similar to PROLINE-RICH PROTEIN MP-3 [M.musculus]	0.081
	133914	N32811	Hs.77542	ESTs	0.081
	102038	U05659	Hs.477	hydroxysteroid (17-beta) dehydrogenase 3	0.081
20	110336	H40338	Hs.174094	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.081
	118637	N70274	Hs.49822	ESTs	0.081
	117966	N51589	Hs.94012	ESTs	0.082
	104424	H87671	Hs.182320	ESTs; Weakly similar to Mouse 19.5 mRNA; complete cds [M.musculus]	0.082
	100361	D78361	Hs.125078	Human mRNA for ornithine decarboxylase antizyme; ORF 1 and ORF 2	0.082
	112974	T17291	Hs.101174	microtubule-associated protein tau	0.082
25	132832	D63482	Hs.57734	KIAA0148 gene product	0.082
	132039	Z39489	Hs.3781	Homo sapiens BAC clone RG118D07 from 7q31	0.082
	113272	T65383	Hs.12807	ESTs	0.082
	104924	AA058532	Hs.28774	ESTs	0.082
	111061	N58054	Hs.36859	ESTs	0.082
30	129269	R45977	Hs.163593	ribosomal protein L18a	0.082
	102453	U48437	Hs.74565	amyloid beta (A4) precursor-like protein 1	0.082
	126204	AJ080388	Hs.134296	ESTs	0.082
	116615	D80666	Hs.45203	ESTs	0.082
35	128856	AA219552	Hs.204144	ESTs; Modly smlr to tumor necrosis factor-alpha-induced prot B12 [H.sapiens]	0.082
	112776	R95850	Hs.34494	ESTs	0.082
	105494	AA256273	Hs.29288	Homo sapiens mRNA; cDNA DKFZp434P174 (from clone DKFZp434P174)	0.082
	117000	H84718	Hs.112236	ESTs; Weakly similar to repressor protein [H.sapiens]	0.082
	112656	R85260	Hs.133151	transient receptor potential channel 7	0.082
	128963	J03890	Hs.1074	surfactant; pulmonary-associated protein C	0.083
40	116957	H79292	Hs.39960	ESTs	0.083
	101057	K03430		Human complement C1q B-chain gene, exon A+1	0.083
	121948	AA429452	Hs.98582	ESTs	0.083
	130822	M80647	Hs.2001	thromboxane A synthase 1 (platelet; cytochrome P450; subfamily V)	0.083
	122743	AA458674	Hs.99478	EST	0.083
45	114569	AA063316		zm2d1.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone IMAGE:512947 3' similar to TR:E198281 E198281 THIOREDOXIN REDUCTASE ;contains Alu repetitive element;; mRNA sequence	0.083
	132270	U70671	Hs.43509	ataxin 2 related protein	0.083
50	108126	AA052951	Hs.47413	ESTs	0.083
	102880	X04325	Hs.2679	gap junction protein; beta 1; 32kD (connexin 32; Charcot-Marie-Tooth neuropathy; X-linked)	0.083
	115365	AA282089	Hs.88599	ESTs	0.083
	114529	AA052980	Hs.206704	ESTs	0.083
	135017	AA249586	Hs.9315	ESTs; Weakly similar to NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN [H.sapiens]	0.083
55	123776	AA610071	Hs.112813	ESTs	0.083
	114454	AA021091	Hs.226208	ESTs	0.083
	101246	L33799	Hs.202097	procollagen C-endopeptidase enhancer	0.083
	107366	U78310	Hs.13501	pescadillo (zebrafish) homolog 1; containing BRCT domain	0.083
60	132779	T89601	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPORTER TYPE 5; SMALL INTESTINE [H.sapiens]	0.083
	129709	AA112209	Hs.1209	acyl-Coenzyme A dehydrogenase; long chain	0.083
	115244	AA278767	Hs.914	Human mRNA for SB classII histocompatibility antigen alpha-chain	0.083
65	123253	AA490878	Hs.111334	ferritin; light polypeptide	0.083
	128469	T23724	Hs.258677	EST	0.083
	132220	AA431847	Hs.42409	ESTs; Highly similar to CGI-146 protein [H.sapiens]	0.083
	111664	R17939	Hs.22344	ESTs	0.083
	102354	U38268		Human cytochrome b pseudogene, partial cds	0.084
	112828	R98774	Hs.194338	ESTs	0.084

5	110410	H47868	Hs.34024	ESTs	0.084
	102620	U66052		Human clone W2-6 mRNA from chromosome X	0.084
	102550	U58087	Hs.14541	cullin 1	0.084
	108417	AA075716		zm89e5.s1 Stratagene ovarian cancer (#937219) H sapiens cDNA clone IMAGE:54512 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequence	0.084
10	113299	T67285	Hs.13089	ESTs	0.084
	117869	N49947	Hs.46990	ESTs	0.084
	113734	T98484	Hs.18377	EST	0.084
	133325	C00424	Hs.7101	periodontal ligament fibroblast protein	0.084
15	123368	AA505022	Hs.124838	ESTs	0.084
	101615	M55153	Hs.8265	transglutaminase 2 (C polypeptide; protein-glutamine -gamma-glutamyltransferase)	0.084
	119352	T65972	Hs.193365	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	0.084
	123828	AA620686	Hs.112884	EST	0.084
20	103611	Z38133	Hs.113973	myosin; heavy polypeptide 8; skeletal muscle; perinatal	0.084
	131289	AA485697	Hs.25334	ESTs; Weakly similar to ION CHANNEL HOMOLOG RIC PRECURSOR [M.musculus]	0.084
	128678	T15896	Hs.103535	ESTs	0.084
	130814	AA256695	Hs.19813	ESTs	0.084
25	133391	X57579	Hs.727	inhibin; beta A (activin A; activin AB alpha polypeptide)	0.084
	129322	AA437153	Hs.110407	ESTs; Weakly similar to coded for by C. elegans;cDNA yk173c12.5 [C.elegans]	0.084
	109284	AA196995	Hs.86092	ESTs	0.084
	116689	F09222	Hs.66099	ESTs	0.085
30	100545	HG2147-HT2217		Mucin 3, Intestinal (Gb:M55405)	0.085
	102634	U66711	Hs.77667	lymphocyte antigen 6 complex; locus E	0.085
	111735	R25389	Hs.23856	ESTs; Weakly similar to FAST kinase [H.sapiens]	0.085
	105181	AA190676	Hs.10974	ESTs; Moderately similar to unknown [R.norvegicus]	0.085
35	122681	AA455350	Hs.99401	EST	0.085
	114543	AA056121	Hs.158419	ESTs	0.085
	133597	AA425908	Hs.75139	partner of RAC1 (araptin 2)	0.085
	121064	AA398647	Hs.97406	ESTs	0.085
40	122231	AA436369	Hs.197728	ESTs; Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]	0.085
	100309	D50550	Hs.95659	lethal giant larvae (Drosophila) homolog 1	0.085
	101727	M73481	Hs.73883	gastrin-releasing peptide receptor	0.085
	131226	AA165400	Hs.24476	ESTs	0.085
45	133580	AA095041	Hs.181073	ESTs	0.085
	102792	U87964	Hs.227576	GTP binding protein 1	0.085
	104976	AA086480	Hs.183669	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.085
	120865	AA350631	Hs.96963	EST	0.085
50	106080	AA418046	Hs.35124	ESTs	0.085
	128571	AA416619	Hs.101661	ESTs	0.085
	101838	M92934	Hs.75511	connective tissue growth factor	0.085
	128514	H84261	Hs.100843	ESTs; Weakly similar to similar to GTP-binding protein [C.elegans]	0.085
55	123099	AA485931	Hs.79	aminoacylase 1	0.085
	134067	Y08200	Hs.78920	Rab geranylgeranyltransferase; alpha subunit	0.085
	116967	H80336	Hs.40124	EST	0.085
	110053	H12586	Hs.89563	nuclear cap binding protein 1; 80kD	0.085
60	114395	AA007313	Hs.110155	ESTs	0.085
	107465	W44681	Hs.251385	murine retrovirus integration site 1 homolog	0.085
	101983	S85655	Hs.75323	prohibitin	0.085
	112544	R70948	Hs.29153	ESTs	0.086
65	111423	R01165	Hs.188507	ESTs	0.086
	127918	AA806043	Hs.115396	Human germline IgD chain gene; C-region; C-delta-1 domain	0.086
	107300	T40348	Hs.90488	ESTs	0.086
	134947	R51194		yj71a08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154166 5' similar to gb:L11284 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (HUMAN);, mRNA sequence.	0.086
70	124579	N68345	Hs.127179	ESTs; Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]	0.086
	130471	Z68280	Hs.183706	adducin 1 (alpha)	0.086
	116596	D60755	Hs.92955	ESTs	0.086
	105069	AA136345	Hs.23617	ESTs; Weakly similar to ZFOC1 gene product [H.sapiens]	0.086
75	102491	U51010		Human nicotinamide N-methyltransferase gene, exon 1 and 5' flanking region	0.086
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	0.086
	130234	AA280413	Hs.157441	spleen locus forming virus (SFFV) proviral integration oncogene spi1	0.086
	120540	AA262992	Hs.96417	ESTs	0.086
80	122508	AA449221	Hs.20432	ESTs	0.086

5	128054	AI205718	Hs.125416	ESTs	0.086
	133020	AA053248	Hs.185182	ESTs; Highly similar to 40S RIBOSOMAL PROTEIN S10 [H.sapiens]	0.086
	130056	AA017356	Hs.171900	arnadillo repeat gene deletes in velocardiofacial syndrome	0.086
	130504	U48865	Hs.158323	CGAAT/enhancer binding protein (C/EBP); epsilon	0.086
	133978	W73859	Hs.78061	transcription factor 21	0.086
10	105265	AA227941	Hs.26088	ESTs	0.086
	133035	T15965	Hs.6333	ESTs	0.086
	100768	HG3636-HT3846		Myosin, Heavy Polypeptide 9, Non-Muscle	0.086
	129338	T56800	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (from clone DKFZp564B176)	0.086
	132789	W23761	Hs.56876	ESTs	0.086
15	116099	AA456309	Hs.58831	regulator of Fas-induced apoptosis	0.086
	100721	HG3355-HT3532		Peroxisome Proliferator Activated Receptor (Gb:Z30972)	0.087
	112569	R73150	Hs.75270	GTP-binding protein homologous to Saccharomyces cerevisiae SEC4	0.087
	130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITAM domains 2	0.087
	100751	HG3527-HT3721		Luteinizing Hormone, Beta Subunit	0.087
20	134550	M27161	Hs.85258	CD8 antigen; alpha polypeptide (p32)	0.087
	130885	AA338646	Hs.20912	adenomatous polyposis coli like	0.087
	101446	M21302	Hs.56306	small proline-rich protein 2A	0.087
	116287	AA487856	Hs.155829	KIAA0676 protein	0.087
	134034	X89267	Hs.78601	uroporphyrinogen decarboxylase	0.087
25	130860	U66061	Hs.241395	protease; serine; 1 (trypsin 1)	0.087
	109901	H04992	Hs.30499	ESTs	0.087
	107537	Z20777	Hs.9857	ESTs; Weakly similar to peroxisomal short-chain alcohol dehydrogenase [H.sapiens]	0.087
	133232	AA496030	Hs.6845	ESTs	0.087
	108559	AA085161		zn12c5.s1 Stratagene hNT neuron (#937233) H sapiens cDNA clone IMAGE:54728 3' similar to TR:G1151228 G1151228 LPG1P. ; mRNA seq	0.087
30	121288	AA401735	Hs.97340	EST	0.087
	108844	AA132916	Hs.177961	Human Chromosome 16 BAC clone CIT987SK-A-388D4	0.087
	129874	AA406488	Hs.181551	ESTs	0.087
	105139	AA164543	Hs.110082	ESTs	0.088
	124789	R43803	Hs.78110	ESTs; Weakly similar to F17A9.2 [C.elegans]	0.088
35	115923	AA441929	Hs.38205	ESTs	0.088
	123640	AA609292	Hs.112681	ESTs	0.088
	131607	AA351409	Hs.172740	microtubule-associated protein; RP/EB family; member 3	0.088
	130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.088
	108752	AA127070	Hs.71055	ESTs	0.088
40	124249	H68077	Hs.108211	ESTs	0.088
	100109	AJ000480	Hs.143513	phosphoprotein regulated by mitogenic pathways	0.088
	104642	AA004662	Hs.184245	KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog	0.088
	131752	AA453311	Hs.31566	ESTs	0.088
	114727	AA132545	Hs.190202	ESTs	0.088
45	120965	AA398089	Hs.179715	ESTs	0.088
	100396	D84361	Hs.151123	Human mRNA for p52 and p64 isoforms of N-Shc; complete cds	0.088
	106218	AA428451	Hs.91146	DKFZP586E0820 protein	0.088
	111582	R09567	Hs.187569	ESTs	0.088
	121219	AA400606	Hs.144344	EST	0.088
50	101187	L20316	Hs.208	glucagon receptor	0.088
	101513	M28210	Hs.27744	RAB3A; member RAS oncogene family	0.088
	116454	AA621071	Hs.42034	ESTs; Moderately similar to T-complex protein 10A [H.sapiens]	0.088
	116171	AA463434	Hs.42658	ESTs	0.089
	117500	N31909	Hs.44278	ESTs	0.089
55	119978	W88623	Hs.59190	EST	0.089
	132005	D58231	Hs.173091	DKFZP434K151 protein	0.089
	109914	H05529	Hs.194704	leucine-rich; glioma inactivated 1	0.089
	130370	M55265	Hs.155140	casein kinase 2; alpha 1 polypeptide	0.089
	104262	AF009801	Hs.105941	bagpipe homeobox (Drosophila) homolog 1	0.089
60	129708	AA417181	Hs.120858	ESTs	0.089
	106398	AA447545	Hs.18268	adenylate kinase 5	0.089
	120884	AA365356	Hs.97041	ESTs	0.089
	130404	X72012	Hs.76753	endoglin (Osler-Rendu-Weber syndrome 1)	0.089
	114072	Z38184	Hs.123633	ESTs	0.089
65	131470	X54938	Hs.2722	inositol 1,4,5-trisphosphate 3-kinase A	0.089
	124573	N67935	Hs.194703	adaptor-related protein complex 4; mu 1 subunit	0.089
	114717	AA131240	Hs.252014	EST	0.089
	133806	M12759	Hs.76325	Human Ig J chain gene	0.09
	130470	AA398552	Hs.15711	KIAA0639 protein	0.09
	133182	Z80787	Hs.240135	H4 histone family; member J	0.09
	116036	AA452572	Hs.43866	ESTs	0.09

	132404	AA393903	Hs.4768	ESTs	0.09
	122695	AA456048	Hs.99403	ESTs; Moderately similar to undulin 2 [H.sapiens]	0.09
	125975	AA495891	Hs.152290	ESTs; Highly similar to PACAP type-3/VIP type-2 receptor [H.sapiens]	0.09
5	110783	N23669	Hs.26407	ESTs	0.09
	129860	AA410343	Hs.129826	tetraspan transmembrane 4 super family	0.09
	120740	AA302650	Hs.96654	EST	0.09
	119564	W38206		Accession not listed in Genbank	0.09
	134474	AA054746	Hs.8379	ESTs	0.09
10	119014	N95435	Hs.55144	ESTs	0.09
	109791	F10669	Hs.13228	DRE-antagonist modulator; calsenillin	0.09
	117605	N35073	Hs.44433	ESTs	0.09
	121589	AA416627	Hs.191598	ESTs	0.09
	104326	D81655	Hs.143067	ESTs	0.09
15	129861	N69507	Hs.129849	DKFZP564M182 protein	0.09
	102795	U88667	Hs.198396	ATP-binding cassette; sub-family A (ABC1); member 4	0.09
	119626	W49499	Hs.184456	ESTs; Wkly smlr to !! ALU SUBFAMILY SX WARNING ENTRY II [H.sapiens]	0.09
	110516	H56894	Hs.37368	EST	0.09
	105382	AA236853	Hs.111801	Homo sapiens mRNA; cDNA DKFZp564H2023 (from clone DKFZp564H2023)	0.09
20	123754	AA609964	Hs.102021	ESTs	0.09
	108008	AA039430	Hs.61920	ESTs	0.09
	121057	AA398619	Hs.142375	ESTs; Moderately similar to putative envelope protein [H.sapiens]	0.091
	123675	AA609474	Hs.112713	EST	0.091
	135194	C20975	Hs.9613	ESTs; Highly similar to angiotensin-related protein [H.sapiens]	0.091
25	127070	AA641812	Hs.190037	ESTs	0.091
	134051	S67070	Hs.78846	heat shock 27kD protein 2	0.091
	133382	AA112532	Hs.7247	ESTs	0.091
	103615	Z46967	Hs.115460	calicin	0.091
	118457	N66593	Hs.49230	EST	0.091
30	118504	N67334	Hs.50158	ESTs	0.091
	112915	T10176	Hs.4254	ESTs	0.091
	132088	AA470121	Hs.243960	HLA-B associated transcript-3	0.091
	101504	M27288	Hs.248156	oncostatin M	0.091
	112550	R71391	Hs.29074	ESTs	0.091
35	128551	H09058	Hs.237323	N-acetylglucosamine-phosphate mutase; DKFZP434B187 protein	0.091
	112879	T03541	Hs.115960	ESTs	0.091
	127079	A1364691	Hs.128628	ESTs; Moderately similar to CL3BC [R.norvegicus]	0.091
	101993	U01062	Hs.77515	inositol 1;4;5-triphosphate receptor; type 3	0.091
	113020	T23830	Hs.7303	ESTs; Weakly similar to PROHIBITIN [H.sapiens]	0.091
40	120465	AA251505	Hs.130861	ESTs	0.091
	130152	U32645	Hs.151139	E74-like factor 4 (ets domain transcription factor)	0.091
	104941	AA065169	Hs.17805	ESTs	0.091
	110090	H16076	Hs.6915	ESTs	0.091
	135375	AA480888	Hs.99741	ESTs; Weakly similar to BRAIN PROTEIN H5 [H.sapiens]	0.091
45	123799	AA620418	Hs.112861	ESTs	0.092
	118966	N93438	Hs.76907	ESTs; Highly similar to HSPC002 [H.sapiens]	0.092
	116969	H80633	Hs.143038	ESTs	0.092
	125147	W38150		Accession not listed in Genbank	0.092
	100836	HG4113-HT4383		Olfactory Receptor Or17-201	0.092
50	114726	AA132509	Hs.103827	EST	0.092
	107311	T57738	Hs.174112	ESTs	0.092
	112863	T03148	Hs.4610	EST	0.092
	129290	AA521407	Hs.110095	ESTs	0.092
	103384	X92762	Hs.79021	tafazzin (cardiomyopathy; dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	0.092
55	112508	R68213	Hs.28847	ESTs	0.092
	111863	R37495	Hs.23578	ESTs	0.092
	131184	AA452705	Hs.23954	ESTs; Weakly similar to KIAA0584 protein [H.sapiens]	0.092
	107420	W26567	Hs.4775	ESTs	0.092
60	111768	R27606	Hs.24185	ESTs	0.092
	112290	R53940	Hs.26016	ESTs	0.092
	130581	AA481982	Hs.16258	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-5A [H.sapiens]	0.092
	120744	AA302772	Hs.228649	EST	0.093
	112226	R50761	Hs.25738	ESTs	0.093
65	116154	AA460951	Hs.57100	ESTs	0.093
	102640	U67674	Hs.194783	solute carrier family 10 (sodium/bile acid cotransporter family); member 2	0.093
	129797	X53595	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	0.093
	102705	U77180	Hs.50002	small inducible cytokine subfamily A (Cys-Cys); member 19	0.093
	132408	AA035547	Hs.47822	KIAA0380 gene product; RhoA-specific guanine nucleotide exchange factor	0.093
	108441	AA079079		zm97c9.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone	0.093

			IMAGE:545872 3' similar to contains element MER22 REPETITIVE element ;, mRNA sequence	0.093
	108145	AA054133	Hs.63085	ESTs
	106466	AA449990	Hs.76057	lysophospholipase II
5	101697	M64358		Human rhom-3 gene, exon
	121294	AA401958	Hs.240170	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
	117824	N49065	Hs.125201	ESTs; Weakly similar to B7 [M.musculus]
	115771	AA422049	Hs.40780	ESTs
10	102303	U33053	Hs.2499	protein kinase C-like 1
	131405	U79255	Hs.26468	amyloid beta (A4) precursor protein-binding; family A; member 2 (X11-like)
	112909	T10069	Hs.101094	ESTs
	124173	H41281	Hs.107619	ESTs
	112488	R66896	Hs.28788	ESTs
15	130554	X59303	Hs.159637	valyl-tRNA synthetase 2
	106413	AA447964	Hs.6311	ESTs
	111711	R22891	Hs.7093	ESTs
	117595	N34933	Hs.44664	EST
	113813	W45174	Hs.31382	ESTs
20	107769	AA018449	Hs.125220	Homo sapiens DNA from chromosome 19-cosmids R30102:R29350:R27740 containing MEF2B; genomic sequence
	114966	AA250743	Hs.92198	ESTs; Highly similar to calcium-regulated heat stable protein CRHSP-24 [H.sapiens]
	130297	H94949	Hs.171955	trophinin-assisting protein (tastin)
25	109589	F02429	Hs.6581	ESTs
	112592	R77631	Hs.29126	ESTs
	102314	U34038	Hs.154299	coagulation factor II (thrombin) receptor-like 1
	116128	AA459915	Hs.112193	mutS (E. coli) homolog 5
30	106809	AA479704	Hs.220324	Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1; -2; MMP21/22A; -B and -C; a novel gene; the alternatively spliced CDC2L2 gene for
	130607	AA043894	Hs.16603	ESTs
	120592	AA281929	Hs.143974	ESTs
35	117230	N20535	Hs.43265	melastatin 1
	105948	AA404587	Hs.7133	ESTs
	101333	L47738	Hs.80313	p53 inducible protein
	101909	S69265		Homo sapiens mRNA for PLE21 protein; complete cds
40	106959	AA497031	Hs.8657	ESTs; Highly similar to CTG7a [H.sapiens]
	127034	AA352389		ESTs; Wkly smlr to glucose-6-phosphatase catalytic subunit [R.norvegicus]
	134430	H52105	Hs.8309	KIAA0747 protein
	120342	AA207105	Hs.45068	Homo sapiens mRNA; cDNA DKFZp434i143 (from clone DKFZp434i143)
	104450	L77564	Hs.103978	serine/threonine kinase 22B (spermiogenesis associated)
45	130902	AA424530	Hs.21061	ESTs
	102708	U77594	Hs.37682	retinoic acid receptor responder (tazarotene induced) 2
	107373	U85773	Hs.154695	phosphomannomutase 2
	123569	AA608952	Hs.195292	ESTs; Weakly similar to RNA helicase HDB/DICE1 [H.sapiens]
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C
50	128888	AA034951	Hs.106893	ESTs
	100283	D43842	Hs.2430	transcription factor-like 1
	102747	U79303	Hs.82482	protein predicted by clone 23882
	107798	AA019346	Hs.60918	EST
	123565	AA608907	Hs.112614	EST
55	116010	AA449450	Hs.56421	ESTs; Weakly similar to Similarity to H.influenza ribonuclease PH [C.elegans]
	117155	H97536	Hs.42391	EST
	133094	AA115572	Hs.64746	chloride intracellular channel 3
	113174	T54659	Hs.9779	ESTs
	102016	U03270	Hs.122511	centrin; EF-hand protein; 1
60	130126	AB002318	Hs.150443	KIAA0320 protein
	134813	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A receptor; beta 1
	132055	N69440	Hs.38132	ESTs
	122229	AA436198	Hs.103902	ESTs
	127574	AA907314	Hs.188905	ESTs
	134432	AA053022	Hs.8312	ESTs
65	128052	AA878398	Hs.190491	ESTs
	101637	M58285	Hs.132834	hematopoietic protein 1
	103386	X92972	Hs.80324	protein phosphatase 6; catalytic subunit
	133079	AA477561	Hs.6449	ESTs
	120328	AA196979	Hs.104129	ESTs; Weakly similar to protease [H.sapiens]

	107640	AA009615	Hs.257808	ESTs	0.096
	123389	AA521176	Hs.221231	ESTs	0.096
	103222	X74795	Hs.77171	minichromosome maintenance deficient (S. cerevisiae) 5 (cell division cycle 46)	0.096
	111704	R22450	Hs.23396	ESTs; Highly similar to ZINC FINGER PROTEIN 140 [H.sapiens]	0.096
5	126856	AA306523		EST177475 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA sequence.	0.733
	127071	AA250806		ESTs	0.096
	114550	AA056755	Hs.151714	ESTs	0.096
	125955	A1356943	Hs.143761	ESTs	0.096
10	134363	M37033	Hs.82212	CD53 antigen	0.096
	128550	W76492	Hs.170142	ESTs	0.096
	122598	AA453465	Hs.99329	ESTs	0.096
	118898	N90703	Hs.4236	KIAA0478 gene product	0.096
	117661	N39092	Hs.44940	ESTs	0.096
	120996	AA398281	Hs.143684	ESTs	0.096
15	123388	AA521172	Hs.134417	ESTs	0.096
	106700	AA463929	Hs.28701	ESTs	0.096
	112962	T16814	Hs.6828	ESTs	0.096
	121262	AA401372	Hs.97723	ESTs	0.096
	134551	R44839	Hs.8526	i-beta-1;3-N-acetylglucosaminyltransferase	0.096
20	112060	R43754	Hs.21164	ESTs	0.096
	134678	AA039935	Hs.182595	dynelin; axonemal; light polypeptide 4	0.096
	100855	HG4234-HT4504		Methylenetetrahydrofolate Reductase	0.097
	132414	N91193	Hs.48145	ESTs	0.097
	112900	T08758	Hs.3813	ESTs	0.097
25	115989	AA447777	Hs.93135	ESTs	0.097
	103561	Z21488	Hs.143434	contactin 1	0.097
	131087	AA009738	Hs.22824	ESTs; Weakly similar to p160 myb-binding protein [M.musculus]	0.097
	120293	AA190859	Hs.191428	ESTs	0.097
	111830	R36081	Hs.25085	EST	0.097
30	113654	T95770	Hs.17666	ESTs	0.097
	132675	AA179338	Hs.5476	serine proteinase inhibitor	0.097
	120182	Z40125	Hs.91968	ESTs	0.097
	132879	U16282	Hs.5881	ELL gene (11-19 lysine-rich leukemia gene)	0.097
	134211	AA056681	Hs.80021	ESTs; Weakly similar to 62D9.p [D.melanogaster]	0.097
35	115448	AA284845	Hs.165051	ESTs	0.097
	118118	N56901	Hs.47995	ESTs	0.097
	107598	AA004528	Hs.169444	ESTs	0.097
	128933	H01824	Hs.760	GATA-binding protein 2	0.097
	114892	AA235988	Hs.86024	ESTs	0.097
40	101922	S75168	Hs.274	megakaryocyte-associated tyrosine kinase	0.097
	105444	AA252374	Hs.19333	ESTs; Weakly similar to ATP(GTP)-binding protein [H.sapiens]	0.097
	128155	AA926843	Hs.143302	ESTs	0.097
	116276	AA485870	Hs.44914	ESTs	0.097
	111964	R41227	Hs.21860	ESTs	0.097
45	135100	AA398926	Hs.251108	Homo sapiens mRNA; chromosome 1 specific transcript KIAA0493	0.097
	124872	R69251	Hs.101506	EST	0.097
	103084	X59932	Hs.77793	c-src tyrosine kinase	0.097
	124138	H23199	Hs.107010	ESTs	0.098
	130048	R31745	Hs.211612	SEC24 (S. cerevisiae) related gene family; member A	0.098
50	100208	D26129	Hs.78224	ribonuclease; RNase A family; 1 (pancreatic)	0.098
	123537	AA608775	Hs.112589	ESTs	0.098
	118999	N95019	Hs.55092	ESTs	0.098
	119847	W80384	Hs.9853	ESTs	0.098
	112819	R98618	Hs.35984	ESTs	0.098
55	131080	J05008	Hs.2271	endothelin 1	0.098
	127353	AA190853	Hs.155360	ESTs	0.098
	132068	X66365	Hs.38481	cyclin-dependent kinase 6	0.098
	105744	AA293436	Hs.12909	ESTs	0.098
	133680	M92357	Hs.101382	tumor necrosis factor; alpha-induced protein 2	0.098
60	122899	AA469960	Hs.178420	ESTs; Highly similar to WASP interacting protein [H.sapiens]	0.098
	128700	U59286	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys); member 11	0.098
	104393	H46486	Hs.226499	nesca protein	0.098
	123320	AA496792	Hs.139572	EST	0.098
	129169	N31641	Hs.109058	ribosomal protein S6 kinase; 90kD; polypeptide 5	0.098
65	135093	U51333	Hs.159237	hexokinase 3 (white cell)	0.098
	113269	T65159	Hs.85044	ESTs	0.098
	124283	H86783	Hs.194136	ESTs; Moderately similar to zinc finger protein RIN ZF [R.norvegicus]	0.098
	114376	GMCSF		Accession not listed in Genbank	0.099
	100881	HG4458-HT4727		Immunoglobulin Heavy Chain, V μ c Regions (Gb123563)	0.099

	116572	D45654	Hs.65582	DKFZP586C1324 protein	0.099
	123956	AA621747	Hs.112847	EST	0.099
	100818	HG4018-HT4288		Opioid-Binding Cell Adhesion Molecule	0.099
5	132754	W47419	Hs.56007	Human DNA from chromosome 19-specific cosmid F25965; genomic sequence	0.099
	112741	R93080	Hs.35035	ESTs	0.099
	112748	R93299	Hs.166492	ESTs	0.099
	130858	S57235	Hs.246381	CD68 antigen	0.099
	124870	R69233	Hs.101504	ESTs	0.099
10	125304	Z39833	Hs.124940	GTP-binding protein	0.099
	121297	AA401995	Hs.97860	ESTs	0.099
	128602	AA046103	Hs.102367	ESTs	0.099
	124062	H00440	Hs.144524	ESTs; Weakly similar to signal transducer and activator of transcription 2 [M.musculus]	0.099
	100547	HG2149-HT2219		Mucin (Gb:M57417)	0.099
15	105652	AA282505	Hs.19015	ESTs	0.099
	133390	AA459945	Hs.72660	KIAA0585 protein	0.099
	133503	M33195	Hs.743	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	0.099
	109461	AA232667	Hs.58210	ESTs	0.099
20	102068	U09117	Hs.80776	phospholipase C; delta 1	0.099
	113464	T86931	Hs.16295	ESTs	0.099
	104240	AB002368	Hs.70500	KIAA0370 protein	0.099
	121113	AA399109	Hs.161813	ESTs	0.1
	122896	AA469952	Hs.97899	ESTs; Weakly similar to dat2; len:343; CAI: 0.17; ALC_YEAST P25335	0.1
25	102405	U43148	Hs.159526	ALLANTOICASE [S.cerevisiae]	0.1
	103599	Z33905	Hs.81218	patched (Drosophila) homolog	0.1
	121079	AA398719	Hs.14169	receptor-associated protein of the synapse; 43kD	0.1
	115820	AA427487	Hs.39619	ESTs; Weakly similar to CREB-binding protein [H.sapiens]	0.1
	125106	T95766	Hs.189760	ESTs; Weakly similar to RETICULOCALBIN 1 PRECURSOR [H.sapiens]	0.781
30	131373	N68116	Hs.26146	ESTs	0.1
	120224	Z41239	Hs.106960	Down syndrome critical region gene 3	0.1
	133090	AA448228	Hs.6468	ESTs	0.1
	132300	AA133244	Hs.44234	ESTs	0.1
	113129	T49384	Hs.8988	EST	0.1
35	110638	H73197	Hs.17241	ESTs	0.1
	131364	R53255	Hs.26010	ESTs	0.1
	105370	AA236476	Hs.22791	ESTs; Weakly similar to transmembrane protein with EGF-like and two follistatin-like domains 1 [H.sapiens]	0.238
40					

TABLE 11A shows the accession numbers for those primekeys lacking unigeneID's for Table 11. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey:	Unique Eos probeset identifier number	
CAT number:	Gene cluster number	
Accession:	Genbank accession numbers	
Pkey	CAT number	Accession
100610	19864_1	AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F00653 AI936671 AA476718 AW772454 AI807703 R44253 AA976667 AI985186 AI650254 H38942 R84829 AA018724 AA001000 H85934 AA019126 H85609 AA017000 AA339355 AW950556 D51397 AA213981 BE548002 AI056359 AA001560 AW952113 AA317769 AI857477 AI857475 AW249771 AW162661 H38943 AA018628 R85885 AI984613 AI934765 AI796172 AW157488 AI929191 R85523 D51221 D53851 H85610 AI749674 F21582 AA323145 AA019127 AA687444 T06745 AI699293 H29532 AA214029 AA223656 NM_016834 X14474 R19697 H09695 R17455 R13812 R19056 AI681231 AI590200 R37671 AA861828 AI990023 AI935669 AW005821 AA324581 H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 AI890696 AA308884 AA507078 R41274 AI365507 T16348 AI560453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W28930 R44098 R51045
100674	21517_2	AW403342 AW248986 BE561709 AA357312 BE311834 BE389496 BE294887 AW732696 BE047868 AI702383 BE019155 AI702367 BE408966 BE280458 BE313759 BE513492 BE535404 BE280258 AC005263 NM_007165 L21990 AW732711 AI564920 AW249094 BE265365 AW607186 AW607346 BE005217 H27211 U46230 BE260066 BE207043 BE546782 AW248659
108559	41469_9	AA085228 AA085161
100721	19818_1	L40904 NM_005037 X90563 AB005526 H21596 AA086517
100748	41861_1	X06096 X05826
100750	15759_1	BE157260 BE157265 R48118 H43827 Z17877 AW379070 AW291778 M20605 J03253 M14206 V00568 AI860465 AW296022 M13930 AL047400 J00120 BE018476 AW675223 T26980 F06694 R22709 R24720 H22753 AI903100 AI903094 AW937823 X00364 D10493 K01904 K01906 K00535 L00058 AA410662 AW384760 AA304930 AI680985 X00198 H58025 AW998901 AV653447 N31654 AW610357 AW610369 AW862480 BE223010 AW384172 AW384219 AW384218 AA298522 BE140421 AW945162 AW751711 AA514409 AW747912 AI214214 W87741 AA972406 AA554513 BE302087 AI249030 AA477850 AV653129 AI281360 AI274110 W87861 AA641366 X66258 AI051600 AA877139 AA527483 AA857219 AI250782 AA625531 AA807892 AI278811 AI224033 H24033 AA593396 AW129709 R45453 N22772 AA235530 T29737 AI016409 AI688907 AA568370 AA722760 AI539329 AA550843 AW674698 AI538452 AI538453 AI337957 AA477744 AA464600 AI140319 AW949294 AI339781 AI828736 AA923634 AA344094 AI278350 AA975567 AA908416 AA857170 AW023520 R43413 R48004 F02958 AI989439 R11207 AA737307 D10493 AW950652 AI093842 AI474024 AA703369 R11264 M13930 M13930 M13930 M13930 J00120 M13930 M13930 X00364 J00120 R19507 AA639812
100751	24700_1	N32759 N29730 N30831 N32604 N31955 AI206390 H87574 R23494 AI186215 N30036 AI741512 J00117 NM_000737 AI453626 AA330974 AI188729 AI188604 AI188964 N30276 AI188947 AI188830 AI188303 AI200457 AI219166 AI192459 AI183280 AI189275 AI188639 AI186353 AI189616 AI184224 AI130720 AI188454 AI188391 AI148857 AI192447 AI209155 AI190013 AI206355 AI188721 AI189429 AI189364 AI186330 AI431595 AI189595 AI188781 AI148647 AI200022 AI221552 AI220923 AI188728 AA233034 AI189807 AI189641 AI219044 AI148774 AI200658 W71989 AI207360 AI188824 AI200559 AI200270 AA644163 AI199943 AI151301 AI189555 AI262724 AI148590 AI148695 AI126906 AI149163 K03183 K03189 AI189842 AI221014 N30608 AI186465 AI220865 AI188498 AI138226 AI189968 AI221019 AI138197 AI149426 AI148904 AI186218 AI188348 AI160579 AI198460 AI149039 AI160936 AI219055 AI184784 AI221580 AI161082 AI160814 AI123896 AI417614 AI126101 AI188872 AI149571 AI168533 AI149072 AI149467 AI131286 N30684 AI160705 AI160692 AI149559 AI273580 AI189442 AI138448 AI149591 N27302 AA400910 AI138431 AI138435 AI128407 N30216 AI128296 AI219589 AI188492 AI149447 AI168482 H95374 AI219009 N31616 AI276216 N32233 AI291937 N30741 AI188689 N27111 R23214 AI221605 AI184348 AI200375 H94451 N26397 AI871881 AA232905 N30833 AI220780 H94446 N30822 H87464 R68815 N30290 AI128424 H12587 T47334 H87631 H87156 AI219133 AI868741 AA330859 H86993 AA330413 H93556 N30817 T90191 H93668 AI200054 H95207 T47316 H95381 T49170 R00880 T49171 N27381 H94107 R63352 T85053 AW451899 H95142 N30313 H94015 H86987 T28278 N29701 C18834 AA331267 AA330939 AI654493 N27073 N29831 R68113 N30758 R26086 N32108 H95135 AA330414 AA330978 AI219422 AI189453 AI199951 X00264 NM_000894 AA371909 AA063496 T29543 AA371971 AA372026 AA371978 AA371346 AI051683 AI186418 AI220659 AI189068 AI219266 AI186552 AI188715 AI149156
100760	1334_7	AW794626 M27126 M27014
100775	18179_3	J05581 M61170 T27692 M34088 M34089 AW860335 AW579047 AW610437 AW610386 AW610422 AW610473 AW579078 AW604897 AW860163 AW579067 AW862410 AI816584 AW177757 AW602769 AI909790 AW860331 AI909787 AI909811

5 AI909813 AW845083 AI905920 AW387919 BE140766 AI909279 AW369405 AA429321 AA429320 AA367451 AA847972
 AW001137 AI567905 T84561 AI631295 AA151351 H02932 AI884519 AA367457 AW369421 AI678846 AW391803 AI610869
 AW192838 AI922289 AI952140 AI910233 AI479474 AW001395 AA488073 AI985760 AW130017 AI858369 AA627845
 AW081805 AA158865 AI624443 AA344985 AA569793 R72486 AI589329 AI903204 AI269893 AA641284 AI279932 AA149270
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 AI561008 F22392 R71279 AA995433 R50725 W24462 R71931 AA464437 AW591731 R25667 R52695 R50810 AI560805
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 AA460662 AA432059 AW016935 F25770 F32549 F36677 F33016 F35992 F36010 AW172497 AA835076 F28727 AA211643
 25 AA453282
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 30 100885 12707_3 X07881 NM_006249 X07637 AA376715 AA376677 X07715 X07704 S80916
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 BE267438 NM_005850 L35013 BE540833 BE390902 BE391494 BE277459 BE385592 BE390612 BE384263 BE387779
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 AI886259 AI612932 AA215437 AI956014 BE541087 BE255652 BE265878 BE394102 W27502
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 126126 1630017_1 W80551 M85370
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 102675 5145_4 U72512 T98357 R31335 F18090
 102753 2226_1 L32961 NM_000663 U80226 S75578 AA425061 AA429317 AI815143 AA910669 AI286022 AI286019
 102799 34624_4 U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
 127034 51148_2 BE397750 AA232171 BE562900 BE384894 BE242228 BE206819 BE261742 AA296468 AW959763 BE276164 BE264109
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 Y10518 Y10514 Z83935 Y10508 AK000055 Y10519 AI142012 AI681175 BE222219 AA890586 BE504347 BE328064 N63044
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 AI088070 AI214349 AA890297 AI494156 AI698598 AA631658 AA504593 AA860733 AI266781 AW663214 AW771231
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 55 127071 188097_1 AA250806 AA458220
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 126856 20669_1 AI084125 AI083773 AI479687 AI939609 AI968662 AF129507 NM_013282 AW971840 AW298508 AA744240 AA811217
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 60 103996 224545_1 AA321355 AW964592 R23284 H73883 R23382 N47914 C01377 H04668 AW606248 R34447 AA847136 AI684489 AI523112
 AW044269 AI379138 N29366 AA761543 N79248 AA960845 AA768316 AI147926 AI718599 AI880620 R67467 AI216016
 AI738663 H04648
 113213 23798_1 NM_001395 Y08302 AI434619 AI470328 AI261807 AW024965 AI806537 AI830549 AI640337 AI219065 AW271700
 AW028488 AI133339 AI859205 R51175 U87167 BE379324 BE392008 AA340819 AA343110 T57275 D59164 AW299312
 65 AI434422 AI936390 AW024975 R40262
 AW269126 R09430 T56590 AI367247 AI253132 BE464248 T58658 AW207785 T58607
 R51194 AI732276 R53587 AI820697
 134947 844579_1 AK000526 BE550084 W30689 AW271859 AA411456 AI341551 AA242990 AA243027 H87046 D20360 AI184053 AA146956
 129311 16078_1 AI721023 AI718944 AA146955 F18215 AA903890 AI700355 AI075430 AA411584 AA878210 AI476760 AW945637 AA630596

		AA431522 AA301989 AI909058 D12149 N41960 BE222214 AA609922 AA828176 AA393359 AA398693 AW024956 BE467805 AW298623 AW264085 AI024454 AI024719 AI431927 T55087 AI611014 T54920 AA131253 AI436344 AA017176 AI359979 AA047836 AA017063 AA016303 AA001545
5	114427 9724_2 114569 110077_1 100106 15621_5 100515 342_1	AA063315 AA063316 AF015910 AA305746 D90187 T63943 AW951154 T29182 AI734941 D13264 AI299239 Z18812 AW299859 W24476 AA933064 AA489759
10	100531 46038_1 100545 22955_11 100574 17320_2	AW888554 AW607282 AA319986 M28590 M55405 AW752552 AA326895 M10036 NM_000365 N84665 H69414 N84657 AA380453 AA329743 AA357367 AA188770 AA376532 AA353653 AA158953 AA083176 BE537313 AA181433 D53373 R57376 AA206698 R14807 H18899 H11191 H93892 R25593 T61134 N93285 AA083081 AA831789 H13137 AA497014 AA079330 AA182861 H13138 W47161 R62913 AA687089 AA211112 AA429237 AL035923 AA100070 AW392898 AI566433 AA866006 AA214002 AW392865 N79454 AA197181 AI680371 AA176501 AA737967 AI089225 F34874 AW571437 AI620620 AA573489 AA423816 AA164917 AA458455 T47072 AI569087 AI261656 AA730919 AI633441 AW195182 AI351622 AW243465 AI872649 AI359227 AA987941 AI693770 T47073 AW779948 AW510580 AI635626 AW627601 AA864326 AA953578 AI341418 BE222853 AI241963 AI094663 AA928380 AA493373 AW043762 AI377783 AW958987 BE619760 AA385240 BE277975 BE280095 AW631443 AA581048 BE618715 BE299610 C14874 BE559858 BE378455 BE618290 BE544585 AI525575 BE548897 BE267110 AA804738 BE269821 AA918133 BE277647 AA599947 BE280735 BE390239 N74150 T12504 AI208197 AW955527 AA113897 N40081 H73835 H70393 AI434041 W22950 AI192661 BE264461 W26486 AA626424 AA196694 T69209 AA857976 AI540287 AA410599 AA864287 AW950564 AA013320 T49283 AI541438 AW804703 AA335534 AA335659 BE562269 BE618802 BE277850 BE546413 BE280994 AA204813 BE561694 BE543524 BE253647 AW001452 W19116 BE542508 AA205894 BE254875 BE270033 AI525906 BE251792 AA975700 BE272138 AW607671 N87686 M10036 BE515060 BE298607 AI745178 U47924 H03193
25	100627 tigr_HT2798 100756 tigr_HT3768 100768 tigr_HT3846 100813 tigr_HT4265 100836 tigr_HT4383 100855 tigr_HT4504	Z25424 M88357 L29141 M69180 M81105 L33999 U04688 U09806
30	102104 entrez_U12139 125091 genbank_T91518 100929 tigr_HT688 125147 _entrez_W38150 102354 entrez_U38268 102491 entrez_U51010 102636 entrez_U67092 118769 genbank_N74496 101046 entrez_K01160 101057 entrez_K03430	U12139 T91518 X65561 W38150 U38268 U51010 U67092 N74496 K01160 K03430
40	108334 genbank_AA070473 108417 483241_1 108441 genbank_AA079079 108786 genbank_AA128999 101655 entrez_M60299 101697 entrez_M64358 117437 genbank_N27645 101798 entrez_M85220 101909 entrez_S69265 103508 entrez_Y10141 103575 entrez_Z26256 119332 genbank_T54095 112161 genbank_R48295 119564 NOT_FOUND_entrez_W38206 114376 NOT_FOUND_entrez_GMCSF	AA070473 AA070853 AA075749 AA075716 AA079079 AA128999 M60299 M64358 N27645 M85220 S69265 Y10141 Z26256 T54095 R48295 W38206 GMCSF
55	100478 tigr_HT1067 100547 tigr_HT2219 100564 tigr_HT2324	M22406 M57417 Z11585

TABLE 12: shows genes, including expression sequence tags, that are down-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu01 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

5	Pkey:	Unique Eos probeset identifier number			
10	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Background subtracted normal prostate : prostate tumor tissue			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	100522	HG1763-HT1780		Prolactin-Induced Protein	17.4
	130803	M81650	Hs.1968	semenogelin I	16.785
	118068	N53943	Hs.13743	ESTs	13.225
20	114251	Z39898	Hs.21948	ESTs	12.7
	112134	R46025	Hs.7413	ESTs	8.735
	101436	M20642	Hs.158295	Human alkali myosin light chain 3 mRNA; complete cds	8.175
	104028	AA361094	Hs.221128	ESTs	8.15
	108944	AA149204	Hs.175783	ESTs; Highly similar to growth arrest inducible gene product [H.sapiens]	7.535
25	103838	AA174173	Hs.12622	ESTs	7.212
	120469	AA251741	Hs.25882	DKFZP586M1824 protein	7.175
	110279	H29231	Hs.27384	ESTs	6.701
	127472	AA761378	Hs.192013	ESTs	6.642
30	133301	N35229	Hs.7037	pallid (mouse) homolog; pallidin	6.411
	102457	U48807	Hs.2359	dual specificity phosphatase 4	6.395
	114011	W90385	Hs.15082	ESTs	6.15
	101249	L33881	Hs.1904	protein kinase C; iota	6
	123265	AA491209	Hs.105265	ESTs; Weakly similar to reverse transcriptase [M.musculus]	6
35	119322	T49655	Hs.241569	ESTs; Modly smlr to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	5.95
	101673	M61906	Hs.6241	phosphoinositide-3-kinase; regulatory subunit; polypeptide 1 (p85 alpha)	5.925
	115586	AA399218	Hs.92423	ESTs	5.7
	120590	AA281780	Hs.111441	ESTs; Weakly similar to similar to Kruppel-like zinc finger protein [C.elegans]	5.7
	109748	F10192	Hs.248323	Tubulin; alpha; brain-specific	5.625
40	134727	X80507	Hs.8939	yes-associated protein 65 kDa	5.5
	129171	AA234048	Hs.7753	calumenin	5.486
	120390	AA233122	Hs.111460	ESTs; Highly similar to multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform [H.sapiens]	5.4
	131699	R68657	Hs.90421	ESTs; Modly smlr to !! ALU SUBFAMILY SX WARNING ENTRY !! [H.sapiens]	5.279
45	104490	N71503	Hs.43087	ESTs; Weakly similar to dystferlin [H.sapiens]	5.266
	102124	U14528	Hs.29981	solute carrier family 26 (sulfate transporter); member 2	5.151
	109280	AA196635	Hs.86081	ESTs	5.134
	109707	F09739	Hs.185701	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 21920	5.075
	108087	AA045709	Hs.40545	ESTs	5.075
50	135006	M21665	Hs.929	myosin; heavy polypeptide 7; cardiac muscle; beta	5.055
	119182	R80664	Hs.77067	ESTs	5.033
	129806	R62444	Hs.173373	KIAA0931 protein	4.675
	101435	M20543	Hs.1288	actin; alpha 1; skeletal muscle	4.626
	125954	R93943		yt72c12.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:275735 5'	4.6
55	113989	W87544	Hs.221184	ESTs	4.559
	104432	J03460	Hs.99949	prolactin-induced protein	4.451
	112326	R56068	Hs.4268	ESTs	4.45
	119063	R16833	Hs.53106	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	4.45
	130376	R40873	Hs.155174	KIAA0432 gene product	4.301
60	122484	AA448286	Hs.98074	ESTs; Highly similar to atrophin-1 interacting protein 4 [H.sapiens]	4.2
	104142	AA447006		ESTs; Moderately similar to !! ALU SUBFAMILY SQ WARNING	4.175
	129413	N32787	Hs.11123	ESTs; Moderately similar to hypothetical protein 2 [H.sapiens]	4.1
	103678	Z84483		Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-134.05	13q12-134.05
	114266	Z40186	Hs.26409	ESTs	4.05
	115206	AA262491	Hs.186572	ESTs	4.048
65	123723	AA609749	Hs.112759	ESTs; Highly similar to unknown protein [R.norvegicus]	4.041
	129130	H97993	Hs.172788	ESTs; Weakly similar to KIAA0512 protein [H.sapiens]	4.028

	120217	Z41078	Hs.66035	ESTs	4.028
	108536	AA084524		zn19d8.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA	4.023
	134460	AA400030	Hs.8360	ESTs; Weakly similar to II ALU CLASS B WARNING ENTRY II [H.sapiens]	3.925
5	120418	AA236010	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323)	3.91
	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15	3.889
	125052	T80174	Hs.222779	ESTs; Moderately similar to similar to NEDD-4 [H.sapiens]	3.85
	108600	AA099585	Hs.41175	ESTs	3.833
	103099	X61100	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme	3.818
	134948	H06773	Hs.93850	protein kinase; AMP-activated; gamma 2 non-catalytic subunit	3.792
10	120511	AA258144	Hs.221576	ESTs	3.779
	111861	R37460	Hs.25231	ESTs	3.768
	113966	W86600	Hs.9842	ESTs	3.75
	131649	AA481254	Hs.30120	ESTs	3.708
	129775	R94659	Hs.12420	ESTs	3.707
15	110191	H20568	Hs.27182	phospholipase A2-activating protein	3.7
	112678	R87160	Hs.33665	ESTs	3.7
	127115	AA375791	Hs.131894	ESTs	3.674
	132892	W92797	Hs.59378	DKFZP434G162 protein	3.653
	115023	AA252079	Hs.63931	dachshund (Drosophila) homolog	3.625
20	114932	AA242751	Hs.16218	KIAA0903 protein	3.62
	106865	AA487228	Hs.19479	ESTs	3.614
	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 5 (13kD; B13)	3.613
	124780	R42493	Hs.220839	ESTs	3.6
	130631	AA025399	Hs.169737	ESTs	3.592
25	134154	AA211320	Hs.79404	neuron-specific protein	3.568
	104160	AA455706	Hs.99722	ESTs; Weakly similar to 78 KD GLUCOSE REGULATED PROTEIN PRECURSOR	3.559
	105524	AA258158	Hs.22153	ESTs; Weakly similar to KIAA0352 [H.sapiens]	3.542
	110168	H19673	Hs.176586	ESTs	3.525
30	109480	AA233299	Hs.72158	ESTs	3.522
	109585	F02367	Hs.27252	ESTs	3.5
	115134	AA257107	Hs.194331	ESTs	3.5
	116083	AA455653	Hs.44581	ESTs; Weakly similar to HEAT SHOCK 70 KD PROTEIN 6 [H.sapiens]	3.459
	120524	AA261852	Hs.192905	ESTs	3.45
35	116932	H74330	Hs.150000	ESTs	3.425
	130746	AA256976	Hs.18800	ESTs; Weakly similar to KIAA0579 protein [H.sapiens]	3.42
	107513	X05451	Hs.158295	Human alkali myosin light chain 3 mRNA; complete cds	3.417
	118641	N70298	Hs.49828	ESTs	3.407
	126584	AI028384	Hs.127331	ESTs	3.399
40	105134	AA159953	Hs.22895	ESTs; Weakly similar to arylsulfatase B precursor [H.sapiens]	3.325
	123502	AA600116	Hs.112526	ESTs	3.318
	132389	N50866	Hs.47135	ESTs	3.317
	105691	AA287097	Hs.75356	transcription factor 4	3.315
	131505	H85897	Hs.27755	ESTs	3.309
45	120775	AA342104	Hs.96777	EST	3.3
	105579	AA278824	Hs.19218	ESTs	3.295
	128190	AA946876	Hs.148376	ESTs	3.292
	100819	HG4020-HT4290		Transglutaminase	3.288
	130217	D29956	Hs.152818	ubiquitin specific protease 8	3.273
50	130068	AA608903	Hs.106220	KIAA0336 gene product	3.269
	134719	L07515	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.266
	110277	H29209	Hs.151231	ESTs; Highly similar to FYVE finger-containing phosphoinositide kinase [M.musculus]	3.26
	127354	AA418680	Hs.185797	ESTs	3.212
	129173	R60523	Hs.109087	ESTs	3.197
55	127464	AA970504	Hs.146103	ESTs	3.179
	124923	R94500	Hs.108046	ESTs	3.175
	122465	AA448164	Hs.99153	ESTs; Highly similar to CGI-73 protein [H.sapiens]	3.151
	122027	AA431302	Hs.98721	EST; Weakly similar to N-copine [H.sapiens]	3.151
	103329	X85134	Hs.72984	retinoblastoma-binding protein 5	3.15
60	129937	M95767	Hs.135578	chitinase; di-N-acetyl-	3.15
	134197	AA057341	Hs.87889	helicase-mol	3.15
	107764	AA018219	Hs.226923	ESTs	3.125
	121775	AA421773	Hs.161008	ESTs	3.125
	114768	AA149007	Hs.182339	Ets homologous factor	3.12
65	132381	N48818	Hs.46884	ESTs	3.11
	123105	AA485973	Hs.143947	ESTs	3.104
	121176	AA400080	Hs.97774	ESTs	3.1
	125053	T80620	Hs.186473	ESTs	3.075
	105909	AA401739	Hs.5111	ESTs	3.066

	119767	W72562	Hs.58119	ESTs	3.057
	115776	AA424038	Hs.58197	ESTs	3.056
	111713	R22988	Hs.220950	ESTs	3.05
	115301	AA280047	Hs.43948	ESTs	3.05
5	118448	N66412	Hs.49189	ESTs	3
	106586	AA456598	Hs.256269	ESTs	2.995
	110415	H48239	Hs.29739	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-3A [H.sapiens]	2.979
	105173	AA182030	Hs.8364	ESTs	2.978
	101102	L07594	Hs.79059	transforming growth factor; beta receptor III (betaglycan; 300kD)	2.976
10	110543	H58383	Hs.258544	ESTs	2.976
	125593	R24464	Hs.202949	KIAA1102 protein	2.964
	100824	HG4058-HT4328		Oncogene Aml1-Evi-1, Fusion Activated	2.957
	106822	AA481068	Hs.31835	ESTs	2.95
	131963	D11930	Hs.3592	ESTs	2.95
15	111221	N68869	Hs.15119	ESTs	2.936
	113620	T93785	Hs.17252	EST	2.917
	105220	AA210695	Hs.17212	ESTs	2.917
	123234	AA490227	Hs.105252	ESTs	2.904
	125250	W87465	Hs.222926	ESTs; Weakly similar to D20922 [C.elegans]	2.9
20	116196	AA465160	Hs.63386	ESTs	2.9
	122100	AA432243	Hs.41086	ESTs; Weakly similar to OXYSTEROL-BINDING PROTEIN [H.sapiens]	2.896
	111712	R22905	Hs.113716	ESTs	2.895
	126589	W78107	Hs.187698	ESTs; Weakly similar to Yer140wp [S.cerevisiae]	2.895
	111132	N64378	Hs.13149	ESTs; Highly similar to unknown function [H.sapiens]	2.894
25	115307	AA280300	Hs.191346	ESTs	2.886
	108989	AA152263	Hs.18827	KIAA0849 protein	2.883
	129486	H03686	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding protein	2.879
	119805	W73788	Hs.43213	ESTs	2.875
	125721	R59881	Hs.7503	ESTs	2.871
30	103704	AA028171	Hs.153688	ESTs	2.868
	128420	AI088155	Hs.14146	ESTs; Weakly similar to unknown [H.sapiens]	2.866
	120571	AA280738	Hs.128679	ESTs	2.863
	123059	AA482019	Hs.238202	EST	2.86
	129462	D84239	Hs.111732	IgG Fc binding protein	2.856
35	125166	W45491	Hs.172609	nucleobindin 1	2.854
	125992	W01626		za36a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	2.852
	109431	AA227972	Hs.43635	ESTs	2.85
	105077	AA142919	Hs.5558	ESTs	2.847
	131388	R34531	Hs.92200	KIAA0480 gene product	2.846
40	121060	AA398720	Hs.177953	ESTs	2.838
	112575	R73816	Hs.17385	ESTs	2.836
	130244	R26206	Hs.153293	KIAA0701 protein	2.825
	134698	AA427783	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	2.816
	116355	AA504356	Hs.88650	ESTs	2.813
45	115316	AA280627	Hs.57846	ESTs	2.806
	129577	U48736	Hs.198891	serine/threonine-protein kinase PRP4 homolog	2.8
	130971	H20332	Hs.28707	signal sequence receptor; gamma (translocon-associated protein gamma)	2.799
	115054	AA252863	Hs.87729	ESTs	2.795
	130285	AA063546	Hs.202968	ESTs	2.792
50	124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142)	2.783
	125502	AA732329	Hs.191959	ESTs	2.778
	114800	AA159825	Hs.131887	ESTs; Weakly similar to ORF YNL227c [S.cerevisiae]	2.768
	128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapiens]	2.766
	130159	H51098	Hs.151310	PDZ domain protein (Drosophila inaD-like)	2.75
55	107127	AA620504	Hs.22119	ESTs	2.742
	113547	T90746	Hs.15233	ESTs	2.734
	104639	AA004622	Hs.18214	ESTs	2.727
	127609	AA622559	Hs.150318	ESTs	2.726
	106922	AA490964	Hs.10056	ESTs	2.725
60	124825	R52088		yg85c3.s1 Soares infant brain 1NIB Homo sapiens cDNA clone	2.725
	124333	H98683	Hs.154054	ESTs	2.708
	117634	N36421	Hs.107854	ESTs; Weakly similar to SODIUM- AND CHLORIDE-DEPENDENTGLYCINE TRANSP	2.706
65	101609	M54927	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbacher disease; spastic paraplegia 2; uncomplicated)	2.704
	117142	H96908	Hs.42251	ESTs	2.7
	112602	R79147	Hs.203365	ESTs	2.695
	106828	AA481505	Hs.13797	ESTs	2.68
	124377	N25996	Hs.179833	ESTs	2.675

	101026	J04970	carboxypeptidase M	2.675
	124560	N66393	Hs.102754 ESTs	2.675
	124066	H02494	Hs.101615 ESTs	2.671
5	130281	R12777	Hs.15395 ESTs; Weakly similar to ARGINYL-TRNA SYNTHETASE [H.sapiens]	2.66
	110949	N49602	Hs.13308 ESTs	2.65
	111031	N54839	Hs.221085 ESTs; Highly similar to mediator [H.sapiens]	2.633
	121770	AA421714	Hs.11469 KIAA0896 protein	2.63
	134132	U32519	Hs.220689 Ras-GTPase-activating protein SH3-domain-binding protein	2.626
10	112424	R62452	Hs.191265 ESTs	2.625
	122544	AA451679	Hs.194410 ESTs	2.625
	134425	X90568	Hs.172004 titin	2.624
	111114	N63391	Hs.9238 ESTs	2.619
	116119	AA459242	Hs.44445 ESTs; Weakly similar to Ketch motif containing protein [H.sapiens]	2.615
	112079	R44164	Hs.23014 ESTs	2.6
15	123033	AA481271	Hs.193945 ESTs	2.591
	124196	H52617	Hs.144167 ESTs	2.586
	125873	H14437	y25a04.r1 Soares breast 3NbHbSt Homo sapiens cDNA clone	2.58
	117684	N40184	Hs.45050 ESTs	2.575
20	134938	D30037	Hs.168326 phosphatidylinositol transfer protein; beta	2.575
	131822	AA215647	Hs.200332 ESTs	2.568
	135185	U71203	Hs.96038 Ric (Drosophila)-like; expressed in many tissues	2.564
	117690	N40467	Hs.93834 ESTs	2.557
	118807	N78582	Hs.50732 protein kinase; AMP-activated; beta 2 non-catalytic subunit	2.552
25	121369	AA405657	Hs.128791 Human DNA sequence from clone 967N21 on chromosome 20p12.3-13. Contains	2.55
	114860	AA235112	Hs.106227 ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens]	2.549
	121857	AA426017	Hs.62694 ESTs; Highly similar to DNA-REPAIR PROTEIN COMPLEMENTING	2.548
	110190	H20560	Hs.244624 ESTs	2.548
	132573	AA045333	Hs.51743 ESTs; Weakly similar to !! ALU SUBFAMILY SB2 WARNING ENTRY !! [H.sapiens]	2.542
30	109706	F09729	Hs.12780 ESTs	2.537
	135109	AA410391	Hs.94592 klotho	2.525
	132810	R37027	Hs.5737 KIAA0475 gene product	2.525
	124879	R73588	Hs.101533 ESTs	2.525
	103840	AA174190	Hs.50932 ESTs	2.525
35	119066	R22196	Hs.34492 ESTs	2.519
	114833	AA234362	Hs.87310 ESTs; Moderately similar to CGI-66 protein [H.sapiens]	2.507
	112998	T23555	Hs.103288 ESTs	2.5
	123312	AA496258	Hs.99601 ESTs	2.499
	121873	AA426270	Hs.145696 splicing factor (CC1.3)	2.491
40	123321	AA496884	Hs.23972 ESTs	2.491
	107760	AA018042	Hs.95078 EST	2.483
	102580	U60808	Hs.152981 CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1	2.481
	103053	X56741	Hs.5947 mel transforming oncogene (derived from cell line NK14)- RAB8 homolog	2.475
	124756	R38100	Hs.106294 ESTs	2.475
45	112936	T15665	Hs.6185 ESTs; Weakly similar to BcDNA.GH12174 [D.melanogaster]	2.475
	125178	W58202	Hs.125731 ESTs	2.475
	112423	R62447	Hs.22123 ESTs	2.471
	123515	AA600323	Hs.112535 EST	2.462
	102842	U95020	Hs.21903 calcium channel; voltage-dependent; beta 4 subunit	2.457
50	102400	U42390	Hs.171957 triple functional domain (PTPRF interacting)	2.455
	113187	T56056	Hs.9992 ESTs	2.452
	131687	L11066	Hs.3069 heat shock 70kD protein 9B (mortalin-2)	2.448
	115314	AA280583	Hs.256501 ESTs	2.437
	128211	AI206427	Hs.166707 ESTs; Highly similar to Ran-binding protein 2 [H.sapiens]	2.43
55	134281	L11005	Hs.81047 aldehyde oxidase 1	2.425
	115985	AA447709	Hs.132094 ESTs; Moderately similar to putative transcription factor CA150 [H.sapiens]	2.425
	111348	N90041	Hs.9585 ESTs	2.418
	129430	AA258842	Hs.197877 Homo sapiens clone 23777 putative transmembrane GTPase mRNA; partial cds	2.418
	133863	C13990	Hs.76930 synuclein; alpha (non A4 component of amyloid precursor)	2.417
60	111164	N66857	Hs.14808 ESTs; Weakly similar to !! ALU CLASS C WARNING ENTRY !! [H.sapiens]	2.416
	132143	AA257056	Hs.7972 KIAA0871 protein	2.412
	130330	M55047	Hs.154679 synaptotagmin 1	2.408
	114219	Z39451	Hs.27369 ESTs	2.406
	117101	H94043	Hs.24341 DKFZP586I1419 protein	2.403
65	125433	AA034325	Hs.54320 ESTs	2.4
	111099	N62506	Hs.21958 ESTs	2.4
	120323	AA195405	Hs.110347 Homo sapiens mRNA for alpha integrin binding protein 80; partial	2.397
	118624	N69998	Hs.21801 ESTs	2.394
	123570	AA608955	Hs.109653 ESTs	2.389
	123562	AA608893	Hs.190065 ESTs	2.388

	131546	AA262821	Hs.28578	muscleblind (Drosophila)-like	2.385
	103143	X66141	Hs.75535	myosin; light polypeptide 2; regulatory; cardiac; slow	2.384
	123645	AA609310	Hs.188691	ESTs	2.383
5	130123	AA001835	Hs.150390	zinc finger protein 262	2.379
	131682	AA428368	Hs.30654	ESTs	2.378
	115909	AA436666	Hs.59761	ESTs	2.375
	125168	W45574	Hs.252497	ESTs	2.372
	123973	C14805	Hs.182151	ESTs	2.361
10	135197	U76456		Homo sapiens tissue inhibitor of metalloproteinase 4 mRNA, complete cds	2.357
	118689	N71545	Hs.184544	ESTs	2.357
	107734	AA016225	Hs.93386	ESTs	2.354
	124590	N69220	Hs.41381	ESTs; Weakly similar to ubiquitin hydrolyzing enzyme I [H.sapiens]	2.35
	111163	N66850	Hs.17606	ESTs	2.348
15	112349	R58877	Hs.22665	ESTs; Moderately similar to dJ83L6.1 [H.sapiens]	2.345
	129076	AA262179	Hs.169343	ESTs	2.345
	134238	R81509	Hs.184571	splicing factor; arginine/serine-rich 11	2.341
	116766	H13260	Hs.95097	ESTs	2.336
	106331	AA436853	Hs.34795	ESTs	2.333
20	129003	AA443752	Hs.10784	ESTs	2.332
	132368	AA599814	Hs.46637	ESTs; Weakly similar to cDNA EST yk289g5.5 comes from this gene [C.elegans]	2.332
	124697	R06273	Hs.186467	ESTs; Modly smlr to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	2.322
	120273	AA176688	Hs.221139	ESTs	2.313
	127110	AA304993	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapiens]	2.307
25	105450	AA252621	Hs.93842	ESTs	2.301
	119819	W74371	Hs.58383	ESTs	2.297
	102302	U33052	Hs.69171	protein kinase C-like 2	2.288
	130596	N74353	Hs.16475	ESTs	2.282
	114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	2.278
30	130542	U64675		Human sperm membrane protein BS-63 mRNA, complete cds	2.277
	104491	N71513	Hs.39328	ESTs	2.275
	116988	H82527		ys69e12.s1 Soares retina N2b4HR Homo sapiens cDNA clone	2.275
	126823	AA370120	Hs.7870	ESTs; Weakly similar to Ylr350wp [S.cerevisiae]	2.273
	108800	AA129731	Hs.90424	ESTs	2.273
35	101310	L41607	Hs.934	glucosaminyl (N-acetyl) transferase 2; l-branching enzyme	2.269
	126842	W19498	Hs.21085	ESTs	2.255
	127251	AA936428	Hs.128638	ESTs	2.251
	124647	N91947	Hs.125033	ESTs	2.249
	127112	AI143906	Hs.125103	ESTs	2.247
40	101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide	2.246
	120999	AA398302	Hs.127437	ESTs	2.245
	130225	AA599583	Hs.15299	HMBA-inducible	2.243
	119980	W88678	Hs.249247	heterogeneous nuclear protein similar to rat helix destabilizing protein	2.243
	124222	H61053	Hs.222644	ESTs	2.24
45	129199	H90914	Hs.128629	ESTs	2.236
	106802	AA479101	Hs.16570	ESTs; Weakly similar to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	2.231
	126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-related protein [H.sapiens]	2.229
	104627	AA001976	Hs.19603	ESTs	2.228
	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from clone DKFZp564C053)	2.226
50	113096	T40927	Hs.8345	ESTs	2.225
	135336	AA452822	Hs.99027	ESTs	2.225
	135344	R62976	Hs.168491	ESTs; Moderately similar to TRF1-interacting ankyrin-related	2.225
	126156	AA508354	Hs.118448	ESTs; Moderately similar to AKT3 protein kinase [H.sapiens]	2.222
	128885	AA397841	Hs.180141	cofilin 2 (muscle)	2.218
55	107900	AA026385	Hs.176600	ESTs; Moderately similar to II ALU SUBFAMILY SB2 WARNING	2.217
	114481	AA033562	Hs.151572	ESTs	2.212
	109292	AA199828	Hs.188662	ESTs	2.212
	104257	AF006265	Hs.9222	estrogen receptor-binding fragment-associated gene 9	2.209
	132932	T15482	Hs.6093	ESTs	2.204
60	127392	AA262728	Hs.14896	Homo sapiens clone 24590 mRNA sequence	2.204
	104641	AA004652	Hs.18564	ESTs	2.2
	122529	AA449828	Hs.99229	ESTs	2.195
	124307	H93562	Hs.162395	proline synthetase co-transcribed (bacterial homolog)	2.193
	133601	S95936	Hs.75155	transferrin	2.193
65	119904	W85709	Hs.128927	ESTs; Weakly similar to II ALU SUBFAMILY SP WARNING ENTRY II [H.sapiens]	2.192
	100348	D64109	Hs.4994	transducer of ERBB2; 2 (TOB2)	2.185
	126871	AA351779	Hs.200334	ESTs	2.18
	127793	AI298835	Hs.30445	ESTs; Weakly similar to transcription regulator Staf-50 [H.sapiens]	2.178
	105149	AA169253	Hs.8958	ESTs	2.177
	121367	AA405648		zw39g8.s1 Soares_totat_fetus_Nb2HF8_9w H sapiens cDNA clone IMAGE:772478	2.177

	111836	R36228	Hs.25119	ESTs	2.175
	133394	R16759	Hs.237225	ribosomal protein S5 pseudogene 1	2.175
	123207	AA489697	Hs.145053	ESTs	2.175
	129801	F11087	Hs.239666	ESTs	2.175
5	103393	X94612	Hs.41749	protein kinase; cGMP-dependent; type II	2.161
	132415	AA043223	Hs.4815	nudix (nucleoside diphosphate linked moiety X)-type motif 3	2.157
	106369	AA443828	Hs.25324	ESTs	2.157
	122963	AA478446	Hs.69559	KIAA1096 protein	2.156
	133473	M19309	Hs.73980	troponin T1; skeletal; slow	2.155
10	134257	C06270	Hs.8078	Homo sapiens mRNA; cDNA DKFZp586L081 (from clone DKFZp586L081)	2.155
	135156	AA056012	Hs.9552	blinder of Arl Two	2.151
	104055	AA393755	Hs.117211	ESTs; Highly similar to CGI-62 protein [H.sapiens]	2.15
	102313	U33921	HSU33921	Clontech adult lung cDNA library (HL1158a) Homo sapiens cDNA	2.15
	109788	F10638	Hs.12432	Homo sapiens clone 24407 mRNA sequence	2.15
15	103507	Y10032	Hs.159640	serum/ghucocorticoid regulated kinase	2.15
	116000	AA448710	Hs.41327	ESTs	2.15
	105858	AA399164	Hs.227676	ESTs; Moderately similar to !! ALU SUBFAMILY SQ	2.137
	103153	X66534	Hs.75295	guanylate cyclase 1; soluble; alpha 3	2.137
	126202	AA652238	Hs.199726	ESTs	2.135
20	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	2.134
	104164	AA458770	Hs.27023	KIAA0917 protein	2.132
	108692	AA121270	Hs.82960	ESTs	2.128
	122878	AA465341	Hs.99640	ESTs	2.126
	134771	L13939	Hs.89576	adaptor-related protein complex 1; beta 1 subunit	2.125
25	104298	D31120	Hs.40368	adaptor-related protein complex 1; sigma 2 subunit	2.125
	104840	AA039595	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817)	2.125
	122180	AA435798	Hs.98835	ESTs; Moderately similar to putative ring zinc finger protein	2.125
	131012	H01992	Hs.202949	KIAA1102 protein	2.125
	134092	H17490	Hs.7905	ESTs; Highly similar to sorting nexin 9 [H.sapiens]	2.123
30	118617	N69666	Hs.183413	ESTs; Modtly smlr to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	2.123
	107155	AA621202	Hs.7946	DKFZP586D1519 protein	2.12
	130925	N71935	Hs.169378	multiple PDZ domain protein	2.12
	135167	U63717	Hs.95821	osteoclast stimulating factor 1	2.118
	105952	AA405263	Hs.181400	ESTs	2.109
35	110308	H38148	Hs.32775	ESTs	2.108
	116368	AA521186	Hs.94217	ESTs	2.107
	132939	U76189	Hs.61152	exostoses (multiple)-like 2	2.102
	117881	N50073	Hs.84926	ESTs; Highly similar to B-IND1 protein [M.musculus]	2.1
	121723	AA419622	Hs.104800	ESTs; Weakly similar to Mouse 19.5 mRNA; complete cds [M.musculus]	2.096
40	103500	Y09443	Hs.22580	alkylglycerone phosphate synthase	2.094
	121428	AA406293	Hs.193498	ESTs	2.093
	134632	AA398710	Hs.174139	chloride channel 3	2.091
	129785	F10980	Hs.184780	ESTs	2.09
	111065	N58193	Hs.18740	ESTs; Weakly similar to 1-evidence	2.089
45	114710	AA129931	Hs.79081	protein phosphatase 1; catalytic subunit; gamma isoform	2.083
	132711	N73702	Hs.238927	ESTs	2.083
	133377	R05490	Hs.7239	SEC24 (S. cerevisiae) related gene family; member B	2.079
	124773	R40923	Hs.106604	ESTs	2.078
	117759	N47587	Hs.97345	ESTs; Weakly similar to TROPOMODULIN [H.sapiens]	2.076
50	127386	A1457411	Hs.106728	ESTs	2.076
	101167	L15309	Hs.193677	zinc finger protein 141 (clone pHZ-44)	2.075
	109597	F02582	Hs.14474	ESTs	2.074
	124390	N29325	Hs.7535	ESTs; Highly similar to COBW-like placental protein [H.sapiens]	2.07
	116225	AA478609	Hs.47278	Human Chromosome 16 BAC clone CIT987SK-A-735G6	2.07
55	131243	R16667	Hs.24752	spectrin SH3 domain binding protein 1	2.069
	130557	T90830	Hs.15981	ESTs; Weakly similar to line-1 protein ORF2 [H.sapiens]	2.067
	134103	D14826	Hs.155924	cAMP responsive element modulator	2.064
	108833	AA131866	Hs.61661	ESTs; Weakly similar to DY3.6 [C.elegans]	2.063
	112286	R53765	Hs.158135	KIAA0981 protein	2.063
60	125624	AA165411	zq49a01.r1	Stratagene hNT neuron (#937233) Homo sapiens cDNA clone	2.061
	124612	N72200	Hs.13913	ESTs	2.058
	116335	AA495830	Hs.87013	ESTs	2.057
	112248	R51361	Hs.23423	ESTs	2.056
	115789	AA424754	Hs.43149	ESTs	2.056
65	107029	AA599219	Hs.187492	ESTs; Weakly similar to ALR [H.sapiens]	2.056
	110294	H30270	Hs.165062	ESTs	2.054
	120532	AA262354	Hs.186648	ESTs	2.054
	118180	N59249	Hs.48349	ESTs	2.052
	132018	AA293194	Hs.3737	ESTs	2.052

	132617	AA171913	Hs.5338	carbonic anhydrase XII	2.05
	131526	N36167	Hs.28274	ESTs	2.05
	113254	T64438	Hs.11449	DKFZP564O123 protein	2.05
	122785	AA459978	Hs.99508	ESTs	2.05
5	107203	D20426	Hs.5656	EST	2.05
	105713	AA291321	Hs.184319	ESTs; Moderately similar to KIAA1006 protein [H.sapiens]	2.046
	129385	D82675	Hs.110950	Homo sapiens clone 25007 mRNA sequence	2.042
	119116	R43845	Hs.64595	DKFZP566E2346 protein	2.04
	116405	AA600253	Hs.55601	ESTs; Highly similar to host cell factor 2 [H.sapiens]	2.04
10	125924	AA526849	Hs.82109	syndecan 1	2.039
	105599	AA279442	Hs.143460	protein kinase C; nu	2.037
	119741	W70205	Hs.43670	kinesin family member 3A	2.037
	101449	M21494	Hs.118843	creatine kinase; muscle	2.036
	107109	AA609943	Hs.32793	ESTs	2.034
15	117040	H89112	yw25e5.s1	Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:25328	2.034
	132906	AA142857	Hs.234896	ESTs; Highly similar to geminin [H.sapiens]	2.031
	105479	AA255546	Hs.23467	ESTs	2.027
	102031	U04898	Hs.2156	RAR-related orphan receptor A	2.027
	119846	W80363	Hs.58446	ESTs	2.024
20	124809	R46482	Hs.106875	ESTs	2.024
	130286	AA041548	Hs.154023	KIAA0573 protein	2.023
	124457	N50114	Hs.128704	ESTs	2.017
	125144	W37999	Hs.24336	ESTs	2.017
	120581	AA281257	Hs.125868	ESTs	2.014
25	104931	AA062731	Hs.108319	thyroid hormone receptor-associated protein; 150 kDa subunit	2.012
	120548	AA278846	Hs.187634	ESTs	2.011
	113933	W81362	Hs.30567	ESTs	2.011
	123072	AA485041	Hs.104308	ESTs	2.009
	123648	AA609323	Hs.112689	ESTs	2.008
30	116875	H67749	Hs.161022	EST	2.003
	103179	X69398	Hs.82685	CD47 antigen (Rh-related antigen; integrin-associated signal transducer)	1.995
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.995
	111007	N53378	Hs.22543	ESTs	1.995
	120470	AA251797	zs11f3.s1	NCI_CGAP_GCB1 Homo sapiens cDNA clone	1.989
35	112280	R53457	Hs.26040	ESTs; Weakly similar to fatty acid omega-hydroxylase [H.sapiens]	1.989
	114127	Z38652	Hs.106961	ESTs; Weakly similar to TYL [H.sapiens]	1.988
	129863	AA151005	Hs.129872	sperm surface protein	1.988
	106320	AA436608		ESTs	1.988
	108933	AA147224	Hs.71814	ESTs	1.986
40	105906	AA401633	Hs.22380	ESTs	1.982
	109029	AA157911	Hs.72200	ESTs	1.982
	118470	N66769	Hs.82781	ESTs	1.975
	115358	AA281886	Hs.88923	ESTs	1.975
	115257	AA279060	Hs.193516	B-cell CLL/lymphoma 10	1.974
45	126879	AA719776	zh38g04.s1	Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414390	1.974
	109547	F01479	Hs.26966	ESTs	1.973
	127111	AA805726	Hs.220509	ESTs	1.969
	101266	L36645	Hs.73964	EphA4	1.966
	129319	AA037467	Hs.30340	ESTs	1.965
50	106211	AA428240	Hs.126083	ESTs	1.962
	112753	R93696	Hs.169882	ESTs	1.961
	120489	AA255538	Hs.190504	ESTs	1.959
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubiquitin-protein ligase Rsp5	1.956
	105425	AA251129	Hs.24416	ESTs	1.953
55	134740	L37362	Hs.89455	opioid receptor; kappa 1	1.95
	109324	AA210700	Hs.86405	Homo sapiens mRNA; cDNA DKFZp564P056 (from clone DKFZp564P056)	1.95
	124303	H93043	Hs.107070	ESTs	1.95
	102337	U36922		Human fork head domain protein (FKHR) mRNA, 3' end	1.948
	109441	AA228100	Hs.86998	nuclear factor of activated T-cells 5	1.946
60	127364	AA179573	Hs.90061	progesterone binding protein	1.942
	105255	AA227498	Hs.3623	ESTs	1.942
	130672	L19783	Hs.177	phosphatidylinositol glycan; class H	1.942
	104301	D45332	Hs.6783	ESTs	1.94
	132442	R62589	Hs.167419	ESTs	1.939
65	105519	AA258063	Hs.23438	ESTs	1.937
	132902	AA490969	Hs.168147	ESTs	1.936
	118873	N89881	Hs.44577	ESTs	1.936
	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0888 protein [H.sapiens]	1.934
	115075	AA255486	Hs.88045	ESTs	1.933

	110695	H93463	Hs.124777	ESTs	1.931
	105360	AA236209	Hs.187626	ESTs	1.931
	124998	T56013	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1.929
	121816	AA424814	Hs.187509	ESTs	1.927
5	111717	R23241	Hs.110776	STAT induced STAT inhibitor-2	1.925
	128874	H06245	Hs.106801	ESTs	1.925
	109391	AA219699	Hs.184245	KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog	1.913
	126129	H82165	Hs.40334	ESTs	1.911
	115553	AA369027	Hs.71414	ESTs	1.905
10	113811	W44928	Hs.4878	ESTs	1.905
	108345	AA070906	zm66d1.s1	Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone	1.904
	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [M.musculus]	1.903
	116602	D80063	Hs.241673	EST	1.901
	121121	AA399371	Hs.189095	ESTs; Weakly similar to zinc finger protein SALL1 [H.sapiens]	1.9
15	125330	AA401804	Hs.114574	ESTs	1.896
	130095	F01831	Hs.14838	ESTs	1.894
	119782	W72982	Hs.58262	ESTs	1.894
	104115	AA428090	Hs.26102	ESTs	1.893
20	131313	C17938	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122)	1.891
	105583	AA278907	Hs.24549	ESTs	1.891
	122825	AA461195	Hs.99580	ESTs	1.887
	119495	W35390	Hs.55533	ESTs	1.886
	130309	AA134289	Hs.15423	Homo sapiens BAC clone RG114B19 from 7q31.1	1.886
	125628	AA418069	Hs.241493	natural killer-tumor recognition sequence	1.886
25	110611	H66947	Hs.14671	ESTs; Highly similar to gene ERCC5 protein [H.sapiens]	1.885
	117301	N22569	Hs.43215	ESTs	1.884
	131406	N92239	Hs.26471	Wnt inhibitory factor-1	1.881
	126428	AA013312	Hs.64988	ESTs	1.881
30	120285	AA182882	Hs.111110	titin-cap (telethonin)	1.878
	112724	R91753	Hs.17757	ESTs	1.878
	103121	X63679	Hs.4147	translocating chain-associating membrane protein	1.875
	124381	N26765	Hs.109008	ESTs	1.875
	117226	N20468	Hs.177322	ESTs; Weakly similar to putative p150 [H.sapiens]	1.875
35	105610	AA279991	Hs.124691	ESTs; Weakly similar to trithorax homologue 2 [H.sapiens]	1.875
	111229	N69113	Hs.110855	ESTs	1.875
	120627	AA285079	Hs.190474	ESTs	1.873
	107048	AA600012	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.sapiens]	1.872
	104041	AA381902	Hs.197114	RNA binding protein	1.872
	115162	AA258366	Hs.227806	ras GTPase activating protein-like	1.872
40	102239	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.87
	100043	M10098	AFFX control	18S ribosomal RNA	1.868
	120296	AA191353	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	1.867
	129011	S72869	Hs.107932	DNA segment; single copy; probe pH4 (transforming sequence; thyroid-1;	1.867
	134851	R44479	Hs.90232	KIAA0552 gene product	1.866
45	117392	N26175	Hs.93405	ESTs	1.864
	114530	AA053027	Hs.191797	ESTs	1.863
	123541	AA608794	Hs.112592	ESTs	1.863
	124890	R78618	Hs.34145	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-8 [H.sapiens]	1.862
	106299	AA233511	Hs.194720	ATP-binding cassette; sub-family G (WHITE); member 2	1.861
50	103560	Z20656	Hs.182787	myosin; heavy polypept 6; cardiac muscle; alpha (cardiomyopathy; hypertrophic 1)	1.861
	113073	T33637	Hs.6841	ESTs	1.86
	120407	AA235040	Hs.107283	ESTs	1.859
	103892	AA243523	Hs.17155	ESTs	1.858
	123795	AA620381	Hs.70488	ESTs	1.857
55	108524	AA084323	Hs.68138	ESTs	1.857
	113953	W85812	Hs.187554	ESTs	1.856
	110721	H97678	Hs.31319	ESTs	1.856
	129426	AA412087	Hs.168272	EST; Highly smlr to prot inhibitor of activated STAT prot PIASx-alpha [H.sapiens]	1.853
	112102	R44840	Hs.21303	ESTs	1.852
60	118502	N67317	Hs.50150	ESTs	1.852
	107619	AA004955	Hs.60015	ESTs	1.851
	100436	D87446	Hs.75912	KIAA0257 protein	1.85
	120652	AA287312	Hs.191648	ESTs	1.85
	121643	AA417078	Hs.193767	ESTs	1.843
65	117387	N26011	Hs.53810	ESTs	1.843
	132084	Y12394	Hs.3886	karyopherin alpha 3 (importin alpha 4)	1.843
	124449	N48593	Hs.121820	ESTs	1.841
	120263	AA173440	Hs.193919	ESTs	1.838
	127226	AA731036	Hs.3463	ribosomal protein S23	1.838

	111837	R38447	Hs.24453	ESTs	1.835
	128727	M54174	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	1.834
	114439	AA018937	Hs.128629	ESTs	1.833
	102332	U35637		Human nebulin mRNA, partial cds	1.83
5	126579	W72979	Hs.146082	ESTs	1.83
	102341	U37122	Hs.8110	adducin 3 (gamma)	1.83
	114246	Z39848	Hs.12079	ESTs	1.828
	131757	D17532	Hs.316	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase; 54kD)	1.823
	108904	AA136521	Hs.71148	ESTs; Weakly similar to putative p150 [H.sapiens]	1.823
10	115084	AA255566	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from clone DKFZp564C053)	1.823
	131957	AA609008	Hs.183232	ESTs	1.822
	100131	D12485	Hs.11951	phosphodiesterase I/nucleotide pyrophosphatase 1 (homologous to mouse Ly-41 antigen)	1.822
	124163	H30539	Hs.189838	ESTs	1.821
15	118204	N59859	Hs.48443	ESTs	1.821
	107727	AA016021	Hs.173091	DKFZP434K151 protein	1.82
	100357	D78156	Hs.241548	RAS p21 protein activator 2	1.82
	116295	AA489016	Hs.91216	ESTs; Highly similar to partial CDS; human putative tumor suppressor [H.sapiens]	1.82
	124833	R54112	Hs.128697	ESTs	1.817
20	122587	AA453255	Hs.6968	ESTs	1.817
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride channel [H.sapiens]	1.815
	111289	N72253	Hs.238246	ESTs	1.813
	110826	N30068	Hs.15347	ESTs	1.812
	104106	AA422123	Hs.42457	ESTs	1.811
25	130043	AA055404	Hs.193953	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	1.253
	115864	AA432080	Hs.81200	ESTs	1.81
	129737	AA056140	Hs.122684	ESTs	1.81
	124477	N53158	Hs.102682	ESTs	1.809
	100782	HG3740-HT4010		Basic Transcription Factor 2, 34 Kda Subunit	1.806
30	106101	AA421053	Hs.34395	ESTs	1.806
	115479	AA287596		zs52h09.s1 NCL_CGAP_GCB1 H sapiens cDNA clone IMAGE:701153	1.804
	116104	AA456635	Hs.78524	ESTs	1.804
	114173	Z39050	Hs.21963	ESTs	1.804
35	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1.803
	119135	R49548	Hs.169681	death effector domain-containing	1.802
	131559	N91087	Hs.28728	ESTs; Weakly similar to F55A12.9 [C.elegans]	1.801
	126922	AA177138	Hs.161671	ESTs	1.8
	117375	N25427	Hs.108812	ESTs	1.8
	103571	Z25535	Hs.211608	nucleoporin 153kD	1.8
40	105978	AA406367	Hs.15973	ESTs	1.8
	125904	H22372	Hs.163586	ESTs	1.799
	133883	AA397915	Hs.77221	choline kinase	1.798
	105777	AA348412	Hs.23096	ESTs	1.797
	110166	H19480	Hs.174309	ESTs	1.796
45	105038	AA130273	Hs.7584	ESTs; Weakly similar to hypothetical protein; similar to [H.sapiens]	1.796
	105427	AA251330	Hs.28248	ESTs	1.795
	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.melanogaster]	1.794
	133104	L13698	Hs.65029	growth arrest-specific 1	1.794
	131170	N48674	Hs.23796	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the	1.792
50	100136	D13540	Hs.22868	protein tyrosine phosphatase; non-receptor type 11	1.791
	127263	AA331157		EST35035 Embryo, 6 week, subtracted (total cDNA) 1 Homo sapiens cDNA	1.79
	114157	Z38878	Hs.24979	ESTs	1.79
	125601	AI096717	Hs.247043	KIAA0525 protein	1.788
	118472	N66818	Hs.42179	ESTs	1.787
55	112456	R63925	Hs.28464	ESTs	1.787
	130236	N69682	Hs.51957	SC35-interacting protein 1	1.786
	133297	AA600057	Hs.70266	KIAA0905 protein	1.784
	125650	R40096	Hs.176578	ESTs	1.784
	132056	T89386	Hs.38176	KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOP)	1.783
60	129093	AA262710	Hs.108614	KIAA0627 protein	1.783
	123176	AA489020	Hs.193424	ESTs	1.782
	106340	AA441792	Hs.22857	chord domain-containing protein 1	1.781
	100598	HG2463-HT2559		Guanine Nucleotide-Binding Protein G25k	1.779
	104038	AA374532		EST86676 HSC172 cells 1 Homo sapiens cDNA 5' end, mRNA sequence	1.778
65	122235	AA436475	Hs.190104	ESTs	1.777
	105104	AA151771	Hs.76941	ATPase; Na+/K+ transporting; beta 3 polypeptide	1.776
	107601	AA004636	Hs.50223	ESTs	1.776
	131467	W68255	Hs.27194	DKFZP434K171 protein	1.776
	118449	N68413	Hs.172466	ESTs; Weakly similar to KIAA0775 protein [H.sapiens]	1.776

	107969	AA034030	Hs.155212	methylmalonyl Coenzyme A mutase	1.775
	115527	AA342079	Hs.252055	ESTs	1.775
	132471	T16305	Hs.49349	beta-site APP-cleaving enzyme	1.775
5	105966	AA406105	Hs.5344	adaptor-related protein complex 1; gamma 1 subunit	1.774
	127548	AA373091	Hs.93832	Homo sapiens clone 24483 unknown mRNA; parital cds	1.774
	106217	AA428379	Hs.24870	ESTs	1.773
	131214	N26777	Hs.172635	ESTs	1.773
	106295	AA435664	Hs.8583	similar to APOBEC1	1.773
10	106328	AA436705	Hs.28020	KIAA0766 gene product	1.772
	124661	N93797	Hs.3090	EphB1	1.772
	122988	AA479166	Hs.105633	ESTs	1.772
	115504	AA291946	Hs.42736	ESTs	1.771
	105168	AA180208	Hs.16606	ESTs; Highly similar to CGI-32 protein [H.sapiens]	1.767
15	129153	AA188618	Hs.181461	ariadne; Drosophila; homolog of	1.766
	105829	AA398290	Hs.21965	ESTs	1.764
	101811	M86917	Hs.24734	oxysterol binding protein	1.764
	100138	D13628	Hs.2463	angiotensin 1	1.764
	124704	R07335		ye96c1.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	1.763
20	122314	AA442257	Hs.192076	ESTs	1.762
	109865	H02566	Hs.191268	Homo sapiens mRNA; cDNA DKFZp434N174 (from clone DKFZp434N174)	1.761
	106206	AA428069	Hs.89519	KIAA1046 protein	1.758
	107135	AA620782	Hs.23247	ESTs	1.757
	105760	AA338960	Hs.28170	ESTs	1.756
25	106288	AA435536	Hs.24336	ESTs	1.756
	103968	AA304566	Hs.3542	ESTs	1.756
	129559	AA234945	Hs.11360	ESTs	1.756
	117885	N50112	Hs.47023	ESTs	1.754
	107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta subunit	1.754
30	124807	R45963	Hs.233811	ESTs; Weakly similar to ORF2 [M.musculus]	1.753
	100276	D42047	Hs.82432	KIAA0089 protein	1.753
	110924	N47938		yy84a09.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone	1.751
	133002	AF006082	Hs.62461	ARP2 (actin-related protein 2; yeast) homolog	1.751
	132530	AA455917	Hs.50785	SEC22; vesicle trafficking protein (S. cerevisiae)-like 1	1.75
35	110759	N21671	Hs.19025	ESTs	1.75
	106138	AA424515	Hs.33264	ESTs	1.75
	107348	U43701	Hs.184776	ribosomal protein L23a	1.75
	115867	AA432162	Hs.165986	DKFZP586B2022 protein	1.749
	135398	AA194075	Hs.99908	nuclear receptor coactivator 4	1.747
40	113783	W19222	Hs.7041	ESTs; Weakly similar to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	1.747
	134898	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	1.745
	132215	T10132	Hs.4236	KIAA0478 gene product	1.744
	104229	AB002346	Hs.61289	synaptotagmin 2	1.743
	116166	AA461556	Hs.202949	KIAA1102 protein	1.743
45	115433	AA284252	Hs.58372	ESTs	1.743
	114908	AA236545	Hs.54973	ESTs	1.742
	127425	AA470941	Hs.143162	ESTs	1.741
	131089	Z38807	Hs.22870	ESTs	1.739
	113498	T88908	Hs.189746	ESTs	1.738
50	116710	F10577	Hs.70312	ESTs	1.735
	127210	R51476		yg76f04.r1 Soares infant brain 1N1B Homo sapiens cDNA clone	1.733
	120554	AA279654	Hs.194524	ESTs	1.733
	129940	U18242	Hs.13572	calcium modulating ligand	1.732
	117023	H88157	Hs.41105	ESTs	1.731
55	111700	R22212	Hs.23361	ESTs	1.731
	116911	H72240	Hs.39292	ESTs; Moderately similar to KIAA0745 protein [H.sapiens]	1.731
	106025	AA412063	Hs.6065	ESTs	1.728
	108626	AA101984	Hs.61697	G-protein coupled receptor	1.728
	111614	R12581	Hs.191146	ESTs	1.726
60	134134	L76703	Hs.173328	protein phosphatase 2; regulatory subunit B (B56); epsilon isoform	1.725
	106886	AA489086	Hs.36545	ESTs	1.725
	117998	N52136	Hs.93828	ESTs	1.725
	121204	AA400422	Hs.55896	ESTs	1.725
	121342	AA404995	Hs.192480	ESTs	1.725
65	131129	R27296	Hs.23240	ESTs	1.725
	116235	AA479181	Hs.186726	ESTs	1.725
	102423	U44754	Hs.179312	small nuclear RNA activating complex; polypeptide 1; 43kD	1.724
	110273	H29050	Hs.24096	ESTs	1.722
	108758	AA127395	Hs.222414	ESTs	1.722
	110672	H88477	Hs.191178	ESTs	1.721

	120271	AA176404	Hs.111092	ESTs; Weakly similar to ZINC FINGER PROTEIN 136 [H.sapiens]	1.72
	100227	D28915	Hs.82316	interferon-induced; hepatitis C-associated microtubular aggregate prot (44kD)	1.719
	129232	W69459	Hs.109655	sex comb on midleg (Drosophila)-like 1	1.719
	134663	W73367	Hs.8750	ESTs	1.717
5	104902	AA055475	Hs.104143	clathrin; light polypeptide (Lca)	1.717
	120582	AA281290	Hs.125287	ESTs; Weakly similar to BC331191_1 [H.sapiens]	1.717
	134891	F03517	Hs.90787	ESTs	1.716
	106219	AA428567	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323)	1.715
	116372	AA521311	Hs.13854	ESTs	1.713
10	107570	AA001870	Hs.237323	N-acetylglucosamine-phosphate mutase; DKFZP434B187 protein	1.713
	106198	AA427816	Hs.11803	ESTs	1.712
	125136	W31479	Hs.129051	ESTs	1.712
	104973	AA085676	Hs.6763	KIAA0942 protein	1.712
	128710	J04813	Hs.104117	cytochrome P450; subfamily IIIA (naphedipine oxidase); polypeptide 5	1.711
15	123994	D20899	Hs.107127	Homo sapiens mRNA; cDNA DKFZp564G022 (from clone DKFZp564G022)	1.711
	127871	AA766511	Hs.128848	ESTs	1.71
	116089	AA455933	Hs.41324	ESTs	1.709
	123337	AA504153	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevisiae]	1.708
	123619	AA609200	Hs.162686	ESTs	1.708
20	104781	AA026617	Hs.21610	ESTs; Highly similar to BA11-associated protein 1 [H.sapiens]	1.707
	115114	AA256468	Hs.88148	ESTs	1.705
	117852	N49408	Hs.136102	KIAA0853 protein	1.705
	127644	T57570	Hs.77039	ribosomal protein S3A	1.704
	111359	N91273	Hs.27179	ESTs	1.702
25	131721	L36644	Hs.31092	EphA5	1.7
	132438	F08925	Hs.48610	ESTs	1.7
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat region mRNA	1.7
	130990	F02488	Hs.21917	KIAA0768 protein	1.7
	128499	AA487503	Hs.100636	ESTs	1.698
30	120780	AA342337	Hs.241569	ESTs; Modtly smlr to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	1.697
	132920	L06133	Hs.606	ATPase; Cu++ transporting; alpha polypeptide (Mankes syndrome)	1.696
	135037	U77948	Hs.184122	general transcription factor II; i	1.696
	110024	H11297	Hs.31050	ESTs	1.695
	134415	AA329274	Hs.82911	protein tyrosine phosphatase type IVA; member 2	1.694
35	102223	U24685	Hs.148226	Human anti-B cell autoantibody IgM heavy chain variable V-D-J region (VH4) gene; clone E11; VH4-63 non-productive rearrangement	1.694
	126712	AA205862	Hs.7942	ESTs	1.694
	101507	M27492	Hs.82112	interleukin 1 receptor; type I	1.692
	106291	AA435551	Hs.30824	ESTs	1.691
40	116826	H58691	Hs.8215	ESTs; Weakly similar to double-stranded RNA-binding nuclear protein DRSP76 [H.sapiens]	1.69
	135339	D59269	Hs.127842	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 783648	1.69
	118250	N62602		y275b6.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE288851 3' similar to contains Alu repetitive element; mRNA sequence	1.689
45	106470	AA450116	Hs.186180	ESTs	1.688
	108203	AA057678	Hs.63408	ESTs	1.687
	119748	W70313	Hs.126906	ESTs	1.686
	116576	D51228	Hs.79404	neuron-specific protein	1.683
	123035	AA481392	Hs.105166	ESTs	1.683
50	126668	AA011616	Hs.184086	ESTs	1.681
	101512	M28209	Hs.250716	RAB1; member RAS oncogene family	1.678
	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.677
	126218	AA256386	Hs.13649	Novel human gene mapping to chromosome 13; similar-to rat RhoGAP	1.676
	111180	N67277	Hs.9403	ESTs	1.676
55	105937	AA404342	Hs.173531	ESTs	1.675
	114118	Z38520	Hs.175930	ESTs	1.675
	109203	AA190634	Hs.108787	endoplasmic reticulum membrane protein	1.675
	125245	W86608	Hs.7243	ubiquitin specific protease 24	1.675
	102906	X06956	Hs.75318	tubulin; alpha 1 (testis specific)	1.675
60	125914	AA262925	Hs.180034	cleavage stimulation factor; 3' pre-RNA; subunit 3; 77kD	1.674
	134294	U63289	Hs.81248	CUG triplet repeat; RNA-binding protein 1	1.674
	109742	F10108	Hs.183333	ESTs	1.673
	134674	D63876	Hs.87726	KIAA0154 protein	1.673
	104079	AA402937	Hs.103238	ESTs	1.671
65	107554	AA001386	Hs.59844	ESTs	1.671
	132439	AA243139	Hs.4863	Homo sapiens clone 25088 mRNA sequence	1.669
	124515	N58172	Hs.109370	ESTs	1.668
	124300	H92575	Hs.105959	ESTs; Weakly similar to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	1.668
	126809	AA743475	Hs.171693	ESTs	1.667

	106095	AA419547	Hs.11713	ESTs	1.664
	101754	M77142	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein	1.663
	105188	AA192306	Hs.23926	ESTs	1.663
	113582	T91371	Hs.16824	EST	1.661
5	119559	W38197		Accession not listed in Genbank	1.661
	119961	W87535	Hs.59015	ring finger protein 9	1.657
	123255	AA490890	Hs.105273	ESTs	1.657
	111078	N59230	Hs.186574	ESTs	1.655
	113082	T40528	Hs.8246	ESTs	1.654
10	119589	W44692	Hs.124177	ESTs	1.652
	104308	D53639	Hs.77904	ribosomal protein S26	1.65
	103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit; alpha type; 6	1.65
	124424	N35314	Hs.107265	ESTs	1.65
	128890	AA096157	Hs.182364	ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens]	1.65
15	119400	T92767		ye27d06.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118955 3', mRNA sequence.	1.65
	131631	AA486868	Hs.29802	sit (Drosophila) homolog 2	1.65
	118229	N62339	Hs.180532	heat shock 90kD protein 1; alpha	1.649
	118533	N67954	Hs.49413	ESTs	1.648
20	130666	AA476307	Hs.194035	KIAA0737 gene product	1.647
	103093	X60708	Hs.44926	dipeptidylpeptidase IV (CD26; adenosine deaminase complexing protein 2)	1.647
	128667	U69140	Hs.103419	fasciculation and elongation protein zeta 2 (zyglin II)	1.646
	112933	T15530	Hs.221439	ESTs	1.646
	114546	AA056263	Hs.132747	ESTs	1.645
25	126705	AA579377	Hs.180532	heat shock 90kD protein 1; alpha	1.644
	114399	AA007595	Hs.220937	ESTs	1.642
	118836	N79820	Hs.50854	ESTs	1.64
	100401	D85423		Homo sapiens mRNA for Cdc5, partial cds	1.64
	105681	AA284865	Hs.171228	KIAA1040 protein	1.639
30	132526	AA460128	Hs.5074	similar to S. pombe dim1+	1.639
	133809	AA034002	Hs.76359	catalase	1.639
	115968	AA447083	Hs.134522	ESTs	1.637
	116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]	1.631
35	109644	F04477	Hs.204802	ESTs; Moderately similar to GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE; LIVER [H.sapiens]	1.627
	103427	X97303		H.sapiens mRNA for Ptg-12 protein	1.627
	132186	T33888	Hs.221040	KIAA1038 protein	1.626
	131428	U17838	Hs.26719	PR domain containing 2; with ZNF domain	1.626
40	126638	AA649257	Hs.188602	ESTs	1.625
	114503	AA039568	Hs.188083	ESTs	1.625
	121242	AA400857	Hs.97509	EST	1.625
	122414	AA446885	Hs.99087	ESTs; Moderately similar to ZINC FINGER PROTEIN 141 [H.sapiens]	1.625
	110632	H72344	Hs.171635	ESTs	1.624
45	111389	N95837	Hs.169111	ESTs; Weakly similar to L82A [D.melanogaster]	1.624
	112449	R63802	Hs.124186	ring finger protein 2	1.623
	113070	T33464	Hs.6298	ESTs	1.622
	107229	D59284	Hs.34644	ESTs	1.618
	132710	W83726	Hs.55279	protease inhibitor 5 (maspin)	1.617
50	124664	N94814	Hs.33540	ESTs; Weakly similar to KIAA0765 protein [H.sapiens]	1.617
	130166	AA350690	Hs.151411	KIAA0916 protein	1.616
	125040	T78451	Hs.199961	ESTs	1.615
	132972	H39627	Hs.164967	ESTs; Weakly similar to !! ALU SUBFAMILY SB WARNING ENTRY !! [H.sapiens]	1.615
	115873	AA433916	Hs.90093	heat shock 70kD protein 4	1.611
55	120408	AA235045	Hs.190151	ESTs	1.61
	120934	AA383773	Hs.191500	ESTs	1.61
	115259	AA279071	Hs.13453	splicing factor 3b; subunit 1; 155kD	1.609
	134330	D20113	Hs.8185	ESTs; Highly similar to CGI-44 protein [H.sapiens]	1.607
	115117	AA256492	Hs.49007	poly(A) polymerase	1.606
60	125162	W44682	Hs.109896	ESTs	1.605
	103946	AA285246	Hs.111650	ESTs; Weakly similar to Prt1 homolog [H.sapiens]	1.604
	133389	AA166917	Hs.72639	ESTs	1.603
	115528	AA342301	Hs.53929	ESTs; Weakly similar to !! ALU CLASS B WARNING ENTRY !! [H.sapiens]	1.602
	129704	W81301	Hs.12064	ubiquitin specific protease 22	1.602
65	109313	AA206800	Hs.86276	ESTs; Moderately similar to zinc finger protein dp [H.sapiens]	1.601
	130457	U58091	Hs.155976	cullin 4B	1.6
	123076	AA485211	Hs.190046	ESTs	1.6
	115113	AA256460	Hs.44810	ESTs	1.6
	117731	N46433	Hs.46609	ESTs	1.6

5	123344	AA504338	Hs.171857	ESTs	1.599
	131798	X86098	Hs.3238	adenovirus 5 E1A binding protein	1.597
	125370	AA256743	Hs.151791	KIAA0092 gene product	1.596
	114918	AA236813	Hs.72324	ESTs; Highly similar to unknown [H.sapiens]	1.596
	114807	AA160805	Hs.199832	ESTs	1.596
10	105103	AA151593	Hs.10130	ESTs	1.594
	125004	T60120		yb68f02.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:76347 3', mRNA sequence.	1.592
	105658	AA282914	Hs.10176	ESTs	1.589
	110455	H52172		y85e8.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:23111 3' similar to contains Alu repetitive element, mRNA sequence	1.589
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical protein [H.sapiens]	1.587
15	126983	AA211537		zn55d01.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562081 5', mRNA sequence.	1.586
	134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalytic; beta	1.584
	105431	AA252033	Hs.15036	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	1.584
	120187	Z40251	Hs.56974	ESTs	1.584
	115830	AA428137	Hs.86434	ESTs	1.581
20	135069	AA456311	Hs.93961	ESTs; Weakly similar to !! ALU CLASS A WARNING ENTRY !! [H.sapiens]	1.581
	122997	AA479295	Hs.106290	Kelch motif containing protein	1.581
	119707	W67569	Hs.44143	ESTs; Weakly similar to SNF2alpha protein [H.sapiens]	1.58
	131934	D80948	Hs.34922	ESTs	1.58
	106141	AA424558	Hs.9302	phosducin-like	1.58
25	115271	AA279422	Hs.5724	ESTs	1.579
	131468	R27598	Hs.27197	KIAA0797 protein	1.577
	131165	R98173	Hs.23763	Max-interacting protein	1.575
	117273	N21680	Hs.43047	ESTs	1.575
	101569	M33772	Hs.182421	troponin C2; fast	1.575
30	116127	AA459703	Hs.79070	v-myc avian myelocytomatosis viral oncogene homolog	1.575
	120022	W90625	Hs.58432	ESTs	1.575
	117512	N32157	Hs.82207	ESTs	1.574
	106511	AA452865	Hs.206713	UDP-Gal-betaGlcNAc beta 1,4- galactosyltransferase; polypeptide 2	1.573
	116415	AA609204	Hs.27973	KIAA0874 protein	1.573
35	127879	AA810215	Hs.189079	ESTs	1.571
	125211	W72798	Hs.103177	ESTs; Wkly smlr to cDNA EST EMBL:D32579 comes from this gene [C.elegans]	1.571
	114746	AA135638	Hs.223756	ESTs	1.571
	122698	AA456112	Hs.99410	ESTs	1.57
	116765	H12636	Hs.121585	ESTs; Weakly similar to reverse transcriptase [H.sapiens]	1.568
40	130895	AA609828	Hs.21015	ESTs; Highly similar to tetracycline transporter-like protein [M.musculus]	1.568
	114338	Z41366	Hs.40109	KIAA0872 protein	1.567
	111005	N53076	Hs.5996	ESTs	1.567
	128135	AA913491	Hs.189143	ESTs; Modrtly smlr to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	1.567
	112046	R43365	Hs.22273	ESTs	1.566
45	132160	AA281770	Hs.184081	seven in absentia (Drosophila) homolog 1	1.566
	111568	R10153	Hs.20561	ESTs	1.566
	127775	H04106	Hs.179902	ESTs; Weakly similar to NG22 [H.sapiens]	1.566
	115359	AA281936	Hs.88914	ESTs	1.566
	121845	AA425734	Hs.165066	ESTs; Weakly similar to hypothetical protein [H.sapiens]	1.565
50	127854	AA769520		ESTs; Weakly similar to REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 [H.sapiens]	1.564
	120287	AA187679	Hs.111114	ESTs	1.563
	114940	AA243012	Hs.75928	ESTs	1.562
	126716	AA031700	Hs.251962	ESTs	1.562
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	1.561
55	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 20 (yeast) homolog	1.561
	115334	AA281244	Hs.65300	ESTs	1.559
	113721	T97931	Hs.18190	EST	1.558
	114895	AA236177	Hs.76591	KIAA0887 protein	1.558
	119341	T62571	Hs.146388	microtubule-associated protein 7	1.558
60	108012	AA039616	Hs.61933	ESTs	1.558
	130335	AA156499	Hs.8454	protein kinase; cAMP-dependent; regulatory; type II; alpha	1.557
	134351	R82074	Hs.82109	syndecan 1	1.557
	133300	D51401	Hs.70333	ESTs	1.553
	106920	AA490899	Hs.24462	ESTs	1.553
65	118744	N74075	Hs.94293	EST	1.552
	126489	W20016	Hs.144228	ESTs; Weakly similar to ZINC FINGER PROTEIN 83 [H.sapiens]	1.55
	115913	AA436720	Hs.65487	ESTs	1.55
	107868	AA025234	Hs.61260	ESTs	1.55
	134520	N21407	Hs.257325	ESTs	1.55

	109703	F09684	Hs.24792	ESTs; Weakly similar to ORF YOR283w [S.cerevisiae]	1.55
	120288	AA187938	Hs.55189	ESTs; Weakly similar to F25B5.3 [C.elegans]	1.548
	106356	AA443277	Hs.31034	peroxisomal biogenesis factor 11A	1.548
5	129460	AA235627	Hs.11171	APG5 (autophagy 5; S. cerevisiae)-like	1.547
	133950	D11961	Hs.77823	ESTs	1.546
	128172	AI400862	Hs.142607	ESTs	1.546
	114162	Z38909	Hs.22265	ESTs	1.545
	101803	M86546	Hs.155691	pre-B-cell leukemia transcription factor 1	1.544
	113617	T93630	Hs.17207	ESTs	1.542
10	104896	AA054228	Hs.23165	ESTs	1.541
	114477	AA032013	Hs.144260	EST	1.54
	110731	H98653	Hs.188006	KIAA0878 protein	1.54
	130367	Z38501	Hs.8768	ESTs; Wkly smlr to !! ALU SUBFAMILY SQ WARNING ENTRY !! [H.sapiens]	1.538
	130539	L07044	Hs.250857	Homo sapiens calcium/calmodulin-dependent protein kinase II mRNA; partial cds	1.538
15	134921	W60186	Hs.169487	Kreislter (mouse) maf-related leucine zipper homolog	1.537
	130583	W24957	Hs.16281	ESTs; Moderately similar to similar to C.elegans protein encoded in cosmid T20D3 [H.sapiens]	1.537
	133723	AA088851	Hs.75744	S-adenosylmethionine decarboxylase 1	1.537
	106450	AA449469	Hs.11859	ESTs	1.536
20	104120	AA429838	Hs.89519	KIAA1046 protein	1.536
	100533	HG1879-HT1919		Ras-Like Protein Tc10	1.535
	130664	R09049	Hs.17625	ESTs	1.535
	127122	AA279153	Hs.190049	ESTs	1.535
	134264	T03391	Hs.8087	ESTs	1.535
25	132319	AA418662	Hs.44625	ESTs	1.535
	115465	AA286941	Hs.43691	ESTs	1.533
	125003	T59442	Hs.100445	ESTs	1.532
	102273	U30888	Hs.75981	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	1.532
	121875	AA426299	Hs.98510	ESTs	1.532
30	114366	Z41747	Hs.469	succinate dehydrogenase complex; subunit A; flavoprotein (Fp)	1.531
	132944	AA054515	Hs.6127	ESTs; Weakly similar to prostate-specific transglutaminase [H.sapiens]	1.53
	111199	N68210	Hs.29822	ESTs	1.53
	113494	T88878	Hs.258738	ESTs	1.529
	129515	AA490882	Hs.112227	ESTs	1.528
35	133124	AA156049	Hs.65490	ESTs	1.528
	104785	AA027163	Hs.7942	ESTs	1.526
	105595	AA279408	Hs.25866	ESTs	1.526
	130198	U67156	Hs.151988	mitogen-activated protein kinase kinase kinase 5	1.526
	114297	Z40758	Hs.173091	DKFZP434K151 protein	1.525
40	112876	T03488	Hs.4842	ESTs	1.525
	127500	AA525014	Hs.162115	ESTs	1.525
	120519	AA258585	Hs.129887	cadherin 19 (NOTE: redefinition of symbol)	1.525
	119859	W80702	Hs.58461	ESTs	1.525
	129944	L00389	Hs.1361	cytochrome P450; subfamily I (aromatic compound-inducible); polypeptide 2	1.524
45	118864	N89670	Hs.42148	ESTs; Weakly similar to Su(P) [D.melanogaster]	1.523
	123964	C13961	Hs.210115	EST	1.523
	111676	R19414	Hs.166459	ESTs	1.522
	128332	AI079523	Hs.134173	ESTs	1.522
	130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltransferase)	1.521
50	125181	W58461	Hs.12396	ESTs	1.521
	127093	AA768241		oa72d02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1317795 3', mRNA sequence.	1.521
	132156	AA157401	Hs.4113	S-adenosylhomocysteine hydrolase-like 1	1.521
	125303	Z39821	Hs.107295	ESTs	1.52
55	132697	AA281951	Hs.5518	Homo sapiens mRNA; cDNA DKFZp566J2146 (from clone DKFZp566J2146)	1.52
	117086	H93135	Hs.41840	ESTs	1.519
	113355	T79203	Hs.14480	ESTs	1.518
	108621	AA101811	Hs.69506	ESTs	1.518
	109384	AA219172	Hs.86849	EST	1.518
60	128510	X94703	Hs.100816	RAB28; member RAS oncogene family	1.517
	132968	N77151	Hs.61638	myosin X	1.515
	117035	H88798	Hs.41182	ESTs	1.515
	116781	H22985	Hs.52132	ESTs	1.513
	108677	AA115629	Hs.118531	ESTs	1.513
65	130214	H78003	Hs.15266	ESTs	1.513
	134700	AA481414	Hs.8868	golgi SNAP receptor complex member 1	1.512
	116618	D80783	Hs.45224	ESTs	1.508
	126257	N99638		tumor necrosis factor receptor superfamily; member 10b	1.508
	125859	AA806808	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	1.508

	113837	W57698	Hs.8888	ESTs	1.507
	114317	Z41038	Hs.469	succinate dehydrogenase complex; subunit A; flavoprotein (Fp)	1.507
	100311	D50640	Hs.184653	phosphodiesterase 3B; cGMP-inhibited	1.507
	126802	AA947601	Hs.97056	ESTs	1.506
5	128661	R82837	Hs.103329	KIAA0970 protein	1.506
	134194	AA233231	Hs.79828	ESTs	1.506
	108953	AA149652	Hs.42128	ESTs	1.504
	133240	D31161	Hs.68613	ESTs	1.502
	132671	X76302	Hs.54649	putative nucleic acid binding protein RY-1	1.501
10	132609	Z48923	Hs.53250	bone morphogenetic protein receptor; type II (serine/threonine kinase)	1.501
	105574	AA278678	Hs.258567	ESTs	1.5
	113718	T97782	Hs.256268	ESTs	1.5
	127824	AI208365	Hs.127811	ESTs	1.5
	130132	U55936	Hs.184376	synaptosomal-associated protein; 23kD	1.5
15	127394	AA453224		ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	1.5
	100485	HG11111-HT1111		Ras-Like Protein Tc21	1.5
	101078	L04510	Hs.792	ADP-ribosylation factor domain protein 1; 64kD	1.5
	128611	AA456845	Hs.102471	KIAA0680 gene product	1.5

TABLE 12A shows the accession numbers for those primekeys lacking unigeneID's for Table 12. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	<hr/>		
	Pkey	CAT number	Accession
	108536	119811_1	AA084524 AA339253 AW966289
	117040	46956_1	AW970600 AA503323 H89218 AF086031 H89112
	100782	18457_1	AA355435 NM_001516 Z30093 T28405 AW949486 AA461142 AA410532 AI652073 AA521208 AI970141 AI968234 AI026102
			AA713583 AW135876 AA936614 AA770300 AI242635 AA377033 AW960263 AW607683 AI273603 AA410287 AI040513
			AA460838 AI803916 AW294095 AW449680 AW798677 AW675048 BE542116 AL120521
	100819	3022_1	L34840 NM_003241 U31905 AI546931 AI791616 AI973065 AI792321 AI546937 AI685880 AI732835 AI682360 AA420653
			AA564047 AI682323 AI824614 AI659889 AI680052 AI970887 AI623108 AA420692 AI418074 AA631018 AI810595 AW291463
			AW449930 AI668908 AI970818
	100824	5_36	AI393237 AI521317 AI761348 AF025841 D43968 AW994987 L34598 AF025841 D89789 D89788 D89790 AW998932
			AI971742 AI310238 X90976 AW139668 AW674280 AI365552 AA877452 AV657554 C75229 AA376077 AI798056 AW609213
			W25586 H30149 BE075089 BE075190 AW580858 H99598 AA425238 AA133916 AW363478 BE158121 BE158127
			AW467960 BE158135 BE158126 BE158145 N92860 AA847246 AI961688 AI361423 AA878154 AA043767 AI863712
			AI559226 AW339007 AI371266 AI368901 AA046624 AA134739 AW449154 AA130232 AI458720 AA962511 AI700627
			R70437 AW004008 AA045229 AI671572 H99599 AA043768 AI685454 AI871685 N29937 X90977 AA524240 AI142114
			AI825750 AI567805 AI631365 AI347893 AA134740 F20669 AA046707 AW793216 AW963298 AW959380 AA363265
			AI784593 AI268201 R69451 AV657618 AI695588
	125004	264197_1	BE312163 AJ230798 AA374482 AI926059 AA622653 AI860704 BE139185 AW296884 T60238 T60120
	102313	27608_1	U33921 AI190489 AA573311
	102337	553_1	AI814663 AA806761 AA765241 AA019317 AA092255 AA035405 T85079 AA890151 AI373959 T85080 BE153728 AA740848
			BE080682 AL048137 AW182316 AI699468 AW274481 AW407538 AA306562 AW950024 AW949943 AL045703 AW843196
			W25132 BE612794 AA304266 AW958054 H25673 AV646563 AV646573 BE172990 AW593488 AA385181 AA164998
			AI246476 AA345406 AI277554 AA134749 AA856624 BE613247 AA299003 AL048138 AA028121 T92510 AI923835
			AW020440 AI401594 AI889401 N93290 AA044247 AA028100 AI582845 AA811151 AI741811 AI925878 AA448277 AA172221
			AI214783 BE220793 AA022746 AI082882 AA022849 AI928385 AA573472 AI420686 AW072902 AI799493 AI873506
			AI468977 AI192079 AI468976 AA044272 AW015701 AW316979 AA933042 AA609017 AI318393 AI424571 AI934945
			AA172023 AW050917 AA846180 AA134748 AI003947 AI766769 AW006697 AA653517 AW575680 AI474214 AA401478
			U36922 AA927064 AA868000 D62654 T91745 AW500202 AA194764 AA746346 AA130464 AW117498 AA054526 N26432
			H02534 H04964 AW303367 BE300931 AI218049 AI208073 AW182749 AA983630 AI147585 AA194765 AA054534 AA922720
			AI436585 AI346535 AA134269 AA280923 AA897422 AA019559 AW274010 AA035406 AA917879 H99327 W32908 AI216046
			AW496823 AA019414 H82288 W35284 AI936621 AI767113 AA866177 AW367874 H82398 AF032885 AW300151 AW467069
			AA809346 AI188507 AI494178 AA872752 AI631631 U02310 NM_002015 AA815006 AI382453 AW197658 AI761654
			AI804396 AI382221 AI813640 AI439635 AI523901 AW517242 AI221705 AW298104 AW204560 AW573095 AW028783
			AW014650 AI766744 AI808294 AI698758 AI041809 AI766667 AI479103 AA872797 AA769305 AA765080 AA334166
			AI472322
	124704	292319_1	R07335 R07640
	116988	185904_1	AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526
	124825	330773_1	AA501669 R52088
	110455	46874_1	H52576 AF085971 H52172
	126257	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
	125624	154135_1	AW968363 AA465492 R34539 AA165411
	104038	264235_1	AA374532 AA421255
	103427	43892_1	BE514383 AA071273 AW247987 AW673286 BE312102 AW749824 BE071985 AW577383 BE071945 BE072005 AW577355
			BE071965 AW239231 BE072000 BE071960 AW577360 AW749830 AW373020 X97303 AW999522 BE000192 BE562219
			BE266655 BE264970
	104142	113242_1	AA074713 AA447006
	127093	47721_1	AW977549 AA256038 AL365415 AW500455 AA768241 AW968097 Z17849 AA256104

125873	10492_1	AW271838 AL133605 C01646 H29959 AA999896 D60676 AW999454 AW961176 AA315244 H14437 AW386118 N46512 AW272021 AJ768516 BE466421 AJ082809 AI804454 AA905101 AW173368 N38942 AW614169 AI080483 N29489 AI500550 AA994475 AA614464 AA707368 AA593145 AA569473 AW627815 AI828244 N63226 N42300
5	125954 4457_1	NM_016353 AB023584 W44753 R09585 AA382865 R23772 AI814257 AA974046 AK001608 AI935638 AW440609 AI420022 AA777386 AA806969 AI554876 AI584006 AI688556 AI688634 AI697997 AI014540 AI806683 AJ741202 AW263154 AW297238 AI149951 AI589076 AW082158 AW614265 AA931887 AA781969 R09490 AA484643 AI207121 AI088390 AI538065 AI619547 AJ741925 AF702846 H40846 R93943 AW747979 AA461348 U30163 AA326023 AI535992 AW242870 AI244025 AI222558 W38425 AW473630 AI624599 AI921226 AI683152 AI096458 AI123822 AW170802 C16447 AI337674 D25726 AW339366 AW771259 AA461174
10	125992 1589048_1 127210 15307_6	H48372 WD1626 AA305278 AA223833 110924 6443_1 AW058463 AF195766 AA680145 T86901 W60373 W60281 NM_007222 AF106862 AI000795 AA167188 AW884503 AW891313 AW891332 AW891312 AI984924 AI123518 N75170 AA131614 H25330 AI913358 AI742277 W25576 R58771 AW445159 AW888628 AW888627 AW274674 AI088482 N52314 N34282 AW001769 AI338943 T66784 AI288963 AW468676 AW237528 H25289 N71690 AA610128 AI143458 AI082599 N49144 AA854773 AW663411 AW610151 N47938 AW601626 AA167189 AA918304 AA805205 BE069496 AA652836 BE069499 AI699298 AW249926 AW888578 BE567635 T10726 AW604715 D54245 D53062 D55610 D55555 AA301376 AI133498 N77788 AI936320 AW090734 AI269977 N50828 AA550814 AI421993 AI005384 N50813 D60292 D59349 AA131710 D81698 D81699
15	127263 232161_1 135197 29440_1	AA331156 AA331157 AA331155 U76456 NM_003256 AF057532 AA193414 AW293304 AW963378 AA313095 AI359841 AI969312 AI080163 AW448926 AI671136 BE466399 AI637957 AI671873 AW196583 AW071635 AI634427 AW296872 AW292470 AA193650 BE161832 AA453224 AA485772 D90391 M55575 AI652268 AA719776
20	127394 304844_1 126879 1860_2 126983 171841_1 120470 188975_1 127854 443883_1 121367 280429_1 106320 6435_1	AA524886 AW971347 AA211537 AW971327 AA524988 AW628653 AA251797 AW976796 AA769520 AA432071 AA405648 AW000908 T16347 AB028957 AL120001 AI267678 H10928 R19844 AW970334 AA393182 F05472 F11711 H09908 N50250 AI815411 BE463679 D61468 AW970253 D60889 C15548 D61011 D60867 AI815795 AA534831 D81386 AW235039 AI382158 D81174 AA416899 AA852310 H09789 H10929 H09813 F09369 R44721 D51515 Z38456 R14004 T66255 F12148 F12139 AW351702 M85350 AI018713 AW972450 AW972645 AA514964 T66172 F09785 F09776 AA436608 T05327 T07118 AA339352 AW301608 N46706 AA649093 AA287595 AW811753 AA287596 N39260 NM_001874 J04970 T91426 AW205201 T84979 AA255727 AA847837 R02164 T91339 AV651884 AV651835 AV651350 AV650118 AV651338 AI272002 AI367796 AA830651 AA262112 AW151198 AI076696 AA219720 AL135197 AA305877 N56376 AA318063 AA130725 AW954903 BE541230 AW383312 U86753 D85423 AI679458 AI122932 AB007892 AI583919 BE160134 F08104 R34903 F13440 AA095444 AA262453 AA191036 R17895 T81266 BE149776 AI279537 AI143113 AA361072 AW959030 AW268817 AA811533 BE275179 AI221677 T65147 R49293 AA249176 BE000290 AA768053 F09494 BE092645 BE172099 Z41177 AA044750 AI909768 BE140795 BE140574 AW845210 AW752452 BE243244 AA843664 AI300080 BE169032 AW189979 BE004869 AA621872 AI951772 AI678897 AI926598 N62813 AI350912 AW608791 AI309602 AI983138 AW875592 AI655073 AW875626 AA130606 AI370827 C75528 C75554 AW263335 AI344426 BE004788 AA576220 AA604824 AI431405 AA749378 R38882 AW955075 AA173821 C75657 AA219672 AW768408 R43141 AI431414 AA483343 AI673792 T17294 AW770187 N74285 AI476404 AI088288 AA654152 AW974864 BE617311 BE243328 BE168049
30	115479 201515_1 101026 11075_1	U64675 AW167507 AW167508 BE218568 AA779360 W85722 AL044843 BE159404 AF012086 AW898611 AW898610 BE159405 BE092191 AW890826 AW369841 AW368064 AW606702 AL044731 R82691 AA119346 AA416558 H96045 AL040450 AI640531 AI808434 AL046613 AW855784 AW362469 AL048881 AL049015 AA094272 AA888908 AA417294 AW237786 R59793 AL044916 D82402 AI216854 AI079342 H96406 AL037845 AI915900 AA972133 AI478783 T31074 Z21135 Z21396 AA352182 R13918 AA430178 C17811 AI371824 AI742256 AA926801 N79156 AA350610 AA081971 N83639 R35544 AA312292 AW952080 N42322 AA171957 AA565297 R89207 AA504106 AI630782 AA826482 AI301579 T36241 AW956618 Z28426 AL043480 AI124636 AA393449 T19504 AW887823 AI289814 N53979 AL043571 AI632764 AI859613 AI986308 AI683212 AI984499 AI133258 C05898 AW512761 AI041260 BE466240 Z19161 AI351190 N67549 AI373374 AA400873 AW440914 AW514879 AA770146 AI358754 R51113 AI283773 AA649886 T30543 D54358 R37750 T03358 T15451 T15880 AA999689 N67396 AI056289 T85597 N62441 R89099 R00035 T85596 R61335 R00128 N63359 AI535964 AI207768 M31468 NM_012250 W01322 AA253280 AA253233 AA293148 AW582106 R79880 AA459547 AA363459 AA234396 N31669 H44468 AA434587 AW363088 AW993541 AA070906 AA070934
35	100401 24827_1	X51501 NM_002652 Y10179 J03460 AI791618 AI821473 AA916588 AA564296 AA916110 AI972286 AI420470 AI568790 AI597724 AW205207 AI659305 AI791620 AA532383 AI821475 AA526498
40	130542 28089_3	NM_012249 M31470 AL043108 AA262561 AA178883 T29433 AA313329 W48807 AW404323 AA453560 AW403227 H94816 W17101 AA165152 W23989 AA091310 AL121734 D54896 AA424269 BE242906 AA362118 BE018454 AI280348 AL048769 M35543 AA757734 AI28865 H20289 H23728 AI203445 H41481 H18237 H44081 H92839 AI928621 H75675 D51148 AI796198 AW390453 D55579 D54145 D53996 D54015 R37664 H17541 AA668681 T65061 R15867 AW468123 R16049 H69030 AA054226 H16070 F09655 R92144 T03521 R05473 H92840 AA018186 R91707 U35637 AA112989 Z19308
45	100485 30576_2	118250 genbank_N62602 N62602 103678 entrez_Z84483 Z84483 119400 genbank_T92767 T92767 119559 entrez_W38197 W38197
50	108345 112277_6 100522 19669_1	
55	100533 32905_1	
60	100598 23902_2	
65	102332 14745_3	

MISSING AT THE TIME OF PUBLICATION

TABLE 13: shows genes, including expression sequence tags, up-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu02 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

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10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Background subtracted normal prostate : prostate tumor tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	333516			CH22_FGENES.173_1	0.028
	337954			CH22_EM:AC005500.GENSCAN.96-3	0.029
	332496	R73299	Hs.204354	ras homolog gene family; member B	0.03
	337944			CH22_EM:AC005500.GENSCAN.89-7	0.033
	334111			CH22_FGENES.330_10	0.033
20	333657			CH22_FGENES.241_2	0.034
	327718			CH.04_hs gjl6525284	0.034
	336355			CH22_FGENES.817_5	0.035
	322011	AL137354		EST cluster (not in UniGene)	0.035
	336377			CH22_FGENES.821_5	0.036
25	300254	AW079607	Hs.188417	ESTs; Weakly similar to ZnT-3 [H.sapiens]	0.037
	330096			CH.19_p2 gjl6015278	0.037
	335191			CH22_FGENES.507_6	0.038
	334040			CH22_FGENES.322_8	0.039
	333586			CH22_FGENES.204_2	0.04
30	333295			CH22_FGENES.132_2	0.042
	313326	AI088120	Hs.122329	ESTs	0.043
	329517			CH.10_p2 gjl3983513	0.043
	333403			CH22_FGENES.144_21	0.043
	335226			CH22_FGENES.513_11	0.044
35	335976			CH22_FGENES.652_11	0.045
	333637			CH22_FGENES.229_2	0.046
	334582			CH22_FGENES.407_5	0.046
	336437			CH22_FGENES.826_4	0.047
	337461			CH22_FGENES.782-1	0.047
40	302892	N58545	Hs.6975	histone deacetylase 3	0.049
	338689			CH22_EM:AC005500.GENSCAN.475-3	0.049
	334721			CH22_FGENES.421_32	0.049
	305867	AA864572		EST singleton (not in UniGene) with exon hit	0.049
	335498			CH22_FGENES.571_7	0.05
45	311596	AI682088	Hs.223368	ESTs	0.05
	326959			CH.21_hs gjl6469836	0.051
	311688	AW025661	Hs.240090	ESTs	0.052
	317298	AI922374	Hs.158549	ESTs	0.052
	332984			CH22_FGENES.54_6	0.052
50	321039	AW247083		EST cluster (not in UniGene)	0.053
	335844			CH22_FGENES.623_4	0.053
	325371			CH.12_hs gjl5866920	0.054
	335667			CH22_FGENES.590_18	0.054
	333635			CH22_FGENES.228_2	0.054
55	336736			CH22_FGENES.110-2	0.055
	335893			CH22_FGENES.635_1	0.055
	333170			CH22_FGENES.94_5	0.055
	329768			CH.14_p2 gjl6015501	0.055
	334030			CH22_FGENES.320_2	0.055
60	323359	AA234172	Hs.137418	ESTs	0.055
	300453	AW051431	Hs.113029	ribosomal protein S25	0.055
	334262			CH22_FGENES.367_12	0.055
	306590	AI000246		EST singleton (not in UniGene) with exon hit	0.055
	331087	R22520	Hs.23398	ESTs	0.055
65	338620			CH22_EM:AC005500.GENSCAN.450-18	0.056
	339045			CH22_DA59H18.GENSCAN.28-5	0.056
	308023	AI452732		EST singleton (not in UniGene) with exon hit	0.057

	339067		CH22_DA59H18.GENSCAN.33-3	0.057
	335689		CH22_FGENES.596_4	0.057
	339069		CH22_DA59H18.GENSCAN.33-5	0.057
5	338176		CH22_EM:AC005500.GENSCAN.219-4	0.057
	328159		CH.06_hs gjl5868065	0.058
	335655		CH22_FGENES.590_6	0.058
	336371		CH22_FGENES.820_1	0.058
	336558		CH22_FGENES.842_3	0.059
10	337738		CH22_EM:AC000097.GENSCAN.100-4	0.059
	334273		CH22_FGENES.369_2	0.059
	335889		CH22_FGENES.633_3	0.059
	327807		CH.05_hs gjl5867968	0.059
	333315		CH22_FGENES.138_7	0.059
15	338825		CH22_DJ246D7.GENSCAN.4-6	0.06
	337612		CH22_C20H12.GENSCAN.22-5	0.06
	333897		CH22_FGENES.293_4	0.06
	335990		CH22_FGENES.655_4	0.06
	334264		CH22_FGENES.367_15	0.06
20	338653		CH22_EM:AC005500.GENSCAN.460-39	0.061
	322303	W07459	EST cluster (not in UniGene)	0.061
	333498		CH22_FGENES.168_8	0.061
	336522		CH22_FGENES.839_3	0.061
	301357	AW295677	Hs.137840 ESTs; Moderately similar to HOMEBOX PROTEIN SIX1 [H.sapiens]	0.062
25	305917	AA876469	Hs.181357 laminin receptor 1 (67kD; ribosomal protein SA)	0.062
	336143		CH22_FGENES.705_5	0.063
	333493		CH22_FGENES.168_2	0.063
	332533	M99487	Hs.1915 folate hydrolase (prostate-specific membrane antigen) 1	0.063
30	325844		CH.16_hs gjl6552453	0.063
	336402		CH22_FGENES.823_17	0.063
	335767		CH22_FGENES.607_1	0.064
	301893	T80334	EST cluster (not in UniGene) with exon hit	0.064
	324019	AW177009	EST cluster (not in UniGene)	0.064
35	305801	AA845997	EST singleton (not in UniGene) with exon hit	0.064
	335188		CH22_FGENES.507_3	0.065
	337533		CH22_FGENES.828-2	0.065
	333311		CH22_FGENES.138_3	0.065
	335668		CH22_FGENES.590_19	0.065
40	306786	AI041589	EST singleton (not in UniGene) with exon hit	0.066
	306365	AA962086	EST singleton (not in UniGene) with exon hit	0.066
	306249	AA933840	EST singleton (not in UniGene) with exon hit	0.066
	335018		CH22_FGENES.474_6	0.066
	333594		CH22_FGENES.210_3	0.066
45	333900		CH22_FGENES.293_7	0.066
	325207		CH.10_hs gjl6552430	0.067
	329888		CH.15_p2 gjl6067149	0.067
	326238		CH.17_hs gjl5867260	0.067
	333658		CH22_FGENES.241_4	0.067
50	335809		CH22_FGENES.617_6	0.068
	307427	AI243437	EST singleton (not in UniGene) with exon hit	0.068
	318428	AI949409	Hs.224583 ESTs	0.069
	327005		CH.21_hs gjl5867664	0.069
	330463	HG998-HT998	Sulfotransferase, Phenol-Preferring	0.069
55	333318		CH22_FGENES.138_10	0.07
	333313		CH22_FGENES.138_5	0.07
	325937		CH.16_hs gjl5867132	0.07
	335663		CH22_FGENES.590_14	0.07
	335349		CH22_FGENES.539_2	0.07
60	303396	AA224470	Hs.25426 ESTs; Weakly similar to unknown [H.sapiens]	0.07
	332603	N66681	Hs.33470 ESTs	0.07
	333310		CH22_FGENES.138_2	0.071
	309924	AW340812	EST singleton (not in UniGene) with exon hit	0.071
	336340		CH22_FGENES.814_15	0.071
65	308025	AI453365	Hs.172928 collagen; type I; alpha 1	0.071
	306805	AI055966	EST singleton (not in UniGene) with exon hit	0.071
	335499		CH22_FGENES.571_8	0.071
	329669		CH.14_p2 gjl6272129	0.071
	321666	D28390	EST cluster (not in UniGene)	0.071
	338174		CH22_EM:AC005500.GENSCAN.219-2	0.072

	336556		CH22_FGENES.842_1	0.072
	305451	AA738105	Hs.140 immunoglobulin gamma 3 (Gm marker)	0.072
	336684		CH22_FGENES.46-1	0.072
5	326943		CH.21_hs gij6004446	0.073
	333947		CH22_FGENES.303_1	0.074
	333214		CH22_FGENES.104_5	0.074
	331917	AA446572	Hs.174007 ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING	0.074
	339102		CH22_DA59H18.GENSCAN.44-9	0.074
10	328122		CH.06_hs gij5868031	0.075
	332250	N62712	Hs.226223 KIAA0618 gene product	0.075
	328506		CH.07_hs gij5868471	0.075
	331756	AA291468	Hs.98504 ESTs	0.075
	335193		CH22_FGENES.507_8	0.076
15	317729	AA971718	Hs.128141 ESTs	0.076
	304515	AA458708	Hs.251577 hemoglobin; alpha 2	0.076
	313644	AI565766	Hs.124960 ESTs	0.076
	326145		CH.17_hs gij5867204	0.076
	336394		CH22_FGENES.823_6	0.077
20	306516	AA989542	EST singleton (not in UniGene) with exon hit	0.077
	300629	AA152119	Hs.155101 ATP synthase; H+ transporting; mitochondrial F1 complex; alpha subunit; isoform 1; cardiac muscle	0.077
	333160		CH22_FGENES.91_2	0.077
	337490		CH22_FGENES.799-5	0.077
25	305403	AA723748	EST singleton (not in UniGene) with exon hit	0.077
	331747	AA281765	Hs.193689 ESTs	0.077
	332792		CH22_FGENES.3_2	0.078
	330513	M81057	Hs.180884 carboxypeptidase B1 (tissue)	0.078
	308905	AI859636	Hs.8102 ribosomal protein S20	0.078
30	337419		CH22_FGENES.759-4	0.078
	333459		CH22_FGENES.157_8	0.078
	334851		CH22_FGENES.440_3	0.078
	329046		CH.X_hs gij5868569	0.078
	327879		CH.06_hs gij5868142	0.079
35	305830	AA857665	EST singleton (not in UniGene) with exon hit	0.079
	302928	AL137719	EST cluster (not in UniGene) with exon hit	0.079
	304321	AA136698	Hs.113029 ribosomal protein S25	0.079
	326390		CH.19_hs gij5867340	0.079
	335230		CH22_FGENES.514_2	0.08
40	334622		CH22_FGENES.412_6	0.08
	335331		CH22_FGENES.535_4	0.08
	304753	AA578840	Hs.77961 major histocompatibility complex; class I; B	0.08
	301863	AI418863	EST cluster (not in UniGene) with exon hit	0.081
	336561		CH22_FGENES.842_6	0.081
45	335611		CH22_FGENES.583_5	0.081
	305060	AA635771	EST singleton (not in UniGene) with exon hit	0.081
	306051	AA905130	EST singleton (not in UniGene) with exon hit	0.082
	308289	AI571211	EST singleton (not in UniGene) with exon hit	0.082
	334365		CH22_FGENES.378_13	0.082
50	335496		CH22_FGENES.571_4	0.082
	332634	S38953	Human unidentified gene complementary to P450c21 gene; partial cds	0.082
	337824		CH22_EM:AC005500.GENSCAN.13-18	0.082
	335822		CH22_FGENES.619_7	0.082
55	334758		CH22_FGENES.428_7	0.082
	309641	AW194230	Hs.253100 EST	0.082
	333064		CH22_FGENES.75_7	0.083
	338695		CH22_EM:AC005500.GENSCAN.477-25	0.083
	331809	AA402482	Hs.97312 ESTs	0.083
60	326138		CH.17_hs gij5867203	0.083
	328304		CH.07_hs gij6004478	0.083
	330570	U60276	Hs.165439 arsA (bacterial) arsenite transporter; ATP-binding; homolog 1	0.083
	334305		CH22_FGENES.373_8	0.083
	335885		CH22_FGENES.632_3	0.083
	325839		CH.16_hs gij6552452	0.083
65	333531		CH22_FGENES.175_18	0.084
	330385	AA449749	Hs.31386 ESTs; Highly similar to secreted apoptosis related protein 1 [H.sapiens]	0.084
	323305	AA811351	Hs.25307 Homo sapiens clone 24812 mRNA sequence	0.084
	331698	Z39929	Hs.65843 ESTs	0.084

	335888		CH22_FGENES.633_2	0.084
	306008	AA894390	EST singleton (not in UniGene) with exon hit	0.084
	334249		CH22_FGENES.365_15	0.084
5	318303	AW451197	Hs.113418 ESTs	0.084
	330171		CH.02_p2 gj6648220	0.084
	336662		CH22_FGENES.41-1	0.085
	320506	Al815668	Hs.157476 suc1-associated neurotrophic factor target 2 (FGFR signaling adaptor)	0.085
10	316974	Al740721	Hs.128292 ESTs	0.085
	336492		CH22_FGENES.832_9	0.085
	335750		CH22_FGENES.602_4	0.085
	335676		CH22_FGENES.594_1	0.086
	336093		CH22_FGENES.691_2	0.086
15	310932	Al933861	Hs.222852 ESTs	0.086
	335160		CH22_FGENES.502_4	0.086
	334306		CH22_FGENES.373_9	0.086
	334793		CH22_FGENES.433_5	0.086
	333936		CH22_FGENES.301_2	0.087
20	336413		CH22_FGENES.823_35	0.087
	333775		CH22_FGENES.272_6	0.087
	335971		CH22_FGENES.652_4	0.087
	301737	Al815981	EST cluster (not in UniGene) with exon hit	0.087
	339101		CH22_DA59H18.GENSCAN.44-6	0.087
25	327612		CH.04_hs gj6525283	0.087
	326241		CH.17_hs gj5867260	0.088
	338386		CH22_EM:AC005500.GENSCAN.331-4	0.088
	327762		CH.05_hs gj5867961	0.088
	305266	AA679772	EST singleton (not in UniGene) with exon hit	0.088
30	334359		CH22_FGENES.378_4	0.088
	335500		CH22_FGENES.571_10	0.088
	329687		CH.14_p2 gj6117856	0.088
	333654		CH22_FGENES.240_2	0.088
	324430	AA464018	EST cluster (not in UniGene)	0.088
35	325999		CH.16_hs gj5867073	0.089
	334832		CH22_FGENES.439_1	0.089
	339115		CH22_DA59H18.GENSCAN.49-3	0.089
	300896	Al916902	Hs.213882 ESTs	0.089
40	328784		CH.07_hs gj5868309	0.089
	335044		CH22_FGENES.480_1	0.089
	329791		CH.14_p2 gj6469354	0.089
	333656		CH22_FGENES.240_4	0.089
	326180		CH.17_hs gj5867211	0.089
	333391		CH22_FGENES.144_6	0.089
45	338324		CH22_EM:AC005500.GENSCAN.306-3	0.089
	305396	AA721052	EST singleton (not in UniGene) with exon hit	0.089
	337483		CH22_FGENES.795-7	0.09
	326424		CH.19_hs gj5867369	0.09
	306454	AA977992	EST singleton (not in UniGene) with exon hit	0.09
50	338893		CH22_DJ3210.GENSCAN.7-6	0.09
	327470		CH.02_hs gj5867772	0.09
	333165		CH22_FGENES.91_7	0.09
	307155	Al186738	Hs.182426 ribosomal protein S2	0.09
	330717	AA233926	Hs.23635 ESTs	0.09
55	335334		CH22_FGENES.535_10	0.09
	335907		CH22_FGENES.636_2	0.09
	333885		CH22_FGENES.292_7	0.09
	331034	N51868	Hs.31965 ESTs; Moderately similar to 40S RIBOSOMAL PROTEIN S20 [H.sapiens]	0.09
60	304660	AA534416	Hs.162185 ESTs	0.09
	328217		CH.06_hs gj5868096	0.091
	336068		CH22_FGENES.684_13	0.091
	302833	AA295381	Hs.44423 ESTs	0.091
	328668		CH.07_hs gj5868254	0.091
65	335309		CH22_FGENES.532_2	0.091
	338481		CH22_EM:AC005500.GENSCAN.377-5	0.091
	306286	AA936892	EST singleton (not in UniGene) with exon hit	0.091
	305070	AA639783	EST singleton (not in UniGene) with exon hit	0.091
	304870	AA594811	Hs.119122 ribosomal protein L13a	0.091
	303856	AA968589	Hs.944 glucose phosphate isomerase	0.091

5	323789	AI459812	Hs.170460	ESTs; Weakly similar to KIAA0990 protein [H.sapiens]	0.092
	334910			CH22_FGENES.455_3	0.092
	326382			CH.19_hs gi 5867327	0.092
	332467	AA489630	Hs.119004	KIAA0665 gene product	0.092
	338534			CH22_EM:AC005500.GENSCAN.402-7	0.092
10	336449			CH22_FGENES.829_6	0.092
	333709			CH22_FGENES.250_24	0.092
	336559			CH22_FGENES.842_4	0.092
	333230			CH22_FGENES.107_10	0.093
	333133			CH22_FGENES.83_9	0.093
15	334885			CH22_FGENES.451_11	0.093
	330605	X02419	Hs.77274	plasminogen activator; urokinase	0.093
	336392			CH22_FGENES.823_4	0.093
	334083			CH22_FGENES.327_38	0.093
	325469			CH.12_hs gi 6017034	0.093
20	331077	R09531	Hs.19039	ESTs	0.093
	303701	AW500732		EST cluster (not in UniGene) with exon hit	0.093
	334218			CH22_FGENES.358_3	0.093
	336542			CH22_FGENES.840_6	0.093
	337151			CH22_FGENES.546-1	0.093
25	333642			CH22_FGENES.231_2	0.093
	336863			CH22_FGENES.297-4	0.093
	334680			CH22_FGENES.419_2	0.093
	326365			CH.18_hs gi 5867297	0.093
	338952			CH22_DJ32110.GENSCAN.23-22	0.093
30	337539			CH22_FGENES.832-4	0.094
	333546			CH22_FGENES.180_2	0.094
	335258			CH22_FGENES.518_3	0.094
	336786			CH22_FGENES.168-19	0.094
	321644	AI204177	Hs.237396	ESTs	0.094
35	335943			CH22_FGENES.646_17	0.094
	327918			CH.06_hs gi 5868165	0.094
	306398	AA970548		EST singleton (not in UniGene) with exon hit	0.094
	335671			CH22_FGENES.592_3	0.094
	335033			CH22_FGENES.475_11	0.094
40	338277			CH22_EM:AC005500.GENSCAN.290-2	0.094
	332061	AA504812	Hs.192824	early B-cell factor	0.094
	305153	AA654582	Hs.77039	ribosomal protein S3A	0.094
	333880			CH22_FGENES.292_2	0.094
	323940	AI864428	Hs.170880	ESTs	0.094
45	313779	AA648796	Hs.129771	ESTs	0.095
	323109	AA169345		EST cluster (not in UniGene)	0.095
	332930			CH22_FGENES.38_4	0.095
	335368			CH22_FGENES.543_6	0.095
	303887	R72672	Hs.193484	ESTs; Weakly similar to Similarity with yeast gene L3502.1 [C.elegans]	0.095
50	336223			CH22_FGENES.727_3	0.095
	311280	AI767957	Hs.197737	ESTs; Weakly similar to Y38A8.1 gene product [C.elegans]	0.095
	337256			CH22_FGENES.648-3	0.095
	308814	AI819263		EST singleton (not in UniGene) with exon hit	0.095
	334659			CH22_FGENES.418_7	0.095
55	335895			CH22_FGENES.635_3	0.095
	321697	AW388061	Hs.4953	golgi autoantigen; golgin subfamily a; 3	0.095
	336010			CH22_FGENES.668_8	0.096
	302824	U21260		EST cluster (not in UniGene) with exon hit	0.096
	333612			CH22_FGENES.217_7	0.096
60	304823	AA584837		EST singleton (not in UniGene) with exon hit	0.096
	335665			CH22_FGENES.590_16	0.096
	306518	AA989598		EST singleton (not in UniGene) with exon hit	0.096
	335243			CH22_FGENES.516_4	0.096
	335436			CH22_FGENES.559_5	0.096
65	300243	AI420256	Hs.161271	ESTs	0.096
	332810			CH22_FGENES.7_12	0.097
	308612	AI735634		EST singleton (not in UniGene) with exon hit	0.097
	335818			CH22_FGENES.618_6	0.097
	325838			CH.16_hs gi 6552452	0.097
	337482			CH22_FGENES.795-6	0.097
	336645			CH22_FGENES.26-1	0.097
	337293			CH22_FGENES.675-1	0.098

	329893		CH.15_p2 gi 6525313	0.098
	326533		CH.19_hs gi 5867441	0.098
	334905		CH22_FGENES.452_20	0.098
5	306347	AA961144	EST singleton (not in UniGene) with exon hit	0.098
	336676		CH22_FGENES.43-4	0.098
	339166		CH22_DA59H18.GENSCAN.69-7	0.098
	335774		CH22_FGENES.607_10	0.098
	339216		CH22_FF113D11.GENSCAN.6-11	0.098
10	335311		CH22_FGENES.532_4	0.098
	329632		CH.11_p2 gi 6729060	0.098
	328595		CH.07_hs gi 5868224	0.098
	326928		CH.21_hs gi 6456782	0.098
	315234	AI079680	Hs.120770 ESTs	0.098
15	306082	AA908508	EST singleton (not in UniGene) with exon hit	0.098
	305710	AA826544	EST singleton (not in UniGene) with exon hit	0.098
	318540	T30280	EST cluster (not in UniGene)	0.099
	337553		CH22_C4G1.GENSCAN.2-1	0.099
	320951	AA344069	Hs.202699 neurexophilin 4	0.099
20	303845	T08033	EST cluster (not in UniGene) with exon hit	0.099
	338981		CH22_DA59H18.GENSCAN.2-5	0.099
	321313	R87365	Hs.26058 ESTs; Weakly similar to p532 [H.sapiens]	0.099
	328348		CH.07_hs gi 5868383	0.099
	332203	H49388	Hs.102082 EST	0.099
25	301780	R07064	EST cluster (not in UniGene) with exon hit	0.099
	332095	AA608838	Hs.162681 EST	0.099
	333227		CH22_FGENES.107_5	0.099
	316442	AA760894	Hs.153023 ESTs	0.099
30	326001		CH.16_hs gi 5867073	0.099
	334363		CH22_FGENES.378_11	0.099
	338895		CH22_DJ32110.GENSCAN.9-2	0.099
	327460		CH.02_hs gi 6004455	0.099
	332705	T59161	Hs.76293 thymosin; beta 10	0.1
	307806	AI351739	EST singleton (not in UniGene) with exon hit	0.1
35	322800	F25037	Hs.225175 ESTs	0.1
	304918	AA602697	EST singleton (not in UniGene) with exon hit	0.1
	334327		CH22_FGENES.375_4	0.1
	318359	AI097439	Hs.135548 ESTs	0.1
40	326644		CH.20_hs gi 5867559	0.1
	334454		CH22_FGENES.388_3	0.1
	327959		CH.06_hs gi 5868210	0.1
	323783	AA330586	Hs.131819 ESTs	0.1
	309198	AI955915	Hs.248038 major histocompatibility complex; class I; C	0.1
	339265		CH22_BA354112.GENSCAN.10-3	0.1
45	320576	AL049977	Hs.162209 Homo sapiens mRNA; cDNA DKFZp564C122 (from clone DKFZp564C122)	0.1
	338132		CH22_EM.AC005500.GENSCAN.200-2	0.1
	333163		CH22_FGENES.91_5	0.101
	337584		CH22_C20H12.GENSCAN.5-1	0.101
50	307588	AI285535	EST singleton (not in UniGene) with exon hit	0.101
	336969		CH22_FGENES.378-2	0.101
	327535		CH.02_hs gi 6525279	0.101
	328732		CH.07_hs gi 5868289	0.101
	336686		CH22_FGENES.46-3	0.101
55	335777		CH22_FGENES.607_13	0.101
	332944		CH22_FGENES.47_3	0.101
	333174		CH22_FGENES.95_1	0.101
	336380		CH22_FGENES.821_8	0.101
60	330571	U60800	Hs.79089 sema domain; immunoglobulin domain (Ig); cytoplasmic domain; (semaphorin) 4D	0.101
	331789	AA398721	Hs.186749 ESTs	0.101
	338915		CH22_DJ32110.GENSCAN.12-1	0.101
	334844		CH22_FGENES.439_24	0.101
	336642		CH22_FGENES.23-4	0.101
65	334906		CH22_FGENES.452_21	0.101
	333188		CH22_FGENES.98_8	0.101
	300088	AW299993	EST cluster (not in UniGene) with exon hit	0.101
	329373		CH.X_hs gi 6682537	0.102
	331120	R46576	Hs.23239 ESTs	0.102
	335856		CH22_FGENES.628_1	0.102

5	331888	AA431337	Hs.98017	ESTs	0.102
	333154			CH22_FGENES.89_4	0.102
	335989			CH22_FGENES.655_2	0.102
	304385	AA235602		EST singleton (not in UniGene) with exon hit	0.102
	338016			CH22_EM:AC005500.GENSCAN.133-1	0.102
10	335190			CH22_FGENES.507_5	0.102
	318595	T39486	Hs.6137	ESTs	0.102
	333697			CH22_FGENES.250_11	0.102
	306526	AA989713		EST singleton (not in UniGene) with exon hit	0.103
	328734			CH.07_hs gi 5868289	0.103
15	307294	AI205612	Hs.73742	ribosomal protein; large; P0	0.103
	327424			CH.02_hs gi 5867751	0.103
	335872			CH22_FGENES.630_3	0.103
	333572			CH22_FGENES.189_1	0.103
	334774			CH22_FGENES.430_6	0.103
20	338660			CH22_EM:AC005500.GENSCAN.462-1	0.103
	326713			CH.20_hs gi 5867595	0.103
	333994			CH22_FGENES.310_18	0.103
	335800			CH22_FGENES.613_4	0.103
	318113	AI187943	Hs.132322	ESTs	0.103
25	337278			CH22_FGENES.665-1	0.103
	336386			CH22_FGENES.822_6	0.103
	334790			CH22_FGENES.432_15	0.103
	303778	AW505368		EST cluster (not in UniGene) with exon hit	0.104
	336524			CH22_FGENES.839_5	0.104
30	328936			CH.08_hs gi 5868500	0.104
	335102			CH22_FGENES.494_7	0.104
	300935	AA513644	Hs.222815	ESTs; Weakly similar to Wiskott-Aldrich Syndrome protein [H.sapiens]	0.104
	307581	AI284415		EST singleton (not in UniGene) with exon hit	0.104
	317301	AW291683	Hs.226056	ESTs	0.104
35	335330			CH22_FGENES.535_3	0.104
	337968			CH22_EM:AC005500.GENSCAN.103-2	0.104
	335627			CH22_FGENES.584_7	0.104
	336274			CH22_FGENES.762_2	0.104
	334730			CH22_FGENES.424_5	0.105
40	334409			CH22_FGENES.383_6	0.105
	327237			CH.01_hs gi 5867544	0.105
	333321			CH22_FGENES.138_13	0.105
	303181	AA452366		EST cluster (not in UniGene) with exon hit	0.105
	333738			CH22_FGENES.261_2	0.105
45	338255			CH22_EM:AC005500.GENSCAN.276-3	0.105
	334282			CH22_FGENES.369_12	0.105
	330190			CH.05_p2 gi 6165182	0.105
	310748	AW014249	Hs.158698	ESTs	0.105
	338150			CH22_EM:AC005500.GENSCAN.207-2	0.105
50	336719			CH22_FGENES.82-6	0.105
	330228			CH.05_p2 gi 6013527	0.105
	327801			CH.05_hs gi 5867924	0.105
	330525	S75168	Hs.274	megakaryocyte-associated tyrosine kinase	0.105
	334972			CH22_FGENES.468_2	0.105
55	335111			CH22_FGENES.494_19	0.106
	334483			CH22_FGENES.395_5	0.106
	328829			CH.07_hs gi 5868337	0.106
	302753	M74299		EST cluster (not in UniGene) with exon hit	0.106
	334512			CH22_FGENES.398_10	0.106
60	330024			CH.16_p2 gi 6671908	0.106
	321030	AI769930	Hs.233617	Homo sapiens (clone B3B3E13) Huntington's disease candidate region	0.107
	338410			CH22_EM:AC005500.GENSCAN.341-6	0.107
	334353			CH22_FGENES.376_5	0.107
	338276			CH22_EM:AC005500.GENSCAN.288-9	0.107
65	329053			CH.X_hs gi 5868574	0.107
	336560			CH22_FGENES.842_5	0.107
	332158	AA621363	Hs.112980	EST	0.107
	336447			CH22_FGENES.829_4	0.107
	333703			CH22_FGENES.250_17	0.107
	326207			CH.17_hs gi 5867222	0.107
	333232			CH22_FGENES.108_1	0.107

	334802		CH22_FGENES.435_1	0.107
	303784	AA704983	EST cluster (not in UniGene) with exon hit	0.107
	338847		CH22_DJ246D7.GENSCAN.10-2	0.107
5	339407		CH22_DJ579N16.GENSCAN.1-9	0.108
	337635		CH22_C20H12.GENSCAN.32-8	0.108
	334650		CH22_FGENES.417_17	0.108
	308511	AI687580	EST singleton (not in UniGene) with exon hit	0.108
	333392		CH22_FGENES.144_8	0.108
10	325840		CH.16_hs gij6552452	0.108
	315044	AW205664	Hs.129568 ESTs	0.108
	333298		CH22_FGENES.133_4	0.108
	335157		CH22_FGENES.501_7	0.108
	333305		CH22_FGENES.137_2	0.108
15	326379		CH.19_hs gij5867327	0.108
	335050		CH22_FGENES.482_1	0.108
	305185	AA663985	Hs.248038 major histocompatibility complex; class I; C	0.108
	335658		CH22_FGENES.590_9	0.108
	323040	AA336609	Hs.10862 ESTs	0.108
20	337326		CH22_FGENES.699-6	0.108
	339262		CH22_BA354112.GENSCAN.9-6	0.108
	321202	H54052	Hs.163639 ESTs; Weakly similar to INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR [H.sapiens]	0.109
	331792	AA398968	Hs.97548 EST	0.109
25	333806		CH22_FGENES.278_2	0.109
	321325	AB033100	EST cluster (not in UniGene)	0.109
	331373	AA435513	Hs.178170 ESTs; Weakly similar to DUAL SPECIFICITY PROTEIN PHOSPHATASE 3	0.87
	328775		CH.07_hs gij5868309	0.109
30	335105		CH22_FGENES.494_10	0.109
	300975	AI283548	Hs.149668 ESTs	0.109
	324893	T31940	EST cluster (not in UniGene)	0.109
	333397		CH22_FGENES.144_15	0.109
	336484		CH22_FGENES.831_3	0.109
35	335507		CH22_FGENES.571_22	0.109
	336373		CH22_FGENES.820_3	0.109
	336188		CH22_FGENES.717_12	0.109
	313455	AW081702	Hs.137329 ESTs	0.109
	335185		CH22_FGENES.506_4	0.109
40	306814	AI066577	EST singleton (not in UniGene) with exon hit	0.109
	311130	AI632322	Hs.195306 ESTs	0.109
	310882	AW080339	Hs.211911 ESTs	0.109
	323383	AI346359	Hs.135209 ESTs	0.11
	300212	AW135925	Hs.184552 biphenylhydrolase-like (serine hydrolase; breast epithelial mucin-assoc.	0.11
45	325675		CH.14_hs gij5867014	0.11
	330095		CH.19_p2 gij6015278	0.11
	331942	AA453261	Hs.99309 ESTs	0.11
	334723		CH22_FGENES.421_34	0.11
50	333614		CH22_FGENES.217_9	0.11
	337316		CH22_FGENES.692-1	0.11
	305057	AA635626	Hs.62954 ferritin; heavy polypeptide 1	0.11
	338704		CH22_EM:AC005500.GENSCAN.480-3	0.11
	335385		CH22_FGENES.543_27	0.11
55	338012		CH22_EM:AC005500.GENSCAN.128-10	0.11
	329449		CH.Y_hs gij5868886	0.11
	338980		CH22_DA59H18.GENSCAN.2-4	0.11
	336553		CH22_FGENES.841_10	0.111
	330021		CH.16_p2 gij6671889	0.111
60	327579		CH.03_hs gij5867824	0.111
	333099		CH22_FGENES.79_4	0.111
	337076		CH22_FGENES.453-4	0.111
	331388	AA456852	Hs.43543 suppressor of white apricot homolog 2	0.111
	306674	AI005542	Hs.180414 heat shock 70kD protein 10 (HSC71)	0.111
	305949	AA884409	EST singleton (not in UniGene) with exon hit	0.111
65	330748	AA419217	Hs.15911 DKFZP586E1422 protein	0.111
	333780		CH22_FGENES.273_2	0.111
	323676	AI702835	EST cluster (not in UniGene)	0.111
	308952	AI868157	Hs.224226 EST	0.111
	309338	AW026946	Hs.181165 eukaryotic translation elongation factor 1 alpha 1	0.111

	329317		CH.X_hs gij6381976	0.112
	333518		CH22_FGENES.173_3	0.112
	306982	AI127883	EST singleton (not in UniGene) with exon hit	0.112
5	336225		CH22_FGENES.728_2	0.112
	333698		CH22_FGENES.250_12	0.112
	302173	AI417947	Hs.14068 ESTs	0.112
	335510		CH22_FGENES.571_25	0.112
	328042		CH.06_hs gij5902482	0.112
10	336512		CH22_FGENES.834_7	0.112
	328541		CH.07_hs gij5868486	0.112
	311265	AW205118	Hs.199214 ESTs	0.112
	323218	AF131846	Hs.13396 Homo sapiens clone 25028 mRNA sequence	0.112
	302002	AF013956	Hs.123085 chromobox homolog 4 (Drosophila Pc class)	0.112
	315088	AA557351	Hs.152448 ESTs; Moderately similar to MULTIFUNCTIONAL PROTEIN ADE2	0.112
15	312581	AI937242	Hs.176590 ESTs	0.112
	322246	AW384710	Hs.125258 ESTs	0.112
	333659		CH22_FGENES.241_5	0.113
	327510		CH.02_hs gij6117815	0.113
20	336520		CH22_FGENES.839_1	0.113
	338682		CH22_EM.AC005500.GENSCAN.472-1	0.113
	334508		CH22_FGENES.398_6	0.113
	322533	T59538	EST cluster (not in UniGene)	0.113
	306873	AI086929	EST singleton (not in UniGene) with exon hit	0.113
	336040		CH22_FGENES.679_2	0.113
25	303898	T23215	EST cluster (not in UniGene) with exon hit	0.113
	312011	AW294868	Hs.187226 ESTs	0.113
	335186		CH22_FGENES.506_5	0.113
	333607		CH22_FGENES.216_2	0.113
30	305549	AA773530	EST singleton (not in UniGene) with exon hit	0.113
	333686		CH22_FGENES.249_4	0.113
	334362		CH22_FGENES.376_3	0.113
	338195		CH22_EM.AC005500.GENSCAN.233-18	0.114
	333588		CH22_FGENES.206_2	0.114
35	339233		CH22_BA354112.GENSCAN.2-3	0.114
	337455		CH22_FGENES.777-1	0.114
	309101	AI925108	EST singleton (not in UniGene) with exon hit	0.114
	328522		CH.07_hs gij5868477	0.114
	323999	AI537333	Hs.252782 ESTs	0.114
40	333517		CH22_FGENES.173_2	0.114
	329935		CH.16_p2 gij6165200	0.114
	326226		CH.17_hs gij5867230	0.114
	335890		CH22_FGENES.633_4	0.114
	336715		CH22_FGENES.77-1	0.114
45	327640		CH.04_hs gij5867890	0.114
	338842		CH22_DJ246D7.GENSCAN.7-1	0.114
	306534	AA991487	EST singleton (not in UniGene) with exon hit	0.114
	336597		CH22_FGENES.266_1	0.114
	321010	Y17456	Hs.227150 Homo sapiens LSFR2 gene; last exon	0.114
50	302294	AA159213	Hs.5337 isocitrate dehydrogenase 2 (NADP+); mitochondrial	0.114
	324895	N44238	Hs.77515 inositol 1;4;5-triphosphate receptor; type 3	0.114
	327358		CH.01_hs gij6552411	0.114
	308792	AI815153	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	0.115
	325886		CH.16_hs gij5867087	0.115
	336850		CH22_FGENES.272-11	0.115
55	305858	AA863103	EST singleton (not in UniGene) with exon hit	0.115
	302569	AC004472	multiple UniGene matches	0.115
	336158		CH22_FGENES.707_2	0.115
	327866		CH.06_hs gij5868131	0.115
60	339157		CH22_DA59H18.GENSCAN.67-3	0.115
	339258		CH22_BA354112.GENSCAN.8-3	0.115
	336129		CH22_FGENES.701_17	0.115
	333684		CH22_FGENES.249_2	0.115
	309618	AW190162	Hs.184776 ribosomal protein L23a	0.115
65	312926	AA954097	Hs.127523 ESTs	0.115
	302640	AB035698	EST cluster (not in UniGene) with exon hit	0.115
	328968		CH.08_hs gij6456775	0.115
	327902		CH.06_hs gij5868158	0.115
	321927	AJ223366	EST cluster (not in UniGene)	0.115
	335962		CH22_FGENES.651_4	0.115

	334927		CH22_FGENES.460_1	0.115
	330535	U11872	Human interleukin-8 receptor type B (IL8RB) mRNA, splice variant IL8RB1	0.856
5	328591		CH.07_hs gi 5868227	0.115
	334902		CH22_FGENES.452_16	0.115
	328525		CH.07_hs gi 5868482	0.115
	325870		CH.16_hs gi 5682492	0.116
	337522		CH22_FGENES.819-1	0.116
10	305079	AA641329	EST singleton (not in UniGene) with exon hit	0.116
	327343		CH.01_hs gi 6017017	0.116
	333918		CH22_FGENES.296_7	0.116
	333600		CH22_FGENES.213_2	0.116
	335846		CH22_FGENES.623_6	0.116
	333510		CH22_FGENES.171_4	0.116
15	327629		CH.04_hs gi 5867872	0.116
	333470		CH22_FGENES.161_6	0.116
	326855		CH.20_hs gi 5552460	0.116
	327008		CH.21_hs gi 5867664	0.117
	337480		CH22_FGENES.795-3	0.117
20	336425		CH22_FGENES.824_10	0.117
	321964	AL079687	Hs.171065 ESTs	0.117
	335651		CH22_FGENES.590_2	0.117
	308164	AI521574	Hs.181165 eukaryotic translation elongation factor 1 alpha 1	0.117
	337927		CH22_EM:AC005500.GENSCAN.80-3	0.117
25	300341	H45095	Hs.153524 ESTs	0.117
	300154	AI245127	Hs.179331 ESTs	0.117
	306295	AA937331	EST singleton (not in UniGene) with exon hit	0.117
	329670		CH.14_p2 gi 6272129	0.117
	335612		CH22_FGENES.583_6	0.117
30	307845	AI363450	EST singleton (not in UniGene) with exon hit	0.117
	330401	D28383	Human mRNA for ATP synthase B chain, 5'UTR (sequence from the 5'cap to the start codon)	0.117
	327127		CH.21_hs gi 6682520	0.117
	333843		CH22_FGENES.290_1	0.117
35	331083	R17762	Hs.22292 ESTs	0.117
	329140		CH.X_hs gi 6017060	0.117
	339338		CH22_BA354112.GENSCAN.27-3	0.117
	331974	AA464518	Hs.99616 ESTs	0.117
40	338631		CH22_EM:AC005500.GENSCAN.454-2	0.117
	330299		CH.06_p2 gi 2905881	0.117
	330351		CH.09_p2 gi 3056622	0.117
	305377	AA715714	Hs.181357 laminin receptor 1 (67kD; ribosomal protein SA)	0.117
	333106		CH22_FGENES.79_12	0.117
45	338514		CH22_EM:AC005500.GENSCAN.392-4	0.117
	327335		CH.01_hs gi 5902477	0.117
	301970	AB028962	Hs.120245 KIAA1039 protein	0.118
	326339		CH.17_hs gi 6056311	0.118
	330612	X15673	Hs.93174 Human endogenous retrovirus pHE.1 (ERV9)	0.118
50	334178		CH22_FGENES.350_6	0.118
	328008		CH.06_hs gi 5902482	0.118
	328976		CH.16_p2 gi 4878063	0.118
	320952	AA897432	Hs.130411 ESTs	0.118
	305621	AA789095	EST singleton (not in UniGene) with exon hit	0.118
55	337850		CH22_EM:AC005500.GENSCAN.34-3	0.118
	333626		CH22_FGENES.224_2	0.118
	337672		CH22_EM:AC000097.GENSCAN.67-1	0.118
	328803		CH.07_hs gi 6004475	0.118
	325922		CH.16_hs gi 5867122	0.118
	334489		CH22_FGENES.397_1	0.118
60	320638	R54766	Hs.101120 ESTs	0.118
	321932	AA569229	EST cluster (not in UniGene)	0.118
	336958		CH22_FGENES.367-1	0.118
	332082	AA600176	Hs.112345 ESTs	0.118
65	306004	AA889992	EST singleton (not in UniGene) with exon hit	0.118
	336803		CH22_FGENES.194-1	0.118
	309107	AI925823	EST singleton (not in UniGene) with exon hit	0.118
	336859		CH22_FGENES.293-9	0.118
	337935		CH22_EM:AC005500.GENSCAN.85-6	0.118
	326492		CH.19_hs gi 5867422	0.118

	327289		CH.01_hs gij5867481	0.119
	325818		CH.14_hs gij6682490	0.119
	310787	AW262580	Hs.159040 ESTs	0.119
5	330028		CH.16_p2 gij6671908	0.119
	325317		CH.11_hs gij5866878	0.119
	335279		CH22_FGENES.523_7	0.119
	331720	AA192173	Hs.221530 ESTs	0.119
	329186		CH.X_hs gij5868711	0.119
10	316012	AA764950	Hs.119898 ESTs	0.119
	338316		CH22_EM:AC005500.GENSCAN.304-2	0.119
	326033		CH.17_hs gij5867178	0.119
	334745		CH22_FGENES.426_3	0.119
	333051		CH22_FGENES.73_5	0.119
15	301763	R01279	EST cluster (not in UniGene) with exon hit	0.12
	304502	AA454809	Hs.172928 collagen; type I; alpha 1	0.12
	335680		CH22_FGENES.594_5	0.12
	304678	AA548556	EST singleton (not in UniGene) with exon hit	0.12
	335441		CH22_FGENES.560_4	0.12
	336187		CH22_FGENES.717_11	0.12
20	309422	AW087175	EST singleton (not in UniGene) with exon hit	0.12
	336047		CH22_FGENES.679_9	0.12
	309651	AW195850	EST singleton (not in UniGene) with exon hit	0.12
	308547	AI695385	Hs.201903 EST	0.12
25	304443	AA399444	EST singleton (not in UniGene) with exon hit	0.12
	336245		CH22_FGENES.746_3	0.12
	302703	H72333	EST cluster (not in UniGene) with exon hit	0.12
	335690		CH22_FGENES.596_5	0.12
	328941		CH.08_hs gij6456765	0.12
	333873		CH22_FGENES.291_9	0.12
30	317246	AW105092	Hs.155690 ESTs	0.12
	339288		CH22_BA354112.GENSCAN.16-6	0.12
	337996		CH22_EM:AC005500.GENSCAN.116-3	0.12
	333304		CH22_FGENES.137_1	0.121
35	308332	AI591235	EST singleton (not in UniGene) with exon hit	0.121
	329319		CH.X_hs gij6381876	0.121
	302086	X57138	multiple UniGene matches	0.121
	333290		CH22_FGENES.129_2	0.121
	323825	AI793080	Hs.123525 ESTs; Weakly similar to NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR [R.norvegicus]	0.121
40	330575	U64105	Hs.252280 Rho guanine nucleotide exchange factor (GEF) 1	0.121
	305274	AA679990	Hs.181165 eukaryotic translation elongation factor 1 alpha 1	0.121
	333647		CH22_FGENES.235_2	0.121
	302251	AA333340	EST cluster (not in UniGene) with exon hit	0.121
45	329777		CH.14_p2 gij6002090	0.121
	333155		CH22_FGENES.89_5	0.121
	326122		CH.17_hs gij5867194	0.121
	335310		CH22_FGENES.532_3	0.121
	335453		CH22_FGENES.562_13	0.122
50	305103	AA643329	Hs.111334 ferritin; light polypeptide	0.122
	337284		CH22_FGENES.667-2	0.122
	337418		CH22_FGENES.758-4	0.122
	313073	AI963740	Hs.46826 ESTs	0.122
	303759	AW504164	EST cluster (not in UniGene) with exon hit	0.122
55	300017			
	M33197		AFFX control: GAPDH	0.122
	316725	AW135084	Hs.127264 ESTs	0.122
	330738	AA293153	Hs.120980 nuclear receptor co-repressor 2	0.122
	336466		CH22_FGENES.829_25	0.122
60	335956		CH22_FGENES.647_3	0.122
	315308	AA780564	Hs.189053 ESTs	0.122
	338925		CH22_DJ32110.GENSCAN.14-3	0.122
	334969		CH22_FGENES.466_2	0.122
	322050	AL137589	EST cluster (not in UniGene)	0.122
65	339084		CH22_DA59H18.GENSCAN.38-2	0.122
	338323		CH22_EM:AC005500.GENSCAN.306-2	0.122
	337003		CH22_FGENES.419-7	0.122
	325470		CH.12_hs gij6017034	0.123
	336503		CH22_FGENES.833_10	0.123
	330786	D60374	Hs.258712 EST	0.123

	329446		CH.Y_hs gij5868886	0.123
	303326	AA229433	Hs.222634 ESTs; Moderately similar to ubiquitin-like protein / ribosomal protein S30	0.123
5	309067	AI916313	Hs.212788 EST	0.123
	317464	AA968472	Hs.130463 ESTs	0.123
	328755		CH.07_hs gij5868301	0.123
	326036		CH.17_hs gij5867178	0.123
	327208		CH.01_hs gij5867447	0.123
	326124		CH.17_hs gij5916395	0.123
10	327509		CH.02_hs gij6117815	0.123
	338398		CH22_EM:AC005500.GENSCAN.336-5	0.123
	304652	AA527782	Hs.84298 CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	0.123
15	335797		CH22_FGENES.612_6	0.124
	336714		CH22_FGENES.76-29	0.124
	327204		CH.01_hs gij5867447	0.124
	331881	AA430672	Hs.123778 ESTs	0.124
	306971	AI126509	EST singleton (not in UniGene) with exon hit	0.124
20	336174		CH22_FGENES.710_1	0.124
	336126		CH22_FGENES.701_13	0.124
	329129		CH.X_hs gij6588026	0.124
	303049	AW407562	EST cluster (not in UniGene) with exon hit	0.124
	335778		CH22_FGENES.607_14	0.124
25	336601		CH22_FGENES.369_2	0.124
	334340		CH22_FGENES.375_17	0.124
	337436		CH22_FGENES.767-1	0.124
	306013	AA896990	EST singleton (not in UniGene) with exon hit	0.124
	339213		CH22_FF113D11.GENSCAN.6-8	0.124
30	335355		CH22_FGENES.541_2	0.124
	336552		CH22_FGENES.841_9	0.124
	336384		CH22_FGENES.822_4	0.124
	310485	AI286202	Hs.149800 ESTs	0.125
	335840		CH22_FGENES.622_3	0.125
35	336444		CH22_FGENES.827_10	0.125
	315703	N36070	EST cluster (not in UniGene)	0.125
	327763		CH.05_hs gij5867961	0.125
	336383		CH22_FGENES.822_3	0.125
	333496		CH22_FGENES.168_6	0.125
40	328662		CH.07_hs gij6004473	0.125
	338986		CH22_DA59H18.GENSCAN.5-1	0.125
	328311		CH.07_hs gij5868371	0.125
	337241		CH22_FGENES.644-2	0.125
	336933		CH22_FGENES.350-7	0.125
45	313483	AW294432	Hs.144252 ESTs	0.125
	326116		CH.17_hs gij5867193	0.125
	330450	HG363-HT363	Epidermal Growth Factor Receptor-Related Protein	0.125
	307491	AI268539	EST singleton (not in UniGene) with exon hit	0.125
50	331852	AA418988	Hs.98314 Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone DKFZp586L0120)	0.125
	330462	HG944-HT944	Dopamine Receptor D4	0.125
	304410	AA284508	EST singleton (not in UniGene) with exon hit	0.125
	336385		CH22_FGENES.822_5	0.125
	336793		CH22_FGENES.176-3	0.125
55	326243		CH.17_hs gij5867261	0.125
	327266		CH.01_hs gij5867462	0.125
	320753	AF070579	Hs.181544 Homo sapiens clone 24487 mRNA sequence	0.125
	336960		CH22_FGENES.369-5	0.125
	329667		CH.14_p2 gij6272129	0.125
60	328168		CH.06_hs gij5868071	0.125
	336534		CH22_FGENES.839_16	0.125
	339289		CH22_BA354I12.GENSCAN.16-9	0.126
	309230	AI970747	EST singleton (not in UniGene) with exon hit	0.126
	339190		CH22_FF113D11.GENSCAN.1-2	0.126
	337086		CH22_FGENES.458-14	0.126
65	319233	R21054	Hs.211522 ESTs	0.126
	339398		CH22_BA232E17.GENSCAN.6-8	0.126
	331930	AA449077	Hs.179765 Homo sapiens mRNA; cDNA DKFZp586H1921 (from clone DKFZp586H192)	0.126
	308099	AI475914	EST singleton (not in UniGene) with exon hit	0.126

	338477		CH22_EM:AC005500.GENSCAN.373-5	0.126
	334286		CH22_FGENES.369_16	0.126
	317245	AI025039	Hs.131732 ESTs	0.126
5	335249		CH22_FGENES.516_10	0.126
	333327		CH22_FGENES.138_20	0.126
	304240	AA009802	EST singleton (not in UniGene) with exon hit	0.126
	335464		CH22_FGENES.562_26	0.126
	335236		CH22_FGENES.515_8	0.126
	334154		CH22_FGENES.340_4	0.126
10	309257	AI984183	EST singleton (not in UniGene) with exon hit	0.126
	310015	AI220122	Hs.201981 ESTs; Weakly similar to breast carcinoma-associated antigen [H.sapiens]	0.126
	328280		CH.07_hs gij5868352	0.126
15	305744	AA831819	EST singleton (not in UniGene) with exon hit	0.126
	327430		CH.02_hs gij5867754	0.126
	328323		CH.07_hs gij5868373	0.126
	333274		CH22_FGENES.123_2	0.126
	337193		CH22_FGENES.575-3	0.127
	334820		CH22_FGENES.437_2	0.127
20	328706		CH.07_hs gij5868270	0.127
	331228	W67267	Hs.174911 ESTs	0.127
	307205	AI192479	EST singleton (not in UniGene) with exon hit	0.127
	337123		CH22_FGENES.519-3	0.127
25	326201		CH.17_hs gij5867216	0.127
	335276		CH22_FGENES.523_2	0.127
	331202	T81115	Hs.191136 ESTs	0.127
	330532	U03187	Hs.121544 interleukin 12 receptor; beta 1	0.127
	321235	N49521	EST cluster (not in UniGene)	0.127
30	301743	F12605	Hs.204529 ESTs; Weakly similar to reverse transcriptase [H.sapiens]	0.127
	328175		CH.06_hs gij5868073	0.127
	306407	AA971985	EST singleton (not in UniGene) with exon hit	0.127
	327145		CH.01_hs gij5867548	0.127
	327649		CH.04_hs gij5867899	0.127
35	335142		CH22_FGENES.498_12	0.127
	333909		CH22_FGENES.295_2	0.127
	330608	X04325	Hs.2679 gap junction protein; beta 1; 32kD (connexin 32; Charcot-Marie-Tooth neuropathy; X-linked)	0.127
	330158		CH.21_p2 gij6580367	0.127
40	320153	AF064594	Hs.120360 phospholipase A2; group VI	0.127
	314407	AA098835	Hs.224432 ESTs	0.127
	333383		CH22_FGENES.143_22	0.127
	320663	AI734242	Hs.244473 ESTs	0.128
	326233		CH.17_hs gij5867232	0.128
45	326598		CH.20_hs gij5867634	0.128
	335174		CH22_FGENES.504_4	0.128
	319843	H29920	Hs.99486 ESTs; Weakly similar to aralar1 [H.sapiens]	0.128
	335458		CH22_FGENES.562_18	0.128
	332997		CH22_FGENES.58_4	0.128
50	334188		CH22_FGENES.352_3	0.128
	329759		CH.14_p2 gij6048280	0.128
	330348		CH.09_p2 gij4544475	0.128
	326958		CH.21_hs gij6469836	0.128
	305263	AA679467	EST singleton (not in UniGene) with exon hit	0.128
55	337693		CH22_EM:AC000097.GENSCAN.78-14	0.128
	326812		CH.20_hs gij6682504	0.128
	333237		CH22_FGENES.108_7	0.128
	333699		CH22_FGENES.250_13	0.128
	311496	AI768677	Hs.209888 ESTs; Weakly similar to phosphatidylserine synthase-2 [M.musculus]	0.128
60	336499		CH22_FGENES.833_4	0.128
	320087	AF032387	Hs.113265 small nuclear RNA activating complex; polypeptide 4; 190kD	0.128
	309989	AI184186	Hs.197813 ESTs	0.128
	301490	AW298468	Hs.250461 ESTs	0.128
	337011		CH22_FGENES.427-6	0.128
65	315052	AA876910	Hs.134427 ESTs	0.128
	301611	W22172	Hs.59038 ESTs	0.128
	336497		CH22_FGENES.833_2	0.129
	302068	Y16280	Hs.132049 endothelin type b receptor-like protein 2	0.129
	334502		CH22_FGENES.397_18	0.129

	304332	AA158884	EST singleton (not in UniGene) with exon hit	0.129
	304522	AA465405	EST singleton (not in UniGene) with exon hit	0.129
	312407	R46180	Hs.153485 ESTs	0.129
	310098	AI685841	Hs.161354 ESTs	0.129
5	301119	AF142579	EST cluster (not in UniGene) with exon hit	0.129
	309268	AI985821	Hs.62954 ferritin; heavy polypeptide 1	0.129
	330989	H42142	Hs.226396 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19 (Dbp5; yeast; homolog)	0.129
	336949		CH22_FGENES.361-4	0.129
10	330115		CH.19_p2 gjl6015202	0.129
	339212		CH22_FF113D11.GENSCAN.6-7	0.129
	326951		CH.21_hs gjl6004446	0.129
	305165	AA662939	EST singleton (not in UniGene) with exon hit	0.129
	308238	AI559492	EST singleton (not in UniGene) with exon hit	0.129
15	337140		CH22_FGENES.537-5	0.13
	321758	U29112	EST cluster (not in UniGene)	0.13
	304619	AA515554	Hs.119598 ribosomal protein L3	0.13
	312469	AA745289	Hs.173088 ESTs	0.13
	339017		CH22_DA59H18.GENSCAN.20-6	0.13
20	330116		CH.19_p2 gjl6015202	0.13
	333312		CH22_FGENES.138_4	0.13
	338004		CH22_EM:AC005500.GENSCAN.121-1	0.13
	314141	AA232134	Hs.190028 ESTs	0.13
	300509	AI239845	Hs.128494 ESTs; Weakly similar to EG:95B7.2 [D.melanogaster]	0.13
25	338530		CH22_EM:AC005500.GENSCAN.398-11	0.13
	335968		CH22_FGENES.652_1	0.13
	314121	AI732100	Hs.187619 ESTs	0.13
	337593		CH22_C20H12.GENSCAN.6-8	0.13
	332881		CH22_FGENES.33_1	0.13
30	305836	AA858043	EST singleton (not in UniGene) with exon hit	0.13
	339059		CH22_DA59H18.GENSCAN.30-5	0.13
	305610	AA782319	EST singleton (not in UniGene) with exon hit	0.13
	305852	AA862455	EST singleton (not in UniGene) with exon hit	0.13
	327409		CH.02_hs gjl5867750	0.13
35	312751	AI613089	Hs.164178 ESTs	0.13
	308726	AI799268	Hs.209929 EST	0.13
	325961		CH.16_hs gjl5867147	0.13
	311159	AW025919	Hs.197636 ESTs	0.13
	322715	AA057230	Hs.182135 ESTs	0.13
40	336441		CH22_FGENES.827_7	0.13
	336339		CH22_FGENES.814_12	0.13
	306911	AI095365	EST singleton (not in UniGene) with exon hit	0.13
	333613		CH22_FGENES.217_8	0.13
45	338489		CH22_EM:AC005500.GENSCAN.384-17	0.131
	326904		CH.21_hs gjl5867684	0.131
	337337		CH22_FGENES.717-1	0.131
	326752		CH.20_hs gjl5867615	0.131
	303977	AW512978	EST singleton (not in UniGene) with exon hit	0.131
	301373	AA595235	EST cluster (not in UniGene) with exon hit	0.131
50	338448		CH22_EM:AC005500.GENSCAN.359-22	0.131
	333774		CH22_FGENES.272_5	0.131
	332986		CH22_FGENES.54_8	0.131
	335362		CH22_FGENES.541_12	0.131
	335896		CH22_FGENES.635_4	0.131
55	337825		CH22_EM:AC005500.GENSCAN.13-19	0.131
	325257		CH.11_hs gjl5866895	0.131
	331188	T50240	Hs.167837 ESTs	0.131
	330645	Y08302	Hs.144879 dual specificity phosphatase 9	0.131
	331760	AA292721	Hs.154434 ESTs; Weakly similar to unknown [H.sapiens]	0.131
60	322995	AA513829	Hs.29797 ribosomal protein L10	0.131
	335497		CH22_FGENES.571_5	0.131
	334824		CH22_FGENES.437_6	0.131
	319480	R06933	Hs.184221 ESTs	0.131
	334842		CH22_FGENES.439_21	0.131
65	333335		CH22_FGENES.139_4	0.131
	317252	AA905178	Hs.130124 ESTs	0.131
	329034		CH.X_hs gjl5868561	0.131
	305188	AA664230	EST singleton (not in UniGene) with exon hit	0.131
	335755		CH22_FGENES.604_4	0.131

	302143	H15270	Hs.189847	putative neuronal cell adhesion molecule	0.131
	334939			CH22_FGENES.465_3	0.131
	318994	C15110	Hs.17802	ESTs	0.131
5	334498			CH22_FGENES.397_14	0.131
	333413			CH22_FGENES.146_2	0.132
	329676			CH.14_p2 gij6272128	0.132
	327277			CH.01_hs gij5867473	0.132
	305022	AA627416		EST singleton (not in UniGene) with exon hit	0.132
	336805			CH22_FGENES.196_3	0.132
10	320121	T93657		EST cluster (not in UniGene)	0.132
	334761			CH22_FGENES.428_10	0.132
	339400			CH22_BA232E17.GENSCAN.7-6	0.132
	330301			CH.06_p2 gij2905862	0.132
15	316822	AA827691	Hs.129967	ESTs; Weakly similar to neuronal thread protein	
				AD7c-NTP [H.sapiens]	0.132
	328020			CH.06_hs gij5902482	0.132
	325327			CH.11_hs gij5866875	0.132
	321163	AA209530		EST cluster (not in UniGene)	0.132
20	336393			CH22_FGENES.823_5	0.132
	325905			CH.16_hs gij5867104	0.132
	305237	AA676286	Hs.2186	eukaryotic translation elongation factor 1 gamma	0.132
	339046			CH22_DA59H18.GENSCAN.28-6	0.132
	325375			CH.12_hs gij5866920	0.132
25	333961			CH22_FGENES.304_7	0.132
	335450			CH22_FGENES.562_8	0.133
	302286	R58438		EST cluster (not in UniGene) with exon hit	0.133
	335116			CH22_FGENES.496_3	0.133
	327333			CH.01_hs gij5902477	0.133
30	308070	AI470948		EST singleton (not in UniGene) with exon hit	0.133
	308311	AI581855		EST singleton (not in UniGene) with exon hit	0.133
	320813	AW360847	Hs.208839	ESTs	0.133
	323665	AW248307		EST cluster (not in UniGene)	0.133
	328318			CH.07_hs gij5868373	0.133
35	320603	R51419		EST cluster (not in UniGene)	0.133
	332791			CH22_FGENES.3_1	0.133
	314976	AA524725	Hs.162108	ESTs	0.133
	303309	AL134164	Hs.224868	ESTs	0.133
	320581	R39753	Hs.170187	ESTs	0.133
40	333944			CH22_FGENES.302_2	0.133
	317992	AI733512	Hs.130901	ESTs	0.133
	330935	F02383	Hs.26492	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	0.133
	336659			CH22_FGENES.36-5	0.133
	338887			CH22_DJ32I10.GENSCAN.6-10	0.133
45	305273	AA679979	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	0.133
	333566			CH22_FGENES.183_2	0.134
	316952	AW450033	Hs.163312	ESTs	0.134
	333818			CH22_FGENES.283_1	0.134
	328687			CH.07_hs gij5868262	0.134
50	302879	H11802		EST cluster (not in UniGene) with exon hit	0.134
	336557			CH22_FGENES.842_2	0.134
	335222			CH22_FGENES.513_5	0.134
	338094			CH22_EM:AC005500.GENSCAN.179-3	0.134
	337384			CH22_FGENES.745-1	0.134
55	327360			CH.01_hs gij6552411	0.134
	328132			CH.06_hs gij5868038	0.134
	323604	AI751438	Hs.182827	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ	
				WARNING ENTRY !!!!	0.134
	337591			CH22_C20H12.GENSCAN.6-6	0.134
60	307018	AI140639		EST singleton (not in UniGene) with exon hit	0.134
	326896			CH.21_hs gij5867680	0.134
	333479			CH22_FGENES.163_5	0.134
	337915			CH22_EM:AC005500.GENSCAN.61-3	0.134
	335110			CH22_FGENES.494_18	0.134
65	333481			CH22_FGENES.163_9	0.134
	327512			CH.02_hs gij6117815	0.134
	300096	AW328639	Hs.83575	ESTs; Weakly similar to ZC328.3 [C.elegans]	0.134
	330163			CH.02_p2 gij6042042	0.135
	335752			CH22_FGENES.604_1	0.135
	334857			CH22_FGENES.443_1	0.135

	301872	H84730	EST cluster (not in UniGene) with exon hit	0.135
	337529		CH22_FGENES.823-29	0.135
	335734		CH22_FGENES.601_4	0.135
	337551		CH22_FGENES.847-8	0.135
5	309078	AI920965	Hs.77961 major histocompatibility complex; class I; B	0.135
	335513		CH22_FGENES.571_28	0.135
	339078		CH22_DA59H18.GENSCAN.37-6	0.135
	321907	N56660	Hs.148722 ESTs; Weakly similar to large tumor suppressor 1 [H.sapiens]	0.135
	337189		CH22_FGENES.571-32	0.135
10	329635		CH.12_p2 gjl5302817	0.135
	308601	AI719930	EST singleton (not in UniGene) with exon hit	0.135
	305020	AA627248	Hs.2064 vimentin	0.135
	333894		CH22_FGENES.293_1	0.135
15	322465	AA137152	Hs.3784 ESTs; Highly similar to phosphoserine aminotransferase [H.sapiens]	0.135
	305601	AA780975	EST singleton (not in UniGene) with exon hit	0.135
	332186	H10781	Hs.141051 ESTs; Moderately similar to !!! ALU SUBFAMILY SB WARNING ENTRY	0.135
	327822		CH.05_hs gjl5867968	0.135
20	310087	AI393914	Hs.160624 ESTs; Weakly similar to similar to CR16; SH3 domain binding protein	0.135
	328752		CH.07_hs gjl5868298	0.135
	337611		CH22_C20H12.GENSCAN.19-4	0.135
	334470		CH22_FGENES.394_1	0.136
25	335115		CH22_FGENES.496_2	0.136
	328730		CH.07_hs gjl5868289	0.136
	330350		CH.09_p2 gjl3056622	0.136
	336971		CH22_FGENES.378-6	0.136
	308258	AI565612	EST singleton (not in UniGene) with exon hit	0.136
30	326745		CH.20_hs gjl5867611	0.136
	335440		CH22_FGENES.560_3	0.136
	320257	AA330746	EST cluster (not in UniGene)	0.136
	328677		CH.07_hs gjl5868256	0.136
	329731		CH.14_p2 gjl6065783	0.136
35	315950	AA700553	Hs.206974 ESTs	0.136
	330049		CH.17_p2 gjl4567182	0.136
	337070		CH22_FGENES.448-3	0.136
	304095	H11324	Hs.31059 EST	0.136
	309304	AW005527	Hs.232820 EST	0.136
40	333458		CH22_FGENES.157_7	0.136
	329899		CH.15_p2 gjl6563505	0.136
	322202	AI275056	Hs.200133 ESTs	0.136
	333991		CH22_FGENES.310_15	0.136
	318617	AW247252	Hs.75514 nucleoside phosphorylase	0.136
45	310623	AI341586	Hs.195588 ESTs	0.136
	330489	M23323	Hs.3003 CD3E antigen; epsilon polypeptide (TIT3 complex)	0.136
	309646	AW194694	EST singleton (not in UniGene) with exon hit	0.136
	331068	R00071	Hs.191199 ESTs	0.136
	334285		CH22_FGENES.369_15	0.136
50	332178	F13689	Hs.100725 EST	0.136
	305724	AA827608	EST singleton (not in UniGene) with exon hit	0.136
	303158	AL138110	Hs.8594 Homo sapiens mRNA containing (CAG)4 repeat; clone CZ-CAG-7	0.136
	334543		CH22_FGENES.403_8	0.136
	335384		CH22_FGENES.543_26	0.136
55	336527		CH22_FGENES.839_8	0.136
	334951		CH22_FGENES.465_20	0.136
	325882		CH.16_hs gjl5867087	0.137
	305134	AA653159	EST singleton (not in UniGene) with exon hit	0.137
	307058	AI148709	EST singleton (not in UniGene) with exon hit	0.137
60	331943	AA453418	Hs.178272 ESTs	0.137
	331116	R44780	Hs.22634 ESTs	0.137
	306094	AA908877	EST singleton (not in UniGene) with exon hit	0.137
	333561		CH22_FGENES.180_18	0.137
	321439	H61962	EST cluster (not in UniGene)	0.137
65	324594	AA497090	EST cluster (not in UniGene)	0.137
	337926		CH22_EM:AC005500.GENSCAN.77-4	0.137
	337353		CH22_FGENES.726-1	0.137
	331836	AA412295	Hs.104774 EST	0.137
	308981	AI873242	EST singleton (not in UniGene) with exon hit	0.137

	329424		CH.Y_hs gij5868879	0.137
	325829		CH.15_hs gij5867052	0.137
	331845	AA416863	Hs.98183 ESTs	0.137
	333854		CH22_FGENES.290_13	0.137
5	306591	AI000248	EST singleton (not in UniGene) with exon hit	0.137
	328948		CH.08_hs gij6456765	0.137
	338935		CH22_DJ32110.GENSCAN.18-12	0.137
	325960		CH.16_hs gij5867147	0.137
	328377		CH.07_hs gij5868390	0.138
10	308851	AI829820	EST singleton (not in UniGene) with exon hit	0.138
	314620	AA424352	Hs.210586 ESTs	0.138
	337592		CH22_C20H12.GENSCAN.6-7	0.138
	338684		CH22_EM:AC005500.GENSCAN.472-3	0.138
	331800	AA400498	Hs.97543 ESTs	0.138
15	304587	AA505535	EST singleton (not in UniGene) with exon hit	0.138
	333981		CH22_FGENES.310_4	0.138
	332452	AA040369	Hs.11170 SYT interacting protein	0.138
	305752	AA835278	EST singleton (not in UniGene) with exon hit	0.138
	311947	T65554	Hs.251591 EST	0.138
20	333783		CH22_FGENES.273_5	0.138
	337406		CH22_FGENES.754-14	0.138
	327976		CH.06_hs gij5868212	0.138
	325593		CH.13_hs gij5866992	0.138
	339425		CH22_DJ579N16.GENSCAN.14-4	0.138
25	304475	AA428879	EST singleton (not in UniGene) with exon hit	0.138
	309488	AW131104	EST singleton (not in UniGene) with exon hit	0.138
	337532		CH22_FGENES.827-6	0.138
	317234	AA904448	Hs.126368 ESTs	0.138
	312261	AA854425	Hs.144455 ESTs	0.138
30	328927		CH.08_hs gij5868500	0.138
	336424		CH22_FGENES.824_9	0.138
	326667		CH.20_hs gij6552455	0.138
	325988		CH.16_hs gij5867064	0.138
	318446	AW300287	EST cluster (not in UniGene)	0.139
35	336511		CH22_FGENES.834_6	0.139
	335204		CH22_FGENES.508_13	0.139
	303244	AA147472	EST cluster (not in UniGene) with exon hit	0.139
	330870	AA115804	Hs.187593 ESTs	0.139
	329376		CH.X_hs gij5868859	0.139
40	304703	AA563898	EST singleton (not in UniGene) with exon hit	0.139
	333653		CH22_FGENES.239_2	0.139
	306799	AI051696	EST singleton (not in UniGene) with exon hit	0.139
	304872	AA595289	EST singleton (not in UniGene) with exon hit	0.139
	330812	AA013001	Hs.60563 ESTs	0.139
45	329568		CH.10_p2 gij3962490	0.139
	319210	AA253074	Hs.146261 ESTs	0.139
	334320		CH22_FGENES.374_5	0.139
	300860	AI916949	Hs.149748 ESTs; Weakly similar to weak similarity to collagens [C.elegans]	0.139
	305866	AA864533	EST singleton (not in UniGene) with exon hit	0.139
50	312943	AA984364	Hs.119064 ESTs	0.139
	330523	M99439	Hs.83958 transducin-like enhancer of split 4; homolog of Drosophila E(sp1)	0.139
	312708	AI076204	Hs.135440 ESTs	0.139
	309366	AW072970	EST singleton (not in UniGene) with exon hit	0.139
	303273	AA316069	EST cluster (not in UniGene) with exon hit	0.139
55	317484	AW274696	Hs.143921 ESTs	0.139
	333239		CH22_FGENES.111_1	0.139
	307126	AI184951	EST singleton (not in UniGene) with exon hit	0.139
	316813	AA826505	Hs.124517 ESTs	0.139
	331746	AA281365	Hs.121640 ESTs; Weakly similar to KIAA0386 [H.sapiens]	0.139
60	308558	AI700145	Hs.172182 poly(A)-binding protein; cytoplasmic	0.139
	310784	AW086142	Hs.159017 ESTs	0.139
	323831	AA335715	Hs.200299 ESTs	0.139
	307692	AI318342	EST singleton (not in UniGene) with exon hit	0.139
	310570	AI318327	EST cluster (not in UniGene)	0.139
65	327934		CH.06_hs gij5868184	0.139
	305232	AA670052	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	0.139
	334756		CH22_FGENES.428_5	0.139
	331838	AA451867	Hs.99255 ESTs	0.139
	301393	AI474722	Hs.150898 ESTs; Weakly similar to KIAA0644 protein [H.sapiens]	0.139

5	312005	T78450	Hs.13941	ESTs	0.139
	338431			CH22_EM:AC005500.GENSCAN.351-4	0.14
	331214	T90496	Hs.16757	ESTs	0.14
	333601			CH22_FGENES.213_4	0.14
	323481	AA278449	Hs.137429	ESTs	0.14
10	336911			CH22_FGENES.344-4	0.14
	338157			CH22_EM:AC005500.GENSCAN.209-5	0.14
	327845			CH.05_hs gjl6531962	0.14
	319109	Z45662	Hs.90797	Homo sapiens clone 23620 mRNA sequence	0.14
	334763			CH22_FGENES.428_12	0.14
15	329384			CH.X_hs gjl5868869	0.14
	302996	AF054663		EST cluster (not in UniGene) with exon hit	0.14
	323751	AW452656	Hs.209824	ESTs	0.14
	329916			CH.16_p2 gjl6223624	0.14
	301993	N49826	Hs.18602	ESTs	0.14
20	338129			CH22_EM:AC005500.GENSCAN.197-2	0.14
	325704			CH.14_hs gjl5867028	0.14
	335656			CH22_FGENES.590_7	0.14
	331673	W72366	Hs.40033	ESTs	0.14
	316807	AI018331	Hs.172444	ESTs; Highly similar to transcription regulator [M.musculus]	0.14
25	310743	AW449754	Hs.158665	ESTs	0.14
	326941			CH.21_hs gjl6004446	0.14
	328809			CH.07_hs gjl5868327	0.14
	323855	AI653164	Hs.128665	ESTs	0.14
	304705	AA564064		EST singleton (not in UniGene) with exon hit	0.14
30	325666			CH.14_hs gjl6469822	0.14
	333747			CH22_FGENES.265_6	0.14
	318287	AW015616	Hs.143321	ESTs	0.141
	332972			CH22_FGENES.51_5	0.141
	305704	AA825266		EST singleton (not in UniGene) with exon hit	0.141
35	315699	AW182805	Hs.189183	ESTs; Weakly similar to Nod1 [H.sapiens]	0.141
	327296			CH.01_hs gjl5867492	0.141
	336400			CH22_FGENES.823_15	0.141
	321033	H26214	Hs.20733	ESTs; Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY	0.141
	316522	AI475995	Hs.122910	ESTs	0.141
40	335715			CH22_FGENES.599_15	0.141
	335959			CH22_FGENES.650_2	0.141
	333259			CH22_FGENES.118_7	0.141
	337382			CH22_FGENES.744-8	0.141
	322346	AA227618	Hs.10882	HMG-box containing protein 1	0.141
45	325378			CH.12_hs gjl5866920	0.141
	338500			CH22_EM:AC005500.GENSCAN.390-1	0.141
	338460			CH22_EM:AC005500.GENSCAN.362-5	0.141
	315279	AW511138	Hs.256581	ESTs	0.141
	314439	AI539443	Hs.137447	ESTs	0.141
50	333624			CH22_FGENES.222_3	0.141
	329237			CH.X_hs gjl5868729	0.141
	330117			CH.19_p2 gjl6015201	0.141
	338017			CH22_EM:AC005500.GENSCAN.134-1	0.141
	337854			CH22_EM:AC005500.GENSCAN.38-12	0.142
55	329984			CH.16_p2 gjl4646193	0.142
	305004	AA622328	Hs.162762	EST	0.142
	302815	N40373		EST cluster (not in UniGene) with exon hit	0.142
	327823			CH.05_hs gjl5867968	0.142
	326753			CH.20_hs gjl5867616	0.142
60	301201	AA904482	Hs.197775	ESTs	0.142
	334303			CH22_FGENES.373_6	0.142
	326453			CH.19_hs gjl5867399	0.142
	311050	AI864581	Hs.215477	ESTs	0.142
	308740	AI802711	Hs.210337	EST; Weakly similar to aldolase A [H.sapiens]	0.142
65	331003	H63959	Hs.142722	ESTs	0.142
	338010			CH22_EM:AC005500.GENSCAN.128-8	0.142
	336326			CH22_FGENES.812_4	0.142
	318100	R44308	Hs.242302	ESTs	0.142
	320641	R55421		EST cluster (not in UniGene)	0.142
	325855			CH.16_hs gjl5867067	0.142
	330425	HG1728-HT1734		Non-Specific Cross Reacting Antigen (Gb:D90277), Alt. Splice Form 2	0.142

	324583	AA425411	Hs.22581	ESTs	0.142
	326268			CH.17_hs gjl5867267	0.142
	331390	AA460341	Hs.45008	ESTs	0.142
5	338904			CH22_DJ32110.GENSCAN.10-16	0.143
	333086			CH22_FGENES.79_1	0.143
	331919	AA446869	Hs.119316	ESTs	0.143
	312214	AJ248004	Hs.125187	ESTs	0.143
	323198	AW179174	Hs.7984	ESTs	0.143
	316107	AJ204001	Hs.184014	ribosomal protein L31	0.143
10	301335	AA885317	Hs.190511	ESTs	0.143
	337392			CH22_FGENES.747-3	0.143
	325543			CH.12_hs gjl6682452	0.143
	305903	AA873085		EST singleton (not in UniGene) with exon hit	0.143
15	332707	L35594	Hs.174185	phosphodiesterase 1/nucleotide pyrophosphatase 2 (autotaxin)	0.143
	337913			CH22_EM:AC005500.GENSCAN.59-10	0.143
	301436	AA961061	Hs.131696	ESTs	0.143
	335078			CH22_FGENES.486_5	0.143
	338451			CH22_EM:AC005500.GENSCAN.359-39	0.143
20	302777	AJ230640		EST cluster (not in UniGene) with exon hit	0.143
	330464	J03068	Hs.78223	N-acylaminoacyl-peptide hydrolase	0.143
	330988	H41411	Hs.33855	ESTs	0.143
	328939			CH.08_hs gjl6004481	0.143
	308015	AI440174	Hs.228907	EST; Weakly similar to GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN	0.143
25				12.3 [H.sapiens]	0.143
	328504			CH.07_hs gjl5868471	0.143
	332599	AA402891	Hs.32951	solute carrier family 29 (nucleoside transporters); member 2	0.143
	335744			CH22_FGENES.601_15	0.143
30	322394	AF077208		EST cluster (not in UniGene)	0.143
	323892	AL042661		EST cluster (not in UniGene)	0.143
	318443	AI939323	Hs.157714	ESTs; Weakly similar to NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN; ALPHA-5 CHAIN PRECURSOR	0.143
				[H.sapiens]	0.143
	336568			CH22_FGENES.843_7	0.143
35	330958	H08815	Hs.159824	EST	0.143
	327672			CH.04_hs gjl5867843	0.143
	335900			CH22_FGENES.635_8	0.144
	336044			CH22_FGENES.679_6	0.144
40	318845	AI815951	Hs.33183	ESTs; Weakly similar to estrogen-responsive finger protein; efp [H.sapiens]	0.144
	333483			CH22_FGENES.165_2	0.144
	333337			CH22_FGENES.139_6	0.144
	305993	AA889197		EST singleton (not in UniGene) with exon hit	0.144
45	335719			CH22_FGENES.599_22	0.144
	325682			CH.14_hs gjl6138923	0.144
	327350			CH.01_hs gjl6249563	0.144
	339291			CH22_BA354112.GENSCAN.18-1	0.144
	326358			CH.18_hs gjl5867293	0.144
	330316			CH.08_p2 gjl6007576	0.144
50	308150	AI499346	Hs.174131	ribosomal protein L6	0.144
	338065			CH22_EM:AC005500.GENSCAN.164-1	0.144
	339009			CH22_DA59H18.GENSCAN.18-7	0.144
	327776			CH.05_hs gjl5867964	0.145
	336664			CH22_FGENES.41-8	0.145
55	321921	AF070619		EST cluster (not in UniGene)	0.145
	319346	T70147	Hs.12024	ESTs	0.145
	304265	AA062892		EST singleton (not in UniGene) with exon hit	0.145
	303818	Z45986	Hs.250178	copine II	0.145
60	327498			CH.02_hs gjl6017023	0.145
	335227			CH22_FGENES.513_13	0.145
	339022			CH22_DA59H18.GENSCAN.22-1	0.145
	302597	H55661	Hs.33026	ESTs; Weakly similar to similar to Enterococcus faecalis TRAB [C.elegans]	0.145
	308550	AI697008	Hs.201811	EST	0.145
65	302175	AA262760	Hs.156015	Homo sapiens chromosome 19; cosmid R29381	0.145
	303252	AA156760		EST cluster (not in UniGene) with exon hit	0.145
	337414			CH22_FGENES.757-2	0.145
	310382	AI734009		EST cluster (not in UniGene)	0.145
	329333			CH.X_hs gjl5868806	0.145

	336857		CH22_FGENES.291-7	0.145
	332565	AA234896	Hs.25272 E1A binding protein p300	0.145
	318634	AI928098	Hs.156832 ESTs	0.145
	336318		CH22_FGENES.801_1	0.145
5	310960	AI923551	Hs.170843 ESTs	0.145
	335346		CH22_FGENES.537_2	0.145
	331196	T65416	Hs.12826 ESTs	0.145
	337607		CH22_C20H12.GENSCAN.17-3	0.146
	331206	T84096	Hs.15284 ESTs	0.146
10	301793	T80698	EST cluster (not in UniGene) with exon hit	0.146
	319590	AA210878	EST cluster (not in UniGene)	0.146
	311394	AI695374	Hs.256231 ESTs	0.146
	324773	AA632554	Hs.163401 ESTs	0.146
	324841	AI142359	Hs.155316 ESTs	0.146
15	332260	N70088	Hs.138467 ESTs	0.146
	329276		CH.X_hs gij5868762	0.146
	335887		CH22_FGENES.633_1	0.146
	338294		CH22_EM:AC005500.GENSCAN.297-1	0.146
	336993		CH22_FGENES.409-4	0.146
20	334135		CH22_FGENES.336_2	0.146
	326251		CH.17_hs gij5867263	0.146
	337396		CH22_FGENES.749-1	0.146
	339167		CH22_DA59H18.GENSCAN.69-8	0.146
	316838	AW135418	Hs.161210 ESTs	0.146
25	325313		CH.11_hs gij5866865	0.146
	331047	N66918	Hs.32205 ESTs	0.146
	323915	AL043362	EST cluster (not in UniGene)	0.146
	302747	AF062275	EST cluster (not in UniGene) with exon hit	0.146
	306317	AA947909	EST singleton (not in UniGene) with exon hit	0.146
30	334399		CH22_FGENES.382_5	0.146
	326472		CH.19_hs gij5867404	0.146
	333061		CH22_FGENES.75_4	0.146
	337072		CH22_FGENES.448-5	0.146
	334328		CH22_FGENES.375_5	0.146
35	327039		CH.21_hs gij6531965	0.146
	325576		CH.12_hs gij6552443	0.147
	315935	AI075804	Hs.132660 ESTs	0.147
	319638	AA323758	EST cluster (not in UniGene)	0.147
	334501		CH22_FGENES.397_17	0.147
40	338238		CH22_EM:AC005500.GENSCAN.264-4	0.147
	308636	AI744063	EST singleton (not in UniGene) with exon hit	0.147
	336567		CH22_FGENES.843_6	0.147
	335819		CH22_FGENES.619_2	0.147
	336950		CH22_FGENES.361-8	0.147
45	307055	AI148477	EST singleton (not in UniGene) with exon hit	0.147
	315134	AW504854	Hs.126714 ESTs	0.147
	335834		CH22_FGENES.621_1	0.147
	327870		CH.06_hs gij5868131	0.147
50	323802	AA332011	Hs.250138 protein phosphatase 2C; magnesium-dependent; catalytic subunit	0.147
	329412		CH.X_hs gij5682553	0.147
	323791	AA333068	EST cluster (not in UniGene)	0.147
	324126	AA385315	EST cluster (not in UniGene)	0.147
	327865		CH.06_hs gij5868130	0.147
	333445		CH22_FGENES.154_2	0.147
55	321302	AA021351	Hs.158497 KIAA0724 gene product	0.147
	336744		CH22_FGENES.118-9	0.147
	323731	AA323414	EST cluster (not in UniGene)	0.148
	320289	H07989	EST cluster (not in UniGene)	0.148
	305488	AA749000	EST singleton (not in UniGene) with exon hit	0.148
60	305592	AA780594	Hs.62954 ferritin; heavy polypeptide 1	0.148
	304094	H11295	EST singleton (not in UniGene) with exon hit	0.148
	325040	AW296368	EST cluster (not in UniGene)	0.148
	339034		CH22_DA59H18.GENSCAN.28-2	0.148
	334504		CH22_FGENES.398_2	0.148
65	334778		CH22_FGENES.431_2	0.148
	320148	U77494	Hs.119687 RAN binding protein 8	0.148
	303584	AW173759	Hs.203401 ESTs	0.148
	325826		CH.15_hs gij5867048	0.148
	331192	T55182	Hs.152571 ESTs; Highly similar to IGF-II mRNA-binding protein 2 [H.sapiens]	0.148

	325785		CH.14_hs gi 5381957	0.148
	333166		CH22_FGENES.91_8	0.148
	336548		CH22_FGENES.841_5	0.148
	337552		CH22_C4G1.GENSCAN.1-4	0.148
5	331775	AA382742	Hs.97151 EST	0.148
	338936		CH22_DJ32110.GENSCAN.19-6	0.148
	331869	AA428554	Hs.104894 ESTs; Weakly similar to fibronectin precursor [H.sapiens]	0.148
	332865		CH22_FGENES.28_5	0.148
10	328663		CH.07_hs gi 5004473	0.148
	328436		CH.07_hs gi 5868417	0.148
	311158	AI634864	Hs.250789 ESTs; Highly similar to similar to NEDD-4 [H.sapiens]	0.148
	336942		CH22_FGENES.354-2	0.148
	302262	R53169	Hs.246091 ESTs	0.149
15	333296		CH22_FGENES.132_3	0.149
	333365		CH22_FGENES.142_2	0.149
	311706	AW452392	Hs.252854 ESTs	0.149
	337109		CH22_FGENES.489-2	0.149
	315062	AW173300	Hs.190201 ESTs	0.149
20	333454		CH22_FGENES.157_3	0.149
	334784		CH22_FGENES.432_9	0.149
	333255		CH22_FGENES.118_3	0.149
	337518		CH22_FGENES.814-7	0.149
	320651	AA489268	EST cluster (not in UniGene)	0.149
25	323437	AA287567	EST cluster (not in UniGene)	0.149
	328761		CH.07_hs gi 5868302	0.149
	328787		CH.07_hs gi 5868309	0.149
	335261		CH22_FGENES.520_2	0.149
	300827	R16689	Hs.106004 ESTs	0.149
30	339263		CH22_BA354112.GENSCAN.10-1	0.149
	337412		CH22_FGENES.756-6	0.149
	334414		CH22_FGENES.384_1	0.149
	332931		CH22_FGENES.38_5	0.149
	310801	AW270980	Hs.106346 novel centrosomal protein RanBPM	0.149
35	305216	AA669056	EST singleton (not in UniGene) with exon hit	0.149
	314779	AA470122	Hs.190261 ESTs	0.149
	338414		CH22_EM:AC005500.GENSCAN.341-27	0.149
	303342	AW247361	EST cluster (not in UniGene) with exon hit	0.149
	337509		CH22_FGENES.806-4	0.149
	306631	AI001149	EST singleton (not in UniGene) with exon hit	0.149
40	302533	L36149	Hs.248116 chemokine (C motif) XC receptor 1	0.149
	336536		CH22_FGENES.839_18	0.149
	324666	T32458	Hs.14285 ESTs	0.149
	310173	AI767433	Hs.170013 ESTs	0.149
45	333595		CH22_FGENES.211_2	0.149
	335975		CH22_FGENES.652_9	0.15
	306654	AI003654	EST singleton (not in UniGene) with exon hit	0.15
	335025		CH22_FGENES.475_3	0.15
	328711		CH.07_hs gi 5868271	0.15
	328274		CH.07_hs gi 5868219	0.15
50	325505		CH.12_hs gi 6682451	0.15
	329641		CH.14_p2 gi 8468233	0.15
	304955	AA613504	EST singleton (not in UniGene) with exon hit	0.15
	339103		CH22_DA59H18.GENSCAN.44-10	0.15
	329636		CH.12_p2 gi 5302817	0.15
55	310118	AI203293	Hs.157489 ESTs	0.15
	326056		CH.17_hs gi 5867184	0.15
	303773	AA769074	EST cluster (not in UniGene) with exon hit	0.15
	303153	U09759	Hs.8325 mitogen-activated protein kinase 9	0.15

TABLE 13A shows the accession numbers for those primekeys lacking unigeneID's for Table 13. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset Identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT number	Accession
20	322050 321439 321666	24275_1 1599424_1 13653_22	AL137589 AA423949 BE222949 BE222694 AI199615 AW873116 AI277950 AW044290 AW630096 H61962 W01567 N75711 BE259906 AA232518 AA013359 AL035788 AW160822 BE387134 BE002954 BE391839 AW161565 AI878841 BE616458 BE409981 BE387308 BE297436 BE315536 AA206924 R12012 AA214169 BE312812 BE387093 H11710 BE312009 BE260569 AA343566 AA219526 R34757 AA219749 BE336733 AA219751 AW411099 AA232408 BE018716 BE398089 AA206253 AA053487 AA114224 AV655868 AW732566 BE394087 AW732574 AA313442 BE336875 AA070548 BE259840 BE019828 AW732341 AA299916 BE019253 BE018238 BE387109 AA232304 BE255589 AW732585 AA181436 AA308777 AA075802 AW732521 AA314526 AA226747 BE409513 AA206168 BE388292 BE298782 BE387086 AA305310 AV652723 AA314918 BE615510 AW951763 BE398104 BE385195 BE407165 BE391336 BE390187 BE389189 BE540650 BE249884 BE385985 BE274245 BE391124 BE260080 AA182600 BE512821 BE390090 BE279398 BE279589 BE263454 BE515194 BE293569 BE272531 BE388814 BE384659 BE271685 BE561043 BE278449 BE302572 AW239076 AI750583 AA376179 AA112632 BE266324 BE266614 R13105 AA132286 BE296305 AI220355 AA205606 AA219527 AA219519 AW804310 AA083286 BE171208 T19693 AA338328 BE185868 AA903024 T92162 AA330119 BE410404 BE314668 AW576245 BE207878 AW299993 AI199558 AI285442 AW299994 AW394242 AW394184 AI357412 AI870708 AI590539 W07459 AW068287 AA310079 BE336702 AA356318 AA360659 AA346785 AW402633 AA311210 AW402909 N76879 AW402913 AW401920 AA321636 AA354474 C17297 C16938 AA311774 M29871 NM_002872 Z82188 AW405674 H94176 R89281 AA214723 AI014482 AW949347 T27749 AW804226 AW786964 AW404581 AF077208 NM_014029 W68830 W79652 AA353375 AW575218 AA552192 AA521232 AA702695 AA033975 AW407827 AA829948 N94402 AW628604 AI523308 N57605 AA641662 H42477 N52784 AI753478 AA768493 AA845729 W47391 N55270 AI090117 R89282 BE206172 AA076650 AA595650 AI218931 BE049397 AI433110 W74114 H94277 AI358627 AI085221 AI862818 AA835967 AW103905 AI640644 AA835507 AA856887 AA694392 AW337542 AI524410 BE045500 AI440060 AI358801 AW028238 AW205248 AI718264 R48618 AA357358 AI695002 AA897549 AW081065 AI433360 AI810783 AI620963 Z82188 AA360224 U29112 AI656540 AI364875 AI656246 AI990940 AI169345 AI762857 AI949997 AI809601 AI681948 AI221079 AW167404 AI347614 AI611090 AI023472 AI347683 AI027467 AW591788 AI380665 AA835735 AA836654 AI244028 AW193159 AI500112 AI818722 AI738693 AI702308 AA805365 AI766842 T59538 T59589 T59598 T59542 AF147374 AF070619 R20302 T80358 AJ223366 BE305086 AW820106 AA621993 BE305208 AI738475 AI380189 AW590847 AI127232 AA622706 AI380858 AA621975 AI587036 AA665743 AW204003 AI692234 AI002242 AI692219 AW137282 AW268783 AW259510 AI308015 AW301462 AI318288 AI318575 AI318117 AI345591 AI249650 AI246934 AI246864 AI246971 AW268311 AI249654 BE041907 AW732776 N72324 N52825 W19526 BE143464 AA376060 M83667 NM_005195 S63168 M83667 AW068039 AW630649 AI338577 AI018125 AI269878 AW242440 AI887823 AI342581 BE222416 AI582847 AI651011 AI660815 AI699574 BE550201 AI926996 AW665855 AI827752 AI761857 BE328168 BE222451 AI762201 AW000929 AW007207 BE042962 BE551843 BE465373 AI279179 AI949945 BE551862 AW051667 BE328076 BE222296 AW007229 AW772332 AI279801 AI934526 AI631938 AI770103 BE041412 AI417900 AI692655 AI869943 AW270119 AI431739 AI703347 AW770568 AW025473 AI701497 AI128026 BE328147 AW203980 BE046793 AW087704 AI674597 AI650732 AI813691 AI472092 AI695224 AI241217 AW207746 AI206840 AI271362 AI631788 AI911883 AI914619 AI380585 AI767501 AI823759 AI564116 AI190991 AI377369 AI814122 AI221623 AI354793 AI081988 AI391740 AI337435 BE467366 AI824347 AI565325 AI280038 AI640455 AI819744 BE467803 BE327524 AI149402 AI313187 BE219684 AW611948 AW665821 AI091260 AW044492 BE220366 AW025381 AW183264 AI694865 AI498474 AI129780 AI202028 AI656792 BE220659 AI928040 AI830696 AI493021 AW612488 AI913152 BE042965 AI631837 AI693873 AI498925 AI768668 AI401544 BE327023 AI693383 AI769874 AI744003 AW082273 AI686501 AI798177 AI985196 AI090033 AI432342 AI689918 AI638308 BE468080 BE219568 AI912119 BE219787 AW005392 BE326564 AI589039 AI860187 AI758143 AI338168 AI702936 BE221985 AI498727 AI918196 AI279735 AW771497 AI860133 AW237834 AW661759 AW028111 BE503416 AI360180 AW611715 AI871777 BE045447 BE326444 AI266547 AI800237 AI823315 AI478368 AI264281 AI675841 AI690041
25	300088 322303 322394	622937_1 704603_1 27492_1	
30			
35			
40	321758 323109	44275_1 155498_1	
45	322533 321921 321927	38937_1 34680_1 21620_1	
50	321932 306971	265316_1 14694_7	
55			
60			
65			

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5		AA827710 W60285 W500038 AI884786 AA827191 AA810075 AW005088 R70248 AI858560 AW078678 AA631306 H52839
		AW085835 AI656182 AA737178 AW136923 AA281028 AA570316 AA722871 AA362737 AI217268 BE242373 R01113
		AA628946 AI394527 AW402308 AI361110 AI917585 T99639 AA805326 N44577 AI394021 AW403385 T23949 AI497766
		T96602 AA834947 AI693908 Z33450 T92127 BE541896 AI933301 BE251540 BE252269 N50968 AI695531 AW575523
		AW296889 N93796 N89924 AI361804 AI085251 AA810694 BE303011 AA743784 R13478 AA358771 AA325294 AW964880
		BE258953 R54116 AW881039 AW602593
10	301793 239325_1	BE265837 AA340632 T96304 T96075 T72780 H51978 R09868
	303049 102592_1	AW408042 AW407562 BE172835 BE396893 BE269184 AA045741 BE004187 AW751261 W74283
	301863 19477_1	BE263301 AI418863 NM_005194 X52560 AW328683 BE298869 D63161
	301872 27494_4	H84730 T73262
	301893 6561_1	T80334 BE292758 AK000854 H16996 BE253691 R88508 AA357663 AW955288 AW579550 N98864 AA595201 AI742967
15		AA602658 AI091433 AA813367 AI983217 AW298007 AI628490 AI708037 AI560654 AI032983 R88509 R38972 AI687783
		AI560153 AW874581 N69891 AA993617 H51180 AI269042 AI281358 AW591213 AI017724 AI262859 H16997 R38991
		AI804355 AI868988 AI669525 AW023081 AL047848
		AI734009 AI263076 AW272255 AI792912
	310382 653318_1	AA452366 AA351338 BE262590 BE262591 AA074050 AA389667 BE161346
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20	302569 17513_2	AA324119 AW246199 BE395368 BE261676 BE382334 BE394701 BE304548 T31940 BE398128 BE398019 BE296693
	324893 4670_1	BE379564 BE269460 BE397065 Z42029 BE305028 AK000549 BE536182 BE314372 AW383349 T50987 AA069735
		BE386997 AW381699 T51050 W95025 AA477678 AA348306 AW956831 AW062919 AL040397 BE305160 AA315419
		AW249929 AA295944 AI635946 AI870259 AI951125 AW028250 AI885184 AW873113 AI077544 AW025091 AI817594
		AI401718 AW008245 AI499064 AA599687 AI016890 AA765638 W93340 AA588708 AW519173 R51917 AA676778 AI084871
25		AA687684 AI860840 AI811921 AW514730 AA477561 N78845 AA779894 AA778559 AI968953 T16188 T32828 AA991426
		AI474472 AI473542 AI828972 AW247906 AA977415 AW591489 AA876008 AW191893 AA074278 AW874099 Z40196
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35	330535	1374_-8	U11872
	332634	10404_2	U24488 NM_007116

TABLE 13B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 13. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

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Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
15	332791	Dunham, I. et al.	Plus	72720-73315
	332792	Dunham, I. et al.	Plus	73381-73768
	332810	Dunham, I. et al.	Plus	304296-304384
20	332944	Dunham, I. et al.	Plus	2414825-2414932
	332972	Dunham, I. et al.	Plus	2572152-2572236
	333133	Dunham, I. et al.	Plus	3360058-3360195
	333154	Dunham, I. et al.	Plus	3615887-3616019
	333155	Dunham, I. et al.	Plus	3616832-3617003
	333227	Dunham, I. et al.	Plus	3992866-3992968
25	333230	Dunham, I. et al.	Plus	3995507-3996507
	333298	Dunham, I. et al.	Plus	4581537-4581947
	333304	Dunham, I. et al.	Plus	4629943-4630242
	333305	Dunham, I. et al.	Plus	4630388-4630645
30	333365	Dunham, I. et al.	Plus	4786883-4787283
	333383	Dunham, I. et al.	Plus	4907179-4907277
	333391	Dunham, I. et al.	Plus	4916697-4916780
	333392	Dunham, I. et al.	Plus	4918294-4918433
	333397	Dunham, I. et al.	Plus	4922466-4922635
35	333403	Dunham, I. et al.	Plus	4925140-4925256
	333413	Dunham, I. et al.	Plus	4943824-4943974
	333445	Dunham, I. et al.	Plus	5097827-5097885
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	329916	6223624	Plus	36396-37195
	330021	6671889	Plus	120938-121032
	330024	6671908	Minus	1005-1270
	330028	6671908	Minus	30015-30144
65	326033	5867178	Plus	37261-37333
	326036	5867178	Minus	120215-120273
	326056	5867184	Minus	181553-181690
	326116	5867193	Plus	45548-45604
	326122	5867194	Plus	144397-144683
	326138	5867203	Minus	179374-179436

	326145	5867204	Minus	52599-52814
	326180	5867211	Minus	182758-183222
	326201	5867216	Minus	166168-166959
5	326207	5867222	Plus	48139-48219
	326226	5867230	Plus	52644-52705
	326233	5867232	Plus	124788-124863
	326238	5867260	Plus	64282-64338
	326241	5867260	Minus	181648-181916
	326243	5867261	Plus	123838-123978
10	326251	5867263	Minus	82716-82822
	326268	5867267	Plus	122114-122765
	326124	5916395	Plus	407102-407560
	326339	6056311	Minus	164637-165251
15	330049	4567182	Minus	314662-315210
	326358	5867293	Plus	9122-9195
	326365	5867297	Minus	96630-96764
	326379	5867327	Plus	32299-32402
	326382	5867327	Minus	50420-50503
20	326390	5867340	Minus	108814-110592
	326424	5867369	Minus	168329-168409
	326453	5867399	Plus	86222-86423
	326472	5867404	Plus	293739-293940
	326492	5867422	Plus	120768-120991
25	326533	5867441	Minus	532153-532280
	330117	6015201	Minus	7340-7680
	330115	6015202	Plus	11403-11677
	330116	6015202	Plus	12109-12418
	330095	6015278	Plus	15343-15814
30	330096	6015278	Plus	49370-49458
	326644	5867559	Plus	42684-42819
	326713	5867595	Plus	121511-121798
	326745	5867611	Plus	127130-127318
	326752	5867615	Minus	1214-1562
35	326753	5867616	Plus	12454-12511
	326598	5867634	Plus	68955-69014
	326667	6552455	Plus	142311-142441
	326855	6552460	Minus	111390-111463
	326812	6682504	Plus	189811-189941
40	327005	5867664	Plus	610847-610907
	327008	5867664	Plus	928737-928811
	326886	5867680	Minus	12032-12122
	326904	5867684	Minus	9280-9606
	326951	6004446	Plus	193812-193998
	326941	6004446	Plus	62018-62896
45	326943	6004446	Minus	89242-89427
	326928	6456782	Minus	291007-291219
	326958	6469836	Minus	42952-43082
	326959	6469836	Minus	43159-43301
50	327039	6531965	Plus	694486-694998
	327127	6682520	Plus	41925-42083
	330158	6580367	Plus	81966-82456
	327204	5867447	Plus	165135-165239
	327208	5867447	Plus	180805-180864
55	327266	5867462	Minus	82400-82615
	327277	5867473	Minus	165616-165715
	327289	5867481	Plus	49296-49536
	327296	5867492	Plus	7627-8166
	327237	5867544	Minus	59702-59813
60	327145	5867548	Minus	40482-40551
	327333	5902477	Minus	141448-141609
	327335	5902477	Minus	142979-143124
	327343	6017017	Minus	12288-12395
	327350	6249563	Minus	41890-41985
65	327358	6552411	Minus	3802-3950
	327360	6552411	Minus	6255-6422
	327409	5867750	Minus	52949-53011
	327424	5867751	Plus	160442-160598
	327430	5867754	Plus	1320-1403
	327470	5867772	Plus	150910-150973

	327460	6004455	Plus	175245-175343
	327498	6017023	Minus	42178-42283
	327509	6117815	Minus	54882-55053
5	327510	6117815	Minus	56824-56944
	327512	6117815	Plus	176256-176325
	327535	6525279	Plus	19105-19175
	330163	6042042	Minus	20321-20385
	330171	6648220	Plus	110889-111575
	327579	5867824	Minus	37229-38335
10	327672	5867843	Minus	69649-69740
	327629	5867872	Plus	49692-49811
	327640	5867890	Plus	9448-9566
	327649	5867899	Plus	205871-205927
	327612	6525283	Plus	2747-2924
15	327718	6525284	Plus	86123-86186
	327801	5867924	Plus	23239-23348
	327762	5867961	Minus	50303-50439
	327763	5867961	Plus	229347-229476
	327776	5867964	Minus	164308-164486
20	327822	5867968	Minus	168886-169633
	327823	5867968	Minus	170359-170433
	327807	5867968	Plus	33745-33811
	327845	6531962	Plus	193402-193549
	330228	6013527	Minus	3719-3787
25	330190	6165182	Plus	36103-36243
	328122	5868031	Plus	158474-158656
	328132	5868038	Minus	126737-126839
	328159	5868065	Minus	52957-53162
	328168	5868071	Plus	60321-60479
30	328175	5868073	Plus	208-271
	328217	5868096	Minus	3742-4362
	327865	5868130	Plus	61503-62205
	327866	5868131	Minus	2893-3046
	327870	5868131	Plus	53558-53757
35	327879	5868142	Minus	77722-77793
	327902	5868158	Minus	133339-133467
	327918	5868165	Plus	547530-547591
	327934	5868184	Plus	41830-42036
	327959	5868210	Minus	46497-46682
40	327976	5868212	Minus	349301-349409
	328020	5902482	Minus	556386-556652
	328042	5902482	Minus	1985085-1986626
	328008	5902482	Plus	296663-297151
	330301	2905862	Minus	4420-5781
45	330299	2905881	Minus	1020-1382
	328274	5868219	Minus	31244-31439
	328595	5868224	Plus	148738-148967
	328591	5868227	Minus	237647-237726
	328668	5868254	Minus	10888-10984
50	328677	5868256	Minus	58708-58950
	328687	5868262	Plus	624479-624585
	328706	5868270	Plus	165501-165614
	328711	5868271	Minus	97797-97990
	328730	5868289	Plus	8068-8214
55	328732	5868289	Plus	37437-37550
	328734	5868289	Plus	50559-50747
	328752	5868298	Minus	114911-115087
	328755	5868301	Minus	145959-146446
	328761	5868302	Minus	239308-239412
60	328775	5868309	Plus	12845-12920
	328784	5868309	Minus	74523-74604
	328787	5868309	Plus	135772-135963
	328809	5868327	Plus	91792-91849
	328829	5868337	Plus	36309-36630
65	328280	5868352	Plus	160563-160631
	328311	5868371	Minus	170560-170826
	328318	5868373	Plus	414945-415620
	328323	5868373	Minus	1080089-1080235
	328348	5868383	Minus	260272-260379

	328377	5868390	Plus	16947-17023
	328436	5868417	Plus	203760-203904
	328504	5868471	Plus	47064-47217
5	328506	5868471	Plus	60716-60830
	328522	5868477	Plus	1972307-1972452
	328525	5868482	Plus	12387-14313
	328541	5868486	Plus	130956-131050
	328662	6004473	Plus	1184773-1184855
	328663	6004473	Plus	1185279-1186634
10	328803	6004475	Minus	291716-291948
	328304	6004478	Minus	3884-3952
	328927	5868500	Minus	428829-428893
	328936	5868500	Minus	1352202-1352259
15	328939	6004481	Minus	131139-131320
	328941	6456765	Minus	9817-9885
	328948	6456765	Plus	28227-28413
	328968	6456775	Plus	117442-118283
	330316	6007576	Minus	119761-119931
20	330350	3056622	Minus	26413-26820
	330351	3056622	Minus	27522-27614
	330348	4544475	Minus	19855-19962
	329034	5868561	Minus	32819-32939
	329046	5868569	Plus	18971-19030
25	329053	5868574	Plus	426453-426541
	329186	5868711	Minus	13108-13225
	329237	5868729	Plus	133238-133339
	329276	5868762	Minus	222629-222709
	329333	5868806	Plus	392666-392746
30	329376	5868859	Plus	52356-52694
	329384	5868869	Minus	116524-116662
	329140	6017060	Plus	290842-290905
	329317	6381976	Plus	614823-615209
	329319	6381976	Plus	721390-721470
35	329129	6588026	Plus	144569-144712
	329373	6682537	Minus	38950-39301
	329412	6682553	Minus	68948-69041
	329424	5868879	Plus	362196-362344
	329446	5868886	Plus	84776-84899
	329449	5868886	Plus	97697-97771

TABLE 14: shows genes, including expression sequence tags, down-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu02 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

10	Pkey:	Unique Eos probeset Identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Background subtracted normal prostate : prostate tumor tissue			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	331328	AA281133	Hs.88808	ESTs	18.53
	320875	D60641	Hs.131921	ESTs	14.55
	300994	AI251936	Hs.146298	ESTs	12.17
	323461	AA418762	Hs.190044	ESTs	10.55
20	301015	AA947682	Hs.217173	ESTs; Weakly similar to Chain A; Cdc42hs-Gdp Complex [H.sapiens]	10.17
	319419	AA543096	Hs.13648	ESTs; Highly similar to mitogen-induced [M.musculus]	9.2
	323486	C05278	Hs.166800	ESTs; Moderately similar to [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 4 PRECURSOR [H.sapiens]	8.87
	324882	AW419080	Hs.250645	ESTs	8
25	330569	U57796	Hs.57679	zinc finger protein 192	7.88
	330126		CH.21_p2	gil6093735	7.8
	316265	AA737400	Hs.142230	ESTs	7.7
	323045	AA148950	Hs.188836	ESTs	7.64
	320668	R58399	Hs.146217	ESTs	7.4
30	330769	AA465192	Hs.16514	ESTs	7.15
	312614	AI766732	Hs.201194	ESTs	7
	314790	AW341754	Hs.189305	ESTs	6.83
	309979	AW452118	Hs.257533	EST	6.74
	314236	AA743396	Hs.189023	ESTs	6.49
35	329192		CH.X_hs	gil5868716	6.1
	324307	AA627642	Hs.4994	transducer of ERBB2; 2 (TOB2)	5.99
	303685	AW500106		EST cluster (not in UniGene) with exon hit	5.82
	314921	AW452382	Hs.257564	ESTs	5.8
	315840	AA679001	Hs.192221	ESTs	5.68
40	332776	AA034364	Hs.256551	ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]	5.43
	313533	AW298141	Hs.157975	ESTs	5.4
	303494	F30712		EST cluster (not in UniGene) with exon hit	5.35
	317490	AI627358	Hs.148367	ESTs	5.31
45	332548	D84454	Hs.21899	solute carrier family 35 (UDP-galactose transporter); member 2	5.25
	334719		CH22_FGENES.421_30		5.25
	300679	AA813958	Hs.207727	ESTs; Moderately similar to KIAA0071 [H.sapiens]	5.22
	311811	AI625304	Hs.190312	ESTs	5.22
	315310	AW511298	Hs.256067	ESTs	5.19
	312871	H86747	Hs.227602	KIAA1116 protein	5.11
50	324715	AI739168		EST cluster (not in UniGene)	4.97
	313870	AW206435	Hs.146057	ESTs	4.97
	321453	N50080	Hs.117827	ESTs	4.78
	316160	AW197887	Hs.253353	ESTs	4.63
	313833	AA766825		EST cluster (not in UniGene)	4.58
55	315850	AW270550	Hs.116957	ESTs	4.53
	303124	AF161350		EST cluster (not in UniGene) with exon hit	4.46
	323346	AL134932	Hs.143607	ESTs	4.4
	301383	AA913591	Hs.126480	ESTs	4.35
	324513	AW501678	Hs.164577	ESTs	4.28
60	303480	AA331906		EST cluster (not in UniGene) with exon hit	4.25
	323591	AA301270		EST cluster (not in UniGene)	4.22
	313603	AW468119		EST cluster (not in UniGene)	4.2
	317863	AI733395	Hs.129124	ESTs	4.1
	312381	RA2049	Hs.195473	ESTs	4.08
65	317514	AW451570	Hs.126850	ESTs	4.03
	319750	AA621606	Hs.117956	ESTs	4.03

	322520	T55958	EST cluster (not in UniGene)	4
	314754	AW026761	Hs.134374 ESTs	4
	316088	AI990652	Hs.208973 ESTs	4
5	318473	AI939339	Hs.146883 ESTs	3.96
	307848	AI364186	EST singleton (not in UniGene) with exon hit	3.95
	300730	AW449204	Hs.257125 ESTs	3.94
	303034	W60843	Hs.31570 ESTs	3.93
	324668	AI679131	Hs.201424 ESTs	3.9
10	324674	AA541323	Hs.115831 ESTs	3.88
	300547	N53442	Hs.143443 ESTs	3.83
	316100	AW203986	Hs.213003 ESTs	3.79
	314801	AA481027	Hs.127336 ESTs; Weakly similar to ORF YGR245c [S.cerevisiae]	3.75
	320856	D59945	EST cluster (not in UniGene)	3.74
15	313188	AI039702	Hs.179573 collagen; type I; alpha 2	3.73
	314187	AA804409	Hs.118920 ESTs	3.73
	311826	AA765470	Hs.122826 ESTs	3.7
	302358	D81150	EST cluster (not in UniGene) with exon hit	3.68
	311441	Z38720	Hs.151014 ESTs	3.66
20	321914	AA011603	EST cluster (not in UniGene)	3.59
	332216	H95082	Hs.102332 EST	3.52
	324771	AA631739	EST cluster (not in UniGene)	3.5
	323691	AA317561	EST cluster (not in UniGene)	3.49
	303525	AW516519	Hs.115130 ESTs	3.47
25	309709	AW242630	EST singleton (not in UniGene) with exon hit	3.46
	300038		AFFX control: MurlL4	3.38
	316526	AI088192	Hs.135474 ESTs; Weakly similar to ATP-DEPENDENT RNA HELICASE A [H.sapiens]	3.36
	313029	AA731520	Hs.170504 ESTs	3.35
	304356	AA196027	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	3.34
30	314610	AI948688	Hs.191805 ESTs	3.33
	329815		CH.14_p2 gi 6624888	3.32
	314949	AI745387	Hs.239124 ESTs	3.31
	300598	N53574	Hs.158932 ESTs	3.3
	329218		CH.X_hs gi 5868726	3.28
35	315706	AW440742	Hs.155556 ESTs	3.28
	303751	AW503637	EST cluster (not in UniGene) with exon hit	3.25
	307783	AI347274	EST singleton (not in UniGene) with exon hit	3.25
	321414	AA324975	Hs.128993 ESTs; Weakly similar to KIAA0465 protein [H.sapiens]	3.25
	312187	AA700439	Hs.188490 ESTs	3.25
40	334061		CH22_FGENES.327_14	3.23
	336036		CH22_FGENES.678_7	3.23
	321477	H67818	Hs.222059 ESTs	3.21
	315760	AW139383	Hs.245437 ESTs	3.2
	316733	AA811713	Hs.163222 ESTs	3.2
45	300855	AW235248	Hs.79828 ESTs	3.2
	323611	AA304986	Hs.145704 ESTs	3.19
	314138	AA740616	EST cluster (not in UniGene)	3.17
	316774	AA814859	EST cluster (not in UniGene)	3.16
	308884	AI833131	Hs.179100 ESTs	3.11
50	331317	AA258222	Hs.87757 ESTs	3.1
	317221	AI989538	Hs.191074 ESTs	3.08
	316386	AA749062	Hs.180285 ESTs	3.08
	321040	H26953	EST cluster (not in UniGene)	3.08
	308828	AI824829	EST singleton (not in UniGene) with exon hit	3.08
55	300778	AA236233	Hs.188716 ESTs	3.07
	316667	AW015940	Hs.232234 ESTs	3.07
	324614	AW503101	EST cluster (not in UniGene)	3.07
	316468	AW293046	Hs.255158 ESTs	3.07
	300671	AI239706	Hs.189886 ESTs	3.06
60	314301	AW297967	Hs.188181 ESTs	3.05
	312335	AW043620	Hs.236993 ESTs	3.03
	322957	AA247755	EST cluster (not in UniGene)	3.01
	316848	AA830053	Hs.126798 ESTs	3.01
	313473	AA009660	Hs.251948 ESTs; Moderately similar to T07D3.7 [C.elegans]	2.99
65	318518	T27119	EST cluster (not in UniGene)	2.98
	313383	AI076370	Hs.134037 ESTs	2.97
	331389	AA458637	Hs.152207 ESTs	2.96
	304257	AA053294	EST singleton (not in UniGene) with exon hit	2.95
	309917	AW340014	EST singleton (not in UniGene) with exon hit	2.95
	319661	H08035	Hs.21398 ESTs; Moderately similar to PUTATIVE GLUCOSAMINE-6-PHOSPHATE	2.95

		ISOMERASE [H.sapiens]	2.95
	321253 AI699484	EST cluster (not in UniGene)	2.93
	321193 AA149508	Hs.103288 ESTs	2.93
	332864	CH22_FGENES.28_4	2.92
5	300027		
	M11507	AFFX control: transferrin receptor	2.91
	324330 AA884766	EST cluster (not in UniGene)	2.88
	320014 AA137114	Hs.170291 ESTs	2.88
	333916	CH22_FGENES.296_5	2.88
10	318885 Z43272	EST cluster (not in UniGene)	2.87
	318146 AI040125	Hs.150521 ESTs	2.87
	323348 AA233056	Hs.191518 ESTs	2.85
	305703 AA825148	Hs.21229 F-box protein Fbw1b	2.84
	335862	CH22_FGENES.629_7	2.83
15	317672 AW205409	Hs.127748 ESTs	2.82
	323416 AI610397	Hs.159560 ESTs	2.81
	312652 AI419909	Hs.160994 ESTs	2.81
	324094 AA382603	EST cluster (not in UniGene)	2.81
	319761 R84237	EST cluster (not in UniGene)	2.8
20	317013 AA864468	Hs.135646 ESTs	2.8
	317383 AA913887	Hs.126511 ESTs	2.78
	314659 AW277121	Hs.254881 ESTs	2.78
	312479 AI950844	Hs.128738 ESTs; Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]	2.77
	332808	CH22_FGENES.7_10	2.75
25	311824 AW293826	Hs.250610 ESTs	2.75
	321992 C06003	Hs.116456 ESTs	2.73
	316074 AW517542	Hs.208382 ESTs	2.73
	309839 AW296076	EST singleton (not in UniGene) with exon hit	2.73
	312071 AA683529	Hs.143119 ESTs	2.73
30	312684 AW294020	Hs.117721 ESTs	2.72
	332668 AA082971	Hs.181161 ESTs; Weakly similar to INHIBITOR OF APOPTOSIS PROTEIN 1 [M.musculus]	2.72
	322139 H53744	EST cluster (not in UniGene)	2.72
	304168 H77679	EST singleton (not in UniGene) with exon hit	2.72
	325602	CH.13_hs gjl5866994	2.71
35	319885 R59096	Hs.136698 ESTs	2.71
	300611 N75450	EST cluster (not in UniGene) with exon hit	2.71
	316854 AA831215	Hs.159066 ESTs; Weakly similar to predicted using Genefinder [C.elegans]	2.69
	318208 AI091458	Hs.134559 ESTs	2.68
	331623 R38715	Hs.153529 Homo sapiens clone 24540 mRNA sequence	2.68
40	324616 AI823999	Hs.162000 ESTs	2.68
	304968 AA614308	EST singleton (not in UniGene) with exon hit	2.67
	314912 AI431345	Hs.161784 ESTs	2.67
	300767 AW193466	Hs.136525 ESTs	2.67
	313463 AI057389	Hs.122536 ESTs	2.65
45	320600 AA135565	Hs.250739 ESTs	2.65
	301180 AI308989	Hs.156939 ESTs	2.65
	324825 AA704457	Hs.255738 ESTs; Moderately similar to gag [H.sapiens]	2.65
	300336 AW292417	Hs.255074 ESTs; Moderately similar to high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha [H.sapiens]	2.64
50	317850 N29974	EST cluster (not in UniGene)	2.64
	339047	CH22_DA59H18.GENSCAN.28-7	2.64
	324580 AA492588	EST cluster (not in UniGene)	2.63
	321142 AI817933	Hs.209584 ESTs	2.62
	319478 R06841	EST cluster (not in UniGene)	2.62
55	300793 AI248571	Hs.186837 ESTs	2.61
	313733 AA836116	EST cluster (not in UniGene)	2.6
	326505	CH.19_hs gjl5867435	2.6
	314987 AW015506	Hs.130730 ESTs	2.6
	303114 AF090948	EST cluster (not in UniGene) with exon hit	2.59
60	318709 H24244	Hs.240763 ESTs; Weakly similar to /prediction	2.58
	312878 AI209108	Hs.143946 ESTs	2.57
	329224	CH.X_hs gjl5868728	2.56
	328018	CH.06_hs gjl5902482	2.56
	323231 AA324437	Hs.177230 ESTs	2.55
65	312887 AW157377	Hs.132910 ESTs	2.55
	315183 AW136134	Hs.220277 ESTs	2.55
	300259 AI479011	Hs.170783 ESTs	2.54
	313240 AI743261	Hs.131860 ESTs	2.54
	316697 AW293174	Hs.252627 ESTs	2.53

	313966	AI807551	Hs.189061	ESTs	2.53
	331263	AA015718		ze31a12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:36574 3', mRNA sequence	2.51
5	310683	AW055233	Hs.160870	ESTs	2.5
	302566	AA085996	Hs.248572	Human PAC clone DJ404F18 from Xq23	2.5
	302697	AJ001408		EST cluster (not in UniGene) with exon hit	2.5
	308362	AI613519		EST singleton (not in UniGene) with exon hit	2.49
	322347	AF086538		EST cluster (not in UniGene)	2.49
10	316240	AA974253	Hs.120319	ESTs	2.49
	323208	AA203415	Hs.136200	ESTs	2.48
	321643	W76005	Hs.32094	ESTs	2.48
	330723	AA243617	Hs.31082	ESTs; Highly similar to db83 [R.norvegicus]	2.48
	323455	AA256675	Hs.200438	ESTs; Weakly similar to atypical PKC specific binding protein [R.norvegicus]	2.47
15	308383	AI624497		EST singleton (not in UniGene) with exon hit	2.47
	328744			CH.07_hs gjl5868290	2.47
	332344	W45574	Hs.252497	ESTs	2.47
	328121			CH.06_hs gjl5868031	2.47
	321915	AI670955	Hs.200151	ESTs	2.46
20	314954	AA521381	Hs.187726	ESTs	2.45
	302821	AA188868	Hs.173933	ESTs; Weakly similar to NUCLEAR FACTOR 1/X [H.sapiens]	2.45
	329454			CH.Y_hs gjl5868887	2.45
	336605			CH22_FGENES.420_4	2.45
	300664	AI444628	Hs.256809	ESTs	2.44
25	323362	AL135067	Hs.117182	ESTs	2.44
	300024	M10098		AFFX control: 18S ribosomal RNA	2.44
	325026	AI671168	Hs.12285	ESTs	2.43
	324510	AI148353	Hs.120849	ESTs	2.43
	313389	AI765182	Hs.119903	ESTs	2.43
30	301309	M78276	Hs.255917	ESTs	2.43
	313570	AA041455	Hs.209312	ESTs	2.43
	316504	AW135854	Hs.132458	ESTs	2.42
	319401	R01342		EST cluster (not in UniGene)	2.42
	312827	AI744361	Hs.205591	ESTs; Weakly similar to zinc finger protein Png-1 [M.musculus]	2.42
35	327871			CH.06_hs gjl5868131	2.41
	337173			CH22_FGENES.565-3	2.41
	302948	AA465635		EST cluster (not in UniGene) with exon hit	2.41
	324303	AL118754		EST cluster (not in UniGene)	2.4
	315527	AI791138	Hs.116768	ESTs	2.4
40	315979	AA830515	Hs.222917	ESTs	2.4
	331310	AA253351	Hs.44439	STAT induced STAT inhibitor-4	2.4
	321095	AA017595	Hs.32844	ESTs	2.4
	308561	AI701559		EST singleton (not in UniGene) with exon hit	2.39
	313035	N36417	Hs.144928	ESTs	2.37
45	322114	AA643791	Hs.191740	ESTs	2.37
	313671	W49823	Hs.145553	ESTs	2.37
	303211	AA099548	Hs.191436	ESTs; Highly similar to dJ1118D24.4 [H.sapiens]	2.37
	301256	AA932948		EST cluster (not in UniGene) with exon hit	2.36
	338165			CH22_EM:AC005500.GENSCAN.212-3	2.36
	324692	AA557952		EST cluster (not in UniGene)	2.35
50	318587	AA779704	Hs.168830	ESTs	2.35
	312378	R41582	Hs.109219	retinal degeneration B beta	2.35
	318625	T48448	Hs.193162	ESTs	2.35
	305181	AA663726	Hs.116922	EST	2.35
	300815	AA286678		EST cluster (not in UniGene) with exon hit	2.34
55	324063	AW292740	Hs.254815	ESTs	2.34
	315859	AA682305	Hs.133268	ESTs	2.33
	305092	AA642912		EST singleton (not in UniGene) with exon hit	2.33
	306598	AI000320		EST singleton (not in UniGene) with exon hit	2.33
60	300307	AI651016	Hs.246311	ESTs	2.33
	321348	Z49979		EST cluster (not in UniGene)	2.33
	325112	AI903770	Hs.124344	ESTs	2.32
	336679			CH22_FGENES.43-7	2.32
	321383	AJ002574		EST cluster (not in UniGene)	2.32
	337357			CH22_FGENES.730-6	2.31
65	300680	AW468066	Hs.257712	ESTs; Weakly similar to KIAA0986 protein [H.sapiens]	2.31
	327120			CH.21_hs gjl6531970	2.31
	302761	AW250553		EST cluster (not in UniGene) with exon hit	2.3
	312132	AI475490	Hs.170577	ESTs	2.3
	315639	AA827652		EST cluster (not in UniGene)	2.3

	312189	T95594	Hs.187435	ESTs	2.3
	306537	AA991705		EST singleton (not in UniGene) with exon hit	2.3
	327061			CH.21_hs gjl6531965	2.3
5	315391	AA759098	Hs.192007	ESTs	2.3
	322384	AI968646	Hs.33862	ESTs	2.29
	323206	AA203339	Hs.220750	ESTs	2.29
	318110	AI680915	Hs.201379	ESTs	2.28
	335250			CH22_FGENES.516_11	2.28
10	331696	Z38907	Hs.91662	KIAA0888 protein	2.28
	318327	AW294013	Hs.200942	ESTs	2.28
	324980	AA969121	Hs.254296	ESTs	2.28
	319429	AI608881	Hs.11482	ESTs; Highly similar to junctional adhesion molecule [H.sapiens]	2.28
	310601	AI970543	Hs.192605	ESTs	2.28
	318905	Z43395		EST cluster (not in UniGene)	2.28
15	323442	AA252753	Hs.164039	ESTs	2.27
	304428	AA342250	Hs.99819	ubiquitin specific protease 16	2.27
	313352	AW292127	Hs.144758	ESTs	2.27
	316491	AA766025	Hs.238794	EST	2.27
20	317751	AI697668	Hs.202241	ESTs	2.26
	314136	AA229781	Hs.221962	ESTs	2.26
	306665	AI004614	Hs.130577	EST	2.26
	303946	AW474196	Hs.221604	ESTs	2.25
	313435	AA769123		EST cluster (not in UniGene)	2.25
25	317679	AA968799	Hs.150289	ESTs	2.25
	322370	AA330095		EST cluster (not in UniGene)	2.25
	306620	AI000929		EST singleton (not in UniGene) with exon hit	2.24
	329109			CH.X_hs gjl5868626	2.24
	311043	AI871209	Hs.177128	ESTs	2.24
30	300228	AI458372	Hs.158748	ESTs; Weakly similar to synapsin Ib [M.musculus]	2.24
	307223	AI193698	Hs.184776	ribosomal protein L23a	2.24
	309023	AI888045		EST singleton (not in UniGene) with exon hit	2.23
	310749	AI493675	Hs.170332	ESTs	2.23
	316769	AI914939	Hs.212184	ESTs	2.22
35	320409	AA356195		EST cluster (not in UniGene)	2.21
	333149			CH22_FGENES.87_8	2.21
	324951	M86125	Hs.137487	ESTs	2.21
	321939	AI791617	Hs.145068	ESTs	2.2
	320594	AI863952	Hs.169436	arginyltransferase 1	2.2
40	320722	R67430	Hs.172787	ESTs	2.2
	321781	D78667		EST cluster (not in UniGene)	2.2
	328903			CH.08_hs gjl5868514	2.2
	303889	T19204		EST cluster (not in UniGene) with exon hit	2.2
	325045	T08845		EST cluster (not in UniGene)	2.2
45	312828	AI865455	Hs.211818	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	2.19
	335109			CH22_FGENES.494_15	2.18
	330878	AA131471	Hs.71440	ESTs	2.18
	311289	AI971362	Hs.231945	ESTs	2.18
	304608	AA513456		EST singleton (not in UniGene) with exon hit	2.18
50	337393			CH22_FGENES.747-4	2.18
	332812			CH22_FGENES.7_14	2.18
	327665			CH.04_hs gjl5867839	2.18
	314581	AW504859	Hs.237849	ESTs	2.17
	326508			CH.19_hs gjl6682496	2.17
55	301242	AW161535	Hs.258803	ESTs	2.17
	312780	AI765651	Hs.172900	ESTs	2.17
	315954	AW276810	Hs.254859	ESTs	2.16
	311179	AI880843	Hs.223333	ESTs	2.16
	315320	AI084182	Hs.186895	ESTs	2.16
60	313017	AI015203	Hs.118015	ESTs	2.16
	312430	AW139117	Hs.117494	ESTs	2.15
	300864	AA406539	Hs.190958	ESTs	2.15
	314753	AA463262		EST cluster (not in UniGene)	2.15
	322574	AF156548		EST cluster (not in UniGene)	2.15
	321409	C03864		EST cluster (not in UniGene)	2.15
65	321205	AA002047		EST cluster (not in UniGene)	2.14
	320406	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	2.14
	337646			CH22_EM:AC000097.GENSCAN.11-2	2.13
	303084	AF174008		EST cluster (not in UniGene) with exon hit	2.13
	312185	AA654772	Hs.186564	ESTs	2.13

	306813	AI066544	EST singleton (not in UniGene) with exon hit	2.13	
	314465	AA602917	Hs.156974 ESTs	2.12	
	318168	AI821782	Hs.220587 ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	2.12	
	315990	AI800041	Hs.190555 ESTs	2.11	
5	320712	R66867	EST cluster (not in UniGene)	2.11	
	318487	AI167877	Hs.143716 ESTs	2.11	
	317462	AW015206	Hs.178784 ESTs	2.11	
	304384	AA235482	Hs.62954 ferritin; heavy polypeptide 1	2.11	
	314544	AA399018	Hs.250835 ESTs	2.1	
10	319881	T72744	EST cluster (not in UniGene)	2.1	
	328078		CH.06_hs gjl5868008	2.1	
	317354	AW090770	Hs.192271 ESTs	2.1	
	308617	AI738720	EST singleton (not in UniGene) with exon hit	2.09	
	311568	AW439969	Hs.218177 ESTs	2.09	
15	313605	AI761786	Hs.204674 ESTs	2.09	
	314289	AA848118	Hs.221216 ESTs	2.08	
	332933		CH22_FGENES.38_7	2.08	
	325498		CH.12_hs gjl5866967	2.08	
20	313659	AW296067	Hs.124106 ESTs	2.08	
	324596	AW149321	Hs.105411 ESTs	2.08	
	324783	AA640770	EST cluster (not in UniGene)	2.07	
	302696	AA347452	EST cluster (not in UniGene) with exon hit	2.07	
	313418	AW450674	Hs.114696 ESTs	2.06	
25	326920		CH.21_hs gjl6456782	2.06	
	327574		CH.03_hs gjl5867818	2.06	
	323207	AI052795	Hs.192201 ESTs	2.06	
	303753	AW503733	Hs.170315 ESTs	2.05	
	305235	AA670480	EST singleton (not in UniGene) with exon hit	2.05	
	316055	AA693880	EST cluster (not in UniGene)	2.05	
30	317194	AW445167	Hs.126036 ESTs	2.05	
	319565	AW408683	Hs.32922 ESTs	2.05	
	335146		CH22_FGENES.499_2	2.05	
	301475	AI678183	Hs.170917 prostaglandin E receptor 3 (subtype EP3)	2.04	
35	312442	AA120970	Hs.143199 ESTs	2.04	
	322502	R62925	Hs.243665 ESTs	2.04	
	303693	AA290875	Hs.30120 ESTs	2.04	
	310179	AI215643	Hs.171381 ESTs	2.03	
	321121	W23285	EST cluster (not in UniGene)	2.03	
40	331330	AA282197	Hs.69002 ESTs; Highly similar to CGI-07 protein [H.sapiens]	2.03	
	306557	AA994530	EST singleton (not in UniGene) with exon hit	2.03	
	317865	AI298794	Hs.129130 ESTs	2.03	
	318667	AI493742	Hs.165210 ESTs	2.02	
	318042	AW294522	Hs.149991 ESTs	2.02	
	323818	AW245528	Hs.134754 ESTs	2.02	
45	331286	AA137062	Hs.103853 ESTs	2.01	
	311262	AI989942	Hs.232150 ESTs	2.01	
	335601		CH22_FGENES.581_41	2.01	
	311351	AI682303	Hs.201274 ESTs	2.01	
50	312996	AA249018	EST cluster (not in UniGene)	2.01	
	328190		CH.06_hs gjl5868077	2	
	338030		CH22_EM:AC005500.GENSCAN.148-16	2	
	333940		CH22_FGENES.301_6	2	
	328227		CH.06_hs gjl5868105	2	
55	331481	N27448	Hs.43944 EST	2	
	335288		CH22_FGENES.527_1	2	
	307513	AI274307	EST singleton (not in UniGene) with exon hit	2	
	323316	AL134620	EST cluster (not in UniGene)	2	
	319479	R21945	Hs.256153 ESTs	2	
60	303482	AA502583	Hs.197271 ESTs	2	
	327489		CH.02_hs gjl6004459	1.99	
	323935	AW175841	Hs.192183 ESTs	1.99	
	309575	AW168096	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	1.99	
	337043		CH22_FGENES.439-19	1.98	
	312897	AI828174	Hs.227049 ESTs	1.98	
65	307881	AI370434	EST singleton (not in UniGene) with exon hit	1.98	
	328656		CH.07_hs gjl6004473	1.98	
	314569	AA813784	Hs.123001 ESTs	1.98	
	332783	W45302	Hs.87889 helicase-moi	1.98	
	315259	AA701499	Hs.148115 ESTs	1.98	

	313171	N67879	Hs.157695	ESTs	1.97
	318060	AI241421	Hs.132236	ESTs	1.97
	332256	N66393	Hs.102754	ESTs	1.97
	312110	AI962180	Hs.226803	ESTs	1.97
5	335864		CH22_FGENES.629_9		1.97
	320389	W00545	Hs.171785	ESTs	1.97
	314065	AA868267	Hs.85524	ESTs	1.96
	323086	H15474	Hs.12214	Homo sapiens clone 23716 mRNA sequence	1.96
	323919	AA862973	Hs.220704	ESTs	1.96
10	310750	AI373163	Hs.170333	ESTs	1.96
	309435	AW090537		EST singleton (not in UniGene) with exon hit	1.96
	300129	AW028820		EST cluster (not in UniGene) with exon hit	1.96
	320130	AI820675	Hs.203804	ESTs	1.95
	323787	AW373446	Hs.169885	ESTs; Weakly similar to cDNA EST EMBL:T02216 comes from this gene [C.elegans]	1.95
15	338112		CH22_EM:AC005500.GENSCAN.185-24		1.95
	313625	AW468402	Hs.254020	ESTs	1.95
	325240		CH.10_hs gij5866848		1.95
	331833	AA412102	Hs.250911	interleukin 13 receptor; alpha 1	1.95
20	332252	N63882		za21f9.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	
			IMAGE:293225 3', mRNA sequence		1.95
	300279	AW237425	Hs.253817	ESTs	1.95
	326023		CH.17_hs gij5867245		1.95
	321609	H86021	Hs.198800	ESTs; Weakly similar to hMmTRA1b [H.sapiens]	1.94
	324183	AA402453	Hs.113011	ESTs	1.94
25	336276		CH22_FGENES.762_5		1.94
	334913		CH22_FGENES.456_3		1.94
	325417		CH.12_hs gij5866925		1.94
	318489	AW043590	Hs.225023	ESTs	1.94
	318455	AI148763		EST cluster (not in UniGene)	1.94
30	306890	AI092235		EST singleton (not in UniGene) with exon hit	1.94
	315073	AW452948	Hs.257631	ESTs	1.94
	321289	R84687	Hs.226306	ESTs	1.94
	308521	AI689808		EST singleton (not in UniGene) with exon hit	1.93
	306382	AA968967		EST singleton (not in UniGene) with exon hit	1.93
35	331320	AA262999	Hs.42788	ESTs	1.93
	324279	AA501412	Hs.191688	ESTs; Weakly similar to Pro-Pol-dUTPase polypeptide [M.musculus]	1.93
	309577	AW168753		EST singleton (not in UniGene) with exon hit	1.93
	327014		CH.21_hs gij5867664		1.93
	303488	AW025860		EST cluster (not in UniGene) with exon hit	1.93
40	306561	AA995223	Hs.129559	EST	1.92
	330694	AA019806	Hs.108447	spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	1.92
	313083	N50545	Hs.159200	ESTs	1.92
	327752		CH.05_hs gij5867949		1.92
	318674	AA295490		EST cluster (not in UniGene)	1.92
45	301267	AW297762	Hs.255690	ESTs	1.91
	332092	AA608787	Hs.112590	ESTs	1.91
	323509	AL036947		EST cluster (not in UniGene)	1.91
	321452	AA317554		EST cluster (not in UniGene)	1.91
	311483	AI765013	Hs.209128	ESTs	1.91
50	300976	AI246374	Hs.185861	ESTs	1.91
	323715	AA322155		EST cluster (not in UniGene)	1.91
	313800	AW296132	Hs.166674	ESTs	1.91
	332029	AA489697	Hs.145053	ESTs	1.91
	304013	AW518573	Hs.156110	Immunoglobulin kappa variable 1D-8	1.91
55	322019	AA354549	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (from clone DKFZp727C191)	1.91
	334150		CH22_FGENES.339_1		1.9
	310094	AW450967	Hs.235240	ESTs	1.9
	316218	AW207642	Hs.174021	ESTs	1.9
	324774	AI031771	Hs.132586	ESTs	1.9
60	326507		CH.18_hs gij5867435		1.9
	314570	AA405696		EST cluster (not in UniGene)	1.9
	336268		CH22_FGENES.758_2		1.9
	315278	AI985544	Hs.116429	ESTs	1.9
	325824		CH.15_hs gij5867048		1.9
65	316277	AA737780	Hs.213392	ESTs	1.9
	323181	AA418583	Hs.143621	ESTs	1.9
	301438	AA961643	Hs.127716	ESTs	1.89
	307050	AI147341	Hs.146734	EST	1.89
	306830	AI075803		EST singleton (not in UniGene) with exon hit	1.89

	302426	AL049925	Hs.225984	DKFZP547G0910 protein	1.89
	320127	H72615	Hs.17268	ESTs	1.89
	337736			CH22_EM:AC000097.GENSCAN.100-2	1.89
5	331319	AA262755	Hs.194264	ESTs	1.88
	310767	AI377505	Hs.158835	ESTs	1.88
	314880	AI732169	Hs.105429	ESTs	1.88
	312539	AI004377	Hs.200360	ESTs	1.88
	309674	AW205604	Hs.168034	ESTs; Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	1.88
	314621	AI627478	Hs.187670	ESTs	1.88
10	319495	AI972146	Hs.192756	ESTs	1.88
	313472	AA007374		EST cluster (not in UniGene)	1.88
	302705	U09060		EST cluster (not in UniGene) with exon hit	1.88
	329511			CH.10_p2 gi 3983514	1.88
	317140	AI699412	Hs.201925	ESTs	1.87
15	302598	AI815985	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homologous to yeast UBC4/5)	1.87
	301153	AA725670	Hs.120485	ESTs; Weakly similar to serine/threonine kinase with SH3 domain; leucine zipper domain and proline rich domain [H.sapiens]	1.87
	332222	N28271	Hs.176618	ESTs	1.87
20	330703	AA055475	Hs.104143	clathrin; light polypeptide (Lca)	1.87
	318470	AI159863	Hs.143713	ESTs	1.87
	314014	AW291847	Hs.121715	ESTs; Weakly similar to HP protein [H.sapiens]	1.87
	300370	AI827817		EST cluster (not in UniGene) with exon hit	1.86
	312329	R84768	Hs.13399	Homo sapiens clone 25032 mRNA sequence	1.86
	325587			CH.12_hs gi 5682462	1.86
25	310237	AI884313	Hs.158906	ESTs	1.86
	318872	R13085		EST cluster (not in UniGene)	1.86
	303431	AA317915		EST cluster (not in UniGene) with exon hit	1.86
	338427			CH22_EM:AC005500.GENSCAN.349-1	1.86
	300452	AI352293	Hs.191098	ESTs	1.85
30	321279	H85330	Hs.146060	ESTs	1.85
	301690	F05865	Hs.249180	ubiquitin-conjugating enzyme E2E 2 (homologous to yeast UBC4/5)	1.85
	307932	AJ230822		EST singleton (not in UniGene) with exon hit	1.85
	318292	AI679966	Hs.150603	ESTs	1.85
	310254	AI239811	Hs.157491	ESTs	1.85
35	311790	AW016437	Hs.233462	ESTs	1.84
	314248	AA278347	Hs.126078	ESTs	1.84
	335586			CH22_FGENES.581_25	1.84
	339209			CH22_FF113D11.GENSCAN.6-4	1.84
	307954	AI419692		EST singleton (not in UniGene) with exon hit	1.84
40	302549	AF055136	Hs.248162	tectorin alpha	1.84
	321629	H87213	Hs.158092	ESTs	1.84
	301239	AA807558		EST cluster (not in UniGene) with exon hit	1.84
	332434	N75542	Hs.75356	transcription factor 4	1.84
	327192			CH.01_hs gi 5867445	1.83
45	310214	AI220072	Hs.165893	ESTs	1.83
	320516	R33857	Hs.181479	ESTs; Weakly similar to E-SELECTIN PRECURSOR [H.sapiens]	1.83
	324231	W60827		EST cluster (not in UniGene)	1.83
	336616			CH22_FGENES.613_5	1.83
	328799			CH.07_hs gi 5868316	1.83
50	324661	AW504181		EST cluster (not in UniGene)	1.83
	313190	AA766707	Hs.153039	ESTs	1.83
	301979	L28168	Hs.121495	potassium voltage-gated channel; Isk-related family; member 1	1.82
	302099	AL021397	Hs.137576	ribosomal protein L34 pseudogene 1	1.82
	320187	T99949		EST cluster (not in UniGene)	1.82
55	320791	R78808	Hs.93961	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens]	1.82
	305733	AA829535	Hs.84298	CD74 antigen (invariant polypept of MHC; class II antigen-associated)	1.82
	308280	AI569349	Hs.180920	ribosomal protein S9	1.81
	321533	W78877	Hs.40111	ESTs	1.81
	312946	AI915122	Hs.204087	ESTs; Weakly similar to F33D11.9b [C.elegans]	1.81
60	319474	H90265	Hs.100636	ESTs	1.81
	329519			CH.10_p2 gi 3983510	1.81
	324685	AA220982		EST cluster (not in UniGene)	1.81
	320697	N62937	Hs.139181	ESTs	1.81
	329246			CH.X_hs gi 5868732	1.81
65	332000	AA481271	Hs.193945	ESTs	1.81
	310811	AI420990	Hs.161303	ESTs	1.81
	325866			CH.16_hs gi 5867076	1.81
	322064	Z78343		EST cluster (not in UniGene)	1.8
	333712			CH22_FGENES.251_1	1.8

	313457	AA576052	Hs.193223	ESTs	1.8
	321591	H85687	Hs.117927	ESTs	1.8
	330260			CH.05_p2 gi6671884	1.8
5	311080	AI656320	Hs.197711	ESTs	1.8
	329522			CH.10_p2 gi3983507	1.8
	322889	AA081924	Hs.211417	ESTs	1.8
	300175	AI275011	Hs.204877	ESTs	1.8
	330976	H20560	Hs.244624	ESTs	1.8
	300208	AI341180	Hs.196115	ESTs; Weakly similar to FIBRILLIN 1 PRECURSOR [H.sapiens]	1.79
10	319635	R17531		EST cluster (not in UniGene)	1.79
	313454	AA730673	Hs.188634	ESTs	1.79
	303093	AI400310	Hs.148958	ESTs	1.79
	309815	AW292760		EST singleton (not in UniGene) with exon hit	1.79
15	326506			CH.19_hs gi5867435	1.79
	319845	AA649011	Hs.187902	ESTs	1.79
	300290	AI623739	Hs.186387	ESTs	1.79
	312180	AI248285	Hs.118348	ESTs	1.79
	313058	D81015	Hs.125382	ESTs	1.79
20	330120			CH.19_p2 gi6671864	1.78
	328412			CH.07_hs gi5868405	1.78
	302345	NM_000565		EST cluster (not in UniGene) with exon hit	1.78
	308100	AI475949		EST singleton (not in UniGene) with exon hit	1.78
	311386	AW205705	Hs.207514	ESTs	1.78
25	330282			CH.05_p2 gi6671910	1.78
	318856	Z43011	Hs.21169	ESTs	1.78
	312486	AA845630	Hs.117904	ESTs	1.78
	325450			CH.12_hs gi5866941	1.78
	321206	H54178	Hs.226469	ESTs	1.78
30	330977	H20826	Hs.31783	ESTs	1.78
	303487	AA333666		EST cluster (not in UniGene) with exon hit	1.77
	310398	AI264671	Hs.164166	ESTs	1.77
	313230	AI540166	Hs.129563	ESTs	1.77
	317747	AI683782	Hs.128245	ESTs	1.77
35	303381	AL038841	Hs.163313	ESTs; Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]	1.77
	336123			CH22_FGENES.701_8	1.77
	300185	AI286182	Hs.208484	ESTs	1.77
	316002	AW451733	Hs.119824	ESTs	1.77
	319850	AA001811	Hs.83722	ESTs	1.77
40	329941			CH.16_p2 gi6165199	1.77
	328329			CH.07_hs gi5868375	1.77
	322934	AI493054	Hs.158968	ESTs	1.77
	325902			CH.16_hs gi5867101	1.76
	322239	W01813	Hs.12109	WD40 protein Clao1	1.76
45	303530	AI274851	Hs.258744	ESTs	1.76
	300980	AI025527	Hs.222097	ESTs	1.76
	331909	AA437300	Hs.178210	ESTs	1.76
	321553	H92449	Hs.116406	ESTs	1.76
	301618	T52760		EST cluster (not in UniGene) with exon hit	1.76
50	319592	AA627356	Hs.163315	ESTs	1.76
	318511	T26528	Hs.227175	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	1.76
	327183			CH.01_hs gi5867442	1.76
	313516	AA029058	Hs.135145	ESTs	1.76
	318644	AI752482		EST cluster (not in UniGene)	1.76
55	321632	AA419617		EST cluster (not in UniGene)	1.76
	324657	AW451142	Hs.255628	ESTs	1.76
	300437	AW449374	Hs.257149	ESTs	1.75
	319775	AA504429	Hs.6211	methyl-CpG binding domain protein 1	1.75
	314775	AI149880	Hs.188809	ESTs	1.75
60	337460			CH22_FGENES.780-5	1.75
	309849	AW297444		EST singleton (not in UniGene) with exon hit	1.75
	301471	AA995014	Hs.129544	ESTs; Weakly similar to ORF YLL027w [S.cerevisiae]	1.75
	312739	AI318426	Hs.155925	ESTs	1.75
	319995	H15355	Hs.60887	ESTs	1.75
65	326495			CH.19_hs gi5867423	1.75
	337497			CH22_FGENES.801-4	1.75
	322633	AA004534	Hs.153981	ESTs	1.75
	332177	F10812	Hs.101433	ESTs	1.75
	326930			CH.21_hs gi6456782	1.75
	316893	AA837332		EST cluster (not in UniGene)	1.75

	324826	AA704806	Hs.143842	ESTs	1.75
	311269	AI656924	Hs.174257	ESTs	1.75
	309375	AW075342		EST singleton (not in UniGene) with exon hit	1.75
5	314171	AI821895	Hs.193481	ESTs	1.75
	311684	AI990741	Hs.252809	ESTs	1.75
	334387			CH22_FGENES.380_1	1.75
	312195	AI300101	Hs.252222	ESTs	1.75
	315707	AA18055	Hs.161160	ESTs	1.74
	324349	AW501470		EST cluster (not in UniGene)	1.74
10	300724	AI762929	Hs.206134	ESTs; Weakly similar to similar to reverse transcriptase [C.elegans]	1.74
	309906	AW339340		EST singleton (not in UniGene) with exon hit	1.74
	303714	AW501336		EST cluster (not in UniGene) with exon hit	1.74
	318704	Z24981		EST cluster (not in UniGene)	1.74
15	303027	AF111178		EST cluster (not in UniGene) with exon hit	1.74
	322601	W92924		EST cluster (not in UniGene)	1.74
	319382	H93199	Hs.33665	ESTs	1.74
	315858	AA737345		EST cluster (not in UniGene)	1.74
	332243	N55484	Hs.220540	ESTs; Highly similar to ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR [H.sapiens]	1.74
20	330951	H02566	Hs.191268	Homo sapiens mRNA; cDNA DKFZp434N174 (from clone DKFZp434N174)	1.74
	324044	AL045752	Hs.211519	ESTs	1.73
	320630	AA199847		EST cluster (not in UniGene)	1.73
	327288			CH.01_hs gjl5867481	1.73
25	314986	AI201367	Hs.142860	ESTs	1.73
	319078	H17255	Hs.144515	ESTs	1.73
	326278			CH.17_hs gjl5867269	1.73
	302552	H49792		EST cluster (not in UniGene) with exon hit	1.73
	322322	AF086431		EST cluster (not in UniGene)	1.73
	327075			CH.21_hs gjl6531965	1.73
30	317392	AI797588	Hs.145459	ESTs	1.73
	300810	AI076890	Hs.186949	ESTs	1.73
	315978	AA830893	Hs.119769	ESTs	1.73
	323903	AA773580	Hs.193598	ESTs	1.73
35	330803	AA004699	Hs.150580	putative translation initiation factor	1.73
	309845	AW296802	Hs.255580	EST	1.73
	314963	AI689617	Hs.200934	ESTs	1.73
	311710	F09774	Hs.175971	ESTs	1.73
	315315	AI984592	Hs.15088	ESTs	1.73
40	300378	AA663560	Hs.235873	ESTs; Weakly similar to K11C4.2 [C.elegans]	1.73
	316141	AW303457		EST cluster (not in UniGene)	1.72
	319826	T71739	Hs.75442	albumin	1.72
	312961	AI033922	Hs.122517	ESTs	1.72
	334379			CH22_FGENES.379_11	1.72
45	305854	AA862733		EST singleton (not in UniGene) with exon hit	1.72
	313031	N34927	Hs.186566	ESTs	1.72
	329728			CH.14_p2 gjl6065785	1.72
	312090	N57692	Hs.118064	ESTs	1.72
	323341	AL134875	Hs.192386	ESTs	1.72
50	302077	AA310580	Hs.132898	Homo sapiens chromosome 11; BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene	1.71
	310766	AI971438	Hs.158824	ESTs	1.71
	311450	AI809985	Hs.203340	ESTs	1.71
	311792	AW238064	Hs.253909	ESTs	1.71
55	321500	H71899		EST cluster (not in UniGene)	1.71
	311948	T78791	Hs.241569	ESTs; Moderately smlr to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	1.71
	302270	R56151		EST cluster (not in UniGene) with exon hit	1.71
	329089			CH.X_hs gjl5868614	1.71
	322331	AF086467		EST cluster (not in UniGene)	1.71
60	318235	AI080361	Hs.134217	ESTs	1.71
	304561	AA489792		EST singleton (not in UniGene) with exon hit	1.71
	312681	AI029149	Hs.193124	pyruvate dehydrogenase kinase; isoenzyme 3	1.71
	310250	AI476629	Hs.158465	ESTs	1.71
	338178			CH22_EM:AC005500.GENSCAN.219-6	1.71
	338910			CH22_DJ32110.GENSCAN.11-2	1.71
65	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (from clone DKFZp564B1462)	1.7
	322289	AA534550	Hs.539	ribosomal protein S29	1.7
	319802	AI701489	Hs.202501	ESTs	1.7
	314022	AW452420	Hs.248678	ESTs	1.7
	314937	AA515602	Hs.152330	ESTs	1.7

	300580	AA761322	Hs.220538	ESTs	1.7
	304398	AA262785		EST singleton (not in UniGene) with exon hit	1.7
	313421	AW339515	Hs.163700	ESTs	1.7
5	309763	AW270182		EST singleton (not in UniGene) with exon hit	1.7
	322092	AF085833		EST cluster (not in UniGene)	1.7
	315603	AA764768	Hs.121158	ESTs	1.7
	325031	T08597		EST cluster (not in UniGene)	1.7
	327157			CH.01_hs gi 5866841	1.7
10	314809	AI741461	Hs.161904	ESTs	1.7
	320361	H67220	Hs.146406	nitrilase 1	1.69
	324721	AW402302	Hs.43616	ESTs	1.69
	328624			CH.07_hs gi 5868246	1.69
	303344	AA255977	Hs.250646	ESTs; Highly similar to ubiquitin-conjugating enzyme [M.musculus]	1.69
	328960			CH.08_hs gi 6456775	1.69
15	315702	AA657501	Hs.146315	ESTs	1.69
	302385	AJ224172	Hs.204096	lipophilin B (uteroglobin family member); prostatein-like	1.68
	319699	R14537		EST cluster (not in UniGene)	1.68
	309506	AW137700		EST singleton (not in UniGene) with exon hit	1.68
20	330417	D84424	Hs.57697	hyaluronan synthase 1	1.68
	315296	AA876905	Hs.125286	ESTs	1.68
	328538			CH.07_hs gi 5868485	1.68
	323923	AA354146		EST cluster (not in UniGene)	1.68
	320303	AL079289	Hs.137154	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 35971	1.68
25	302987	AI927068	Hs.110853	ESTs; Weakly similar to R10D12.12 [C.elegans]	1.68
	310695	AI472124	Hs.157757	ESTs	1.68
	307512	AI273815	Hs.242463	keratin 8	1.68
	338506			CH22_EM:AC005500.GENSCAN.390-10	1.68
	331722	AA195405	Hs.110347	Homo sapiens mRNA for alpha integrin binding protein 80; partial	1.68
	301431	R05385		EST cluster (not in UniGene) with exon hit	1.68
30	318853	Z42977	Hs.21062	ESTs	1.68
	323032	AW244073	Hs.145946	ESTs	1.68
	317538	AW137772	Hs.185980	ESTs	1.68
	325780			CH.14_hs gi 6381953	1.67
35	321739	AL080280		EST cluster (not in UniGene)	1.67
	319808	T58960		EST cluster (not in UniGene)	1.67
	313443	AA249037		EST cluster (not in UniGene)	1.67
	331366	AA424754	Hs.43149	ESTs	1.67
	316443	AI797592	Hs.207407	ESTs	1.67
40	322878	AA081820		EST cluster (not in UniGene)	1.67
	330320			CH.08_p2 gi 5932415	1.67
	329081			CH.X_hs gi 5868602	1.67
	334026			CH22_FGENES.318_3	1.67
	317791	AI801500	Hs.128457	ESTs	1.67
	322235	AF086106		EST cluster (not in UniGene)	1.66
45	331148	R73816	Hs.17385	ESTs	1.66
	325452			CH.12_hs gi 5866941	1.66
	315106	AW452184	Hs.232100	ESTs	1.66
	326014			CH.16_hs gi 5867160	1.66
	307130	AJ185234		EST singleton (not in UniGene) with exon hit	1.66
50	300943	AA524545	Hs.224630	ESTs	1.66
	319402	W21298		EST cluster (not in UniGene)	1.66
	310889	AI457946	Hs.170437	ESTs; Weakly similar to hyperpolarization-activated; cyclic nucleotide-gated channel 2 [H.sapiens]	1.66
	323371	AL135118		EST cluster (not in UniGene)	1.66
55	335568			CH22_FGENES.581_4	1.66
	320654	AW263086	Hs.118112	ESTs	1.66
	338983			CH22_DA59H18.GENSCAN.3-1	1.65
	330002			CH.16_p2 gi 6623963	1.65
60	315343	AW205477	Hs.179891	ESTs	1.65
	334487			CH22_FGENES.395_9	1.65
	312169	AI064824	Hs.193385	ESTs	1.65
	309668	AW204480	Hs.253414	EST	1.65
	309518	AW148928	Hs.248895	EST	1.65
	307965	AI421641		EST singleton (not in UniGene) with exon hit	1.65
65	316787	AW369770	Hs.130351	ESTs	1.65
	300835	AA401858	Hs.224843	ESTs	1.65
	338763			CH22_EM:AC005500.GENSCAN.517-16	1.65
	303327	AA232729	Hs.154302	ESTs	1.65
	313231	AW139993	Hs.163682	ESTs	1.65

	334073		CH22_FGENES.327_28	1.65
	319901 T77136	Hs.8765	RNA helicase-related protein	1.65
	326530		CH.19_hs gjl5867441	1.65
5	301126 AI802877	Hs.210843	ESTs; Weakly similar to dJ1039K5.2 [H.sapiens]	1.65
	314043 AA827082		EST cluster (not in UniGene)	1.65
	304387 AA236027		EST singleton (not in UniGene) with exon hit	1.65
	322932 AA099732		EST cluster (not in UniGene)	1.65
	337272		CH22_FGENES.660-1	1.64
10	332694 AA262768	Hs.243901	KIAA1067 protein	1.64
	318996 Z44266		EST cluster (not in UniGene)	1.64
	315336 AW342028	Hs.256112	ESTs	1.64
	313329 AW293704	Hs.122658	ESTs	1.64
	318088 AW295409	Hs.137945	ESTs	1.64
	313835 AI538438	Hs.159087	ESTs	1.64
15	320035 AA378974	Hs.130720	ESTs; Weakly similar to CELLULAR NUCLEIC ACID BINDING PROTEIN [H.sapiens]	1.64
	309372 AW074330		EST singleton (not in UniGene) with exon hit	1.63
	324157 AW402236		EST cluster (not in UniGene)	1.63
	323929 AA354940	Hs.145958	ESTs	1.63
	302490 AA885502	Hs.187032	ESTs	1.63
20	333942		CH22_FGENES.301_8	1.63
	327469		CH.02_hs gjl5867772	1.63
	301918 AAA76777		EST cluster (not in UniGene) with exon hit	1.63
	315664 AJ744068	Hs.160712	ESTs	1.63
25	304405 AA282572		EST singleton (not in UniGene) with exon hit	1.63
	310624 AI341594	Hs.157522	ESTs; Moderately similar to env protein [H.sapiens]	1.63
	319250 F11623		EST cluster (not in UniGene)	1.63
	310608 AI962234	Hs.196102	ESTs	1.63
	317348 AI348076	Hs.831	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	1.63
30	306513 AA989230		EST singleton (not in UniGene) with exon hit	1.63
	320807 AA086110	Hs.188536	Homo sapiens clone 24838 mRNA sequence	1.63
	303710 AI269069	Hs.250852	ESTs; Highly similar to ubiquitin hydrolyzing enzyme I [H.sapiens]	1.63
	328291		CH.07_hs gjl5868363	1.63
	304236 W93278		EST singleton (not in UniGene) with exon hit	1.63
35	317683 AI791700	Hs.127893	ESTs	1.63
	311960 AW440133	Hs.189690	ESTs	1.62
	312834 AI028309	Hs.114246	ESTs	1.62
	325326		CH.11_hs gjl5866875	1.62
	313663 AI953261	Hs.169813	ESTs	1.62
	327526		CH.02_hs gjl6381882	1.62
40	300429 AW449679	Hs.156739	ESTs; Highly similar to XG GLYCOPROTEIN PRECURSOR [H.sapiens]	1.62
	305169 AA663131		EST singleton (not in UniGene) with exon hit	1.62
	316621 AI021996	Hs.122138	ESTs	1.62
	329666		CH.14_p2 gjl6272129	1.62
	318035 AI744130	Hs.131201	ESTs	1.62
45	300492 AL031709		multiple UniGene matches	1.62
	316532 AJ307228	Hs.184304	ESTs	1.62
	332048 AA496019	Hs.201591	ESTs	1.62
	307113 AI183686		EST singleton (not in UniGene) with exon hit	1.62
	319127 N49476		EST cluster (not in UniGene)	1.62
50	331155 R87650	Hs.33439	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	1.61
	338220		CH22_EM:AC005500.GENSCAN.246-9	1.61
	315763 AW515270	Hs.118342	ESTs	1.61
	323571 AA984133	Hs.153260	c-Cbl-interacting protein	1.61
55	312240 R28628	Hs.203669	ESTs	1.61
	304569 AA480934		EST singleton (not in UniGene) with exon hit	1.61
	313179 AI076101	Hs.131704	ESTs	1.61
	326858		CH.20_hs gjl6552462	1.61
	317276 AI823847	Hs.129986	ESTs	1.61
	312572 AA350125	Hs.187499	ESTs	1.61
60	311832 AW451654	Hs.257482	ESTs	1.61
	302103 AA452310	Hs.26090	ESTs; Weakly similar to T20B12.1 [C.elegans]	1.61
	308413 AI636253	Hs.196511	EST	1.61
	310077 AI620617	Hs.148565	ESTs	1.61
65	337780		CH22_EM:AC000097.GENSCAN.121-2	1.61
	327796		CH.05_hs gjl5867982	1.61
	308352 AI610791		EST singleton (not in UniGene) with exon hit	1.61
	324539 AI378032	Hs.125892	ESTs	1.61
	303232 AA437414		EST cluster (not in UniGene) with exon hit	1.61
	337884		CH22_EM:AC005500.GENSCAN.54-2	1.61

	303620	AA397546	Hs.119151	ESTs	1.61
	303481	AA336839		EST cluster (not in UniGene) with exon hit	1.61
	314481	AA548589	Hs.105846	ESTs	1.61
	300327	AI908894	Hs.245893	ESTs	1.6
5	323473	AA262442		EST cluster (not in UniGene)	1.6
	326154			CH.17_hs gjl5867170	1.6
	331920	AA446885	Hs.99087	ESTs; Moderately similar to ZINC FINGER PROTEIN 141 [H.sapiens]	1.6
	323827	AW406878		EST cluster (not in UniGene)	1.6
	322452	W56710		EST cluster (not in UniGene)	1.6
10	310597	AI739071	Hs.158515	ESTs	1.6
	307871	AI368665		EST singleton (not in UniGene) with exon hit	1.6
	322215	AF088005		EST cluster (not in UniGene)	1.6
	318420	AI139857	Hs.143837	ESTs	1.6
	332217	H98987	Hs.102383	EST	1.6
15	324937	M79230	Hs.192398	ESTs	1.6
	320543	AF052176	Hs.158529	Homo sapiens clone 24457 mRNA sequence	1.6
	300674	AW467388		EST cluster (not in UniGene) with exon hit	1.6
	315193	AI241331	Hs.131765	ESTs	1.6
	319713	R24204		EST cluster (not in UniGene)	1.6
20	301210	AI379982	Hs.158944	ESTs	1.6
	309365	AW072861		EST singleton (not in UniGene) with exon hit	1.6
	321403	AW451454	Hs.247568	adenylate kinase 3	1.6
	321908	AA376936	Hs.20998	ESTs	1.6
	303349	AA382661		EST cluster (not in UniGene) with exon hit	1.6
25	324338	AL138357	Hs.247514	ESTs	1.6
	310599	AW300144		EST cluster (not in UniGene)	1.6
	333193			CH22_FGENES.98_15	1.6
	336433			CH22_FGENES.825_12	1.6
	312097	AI352096	Hs.157169	ESTs	1.6
30	311445	AW204237	Hs.192703	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	1.59
	317736	AI361722	Hs.192410	ESTs	1.59
	308147	AI498991		EST singleton (not in UniGene) with exon hit	1.59
	313489	AA017492	Hs.135655	ESTs	1.59
	316289	AA902488	Hs.122952	ESTs	1.59
35	326983			CH.21_hs gjl5867657	1.59
	314781	AW205298	Hs.202372	ESTs	1.59
	328397			CH.07_hs gjl5868397	1.59
	331970	AA461084	Hs.187677	ESTs	1.59
	321744	N91419	Hs.12028	ESTs	1.59
40	310509	AI292181	Hs.150036	ESTs	1.59
	315921	AI147545	Hs.114172	ESTs	1.59
	322049	AI928242	Hs.144383	ESTs	1.59
	301161	AA731518		EST cluster (not in UniGene) with exon hit	1.59
	300548	AI026836	Hs.114689	ESTs	1.59
45	319142	F07366		EST cluster (not in UniGene)	1.59
	313526	AW152263	Hs.249243	ESTs	1.59
	305937	AA883238		EST singleton (not in UniGene) with exon hit	1.58
	330123			CH.19_p2 gjl6671869	1.58
	327819			CH.05_hs gjl5867968	1.58
50	318250	AI478814	Hs.134603	ESTs	1.58
	306760	AI034094	Hs.169476	tubulin; alpha; ubiquitous	1.58
	322358	AA220235	Hs.246836	ESTs	1.58
	317866	AI690269	Hs.201345	ESTs	1.58
	320725	AA703319	Hs.120967	ESTs	1.58
55	311332	AW292247	Hs.255052	ESTs	1.58
	334893			CH22_FGENES.452_7	1.58
	318730	AA398215		EST cluster (not in UniGene)	1.58
	315889	AW271639	Hs.221744	ESTs	1.58
	303702	AW500748	Hs.224961	ESTs; Weakly similar to 73 kDA subunit of cleavage and polyadenylation specificity factor [H.sapiens]	1.57
60	315086	AI492660	Hs.170935	ESTs	1.57
	332514	AA156499	Hs.8454	protein kinase; cAMP-dependent; regulatory; type II; alpha	1.57
	335549			CH22_FGENES.576_10	1.57
	329532			CH.10_p2 gjl3983505	1.57
65	323140	AA180467		EST cluster (not in UniGene)	1.57
	313166	AI801098	Hs.151500	ESTs	1.57
	337896			CH22_EM:AC005500.GENSCAN.56-3	1.57
	330658	AA319514	Hs.211093	ESTs	1.57
	324585	AI823969	Hs.132678	ESTs	1.57

	317151	AW298195	Hs.255735	ESTs	1.57
	308818	AI819700	Hs.208231	EST	1.57
	326547		CH.19_hs	gij5867307	1.57
5	318833	H06234	Hs.24888	ESTs	1.57
	320488	R31386		EST cluster (not in UniGene)	1.57
	306929	AI124514		EST singleton (not in UniGene) with exon hit	1.57
	338083			CH22_EM:AC005500.GENSCAN.174-1	1.57
	316868	AI660898	Hs.195602	ESTs	1.57
10	310937	AI472880	Hs.170480	ESTs	1.57
	328638		CH.07_hs	gij6004473	1.57
	310074	AI651039	Hs.148559	ESTs	1.56
	327058		CH.21_hs	gij6531965	1.56
	320076	AI653733	Hs.204079	ESTs	1.56
	322345	AF086529		EST cluster (not in UniGene)	1.56
15	314731	AI745498	Hs.204579	ESTs	1.56
	318687	H49619	Hs.127301	ESTs	1.56
	303841	AI934464		EST cluster (not in UniGene) with exon hit	1.56
	302370	AJ009849	Hs.199297	Homo sapiens GNAS1 gene encoding NESP55	1.56
	322571	AF156271		EST cluster (not in UniGene)	1.56
20	318050	AI052093	Hs.133132	ESTs	1.56
	303388	AL039604		EST cluster (not in UniGene) with exon hit	1.56
	323758	AA833858		EST cluster (not in UniGene)	1.56
	328369		CH.07_hs	gij5868388	1.56
	329415		CH.Y_hs	gij5868874	1.56
25	303915	AW468839	Hs.257767	EST	1.56
	338794		CH22_EM:AC005500.GENSCAN.528-1		1.56
	303074	AA243481	Hs.127320	ESTs; Weakly similar to KIAA0346 [H.sapiens]	1.56
	318807	F08434		EST cluster (not in UniGene)	1.56
	334287		CH22_FGENES.369_17		1.56
30	311928	AW024798	Hs.233374	ESTs	1.55
	304592	AA505833	Hs.162017	EST	1.55
	300785	AA682913	Hs.247179	ESTs; Weakly similar to KIAA0319 [H.sapiens]	1.55
	304921	AA603092		EST singleton (not in UniGene) with exon hit	1.55
	324605	AW502851	Hs.249978	ESTs	1.55
35	324473	AW501163		EST cluster (not in UniGene)	1.55
	300566	H86709	Hs.21371	son of sevenless (Drosophila) homolog 1	1.55
	314165	AA761265	Hs.221281	ESTs	1.55
	302868	AA157392		EST cluster (not in UniGene) with exon hit	1.55
	314034	AI299137	Hs.154214	ESTs	1.55
40	325389		CH.12_hs	gij5866921	1.55
	331849	AA417078	Hs.193767	ESTs	1.55
	320536	AA331732	Hs.137224	ESTs	1.55
	303347	AA258033		EST cluster (not in UniGene) with exon hit	1.55
	315769	AA744875	Hs.189413	ESTs	1.55
45	317031	AA973297	Hs.126101	ESTs	1.55
	300203	AI827065	Hs.224877	ESTs	1.55
	304037	T26438		EST singleton (not in UniGene) with exon hit	1.55
	322613	AW160507		EST cluster (not in UniGene)	1.54
	317987	AW138174	Hs.130651	ESTs	1.54
50	322313	AF086386		EST cluster (not in UniGene)	1.54
	323992	AW411383	Hs.169688	ESTs	1.54
	325303		CH.11_hs	gij5866908	1.54
	312701	AI457663	Hs.128127	ESTs	1.54
	304787	AA582678		EST singleton (not in UniGene) with exon hit	1.54
55	305849	AA861571		EST singleton (not in UniGene) with exon hit	1.54
	314557	AA401367	Hs.128647	ESTs	1.54
	316507	AI381515	Hs.158381	ESTs	1.54
	315023	AA533505	Hs.185844	ESTs	1.54
	314920	AA513406	Hs.152307	ESTs	1.54
60	323097	Z44354	Hs.180950	guanine nucleotide binding protein (G protein); q polypeptide	1.54
	325043	W27919	Hs.32944	inositol polyphosphate-4-phosphatase; type I; 107kD	1.54
	307892	AI376086	Hs.158759	EST	1.54
	324573	AA491600	Hs.161942	ESTs	1.54
	313092	AI923673	Hs.212827	ESTs	1.54
65	324696	AA641092	Hs.257339	ESTs	1.54
	303019	AF098363		EST cluster (not in UniGene) with exon hit	1.54
	317158	AI459140	Hs.129109	ESTs	1.54
	309536	AW151933		EST singleton (not in UniGene) with exon hit	1.54
	301568	AI146423	Hs.146709	ESTs	1.53

	315674	AA651923	Hs.191850	ESTs	1.53
	321861	N79341		EST cluster (not in UniGene)	1.53
	310890	AI184510	Hs.143728	ESTs	1.53
5	330036			CH.17_p2 gjl6042048	1.53
	316907	AA843868	Hs.190567	ESTs	1.53
	312299	AA972712	Hs.174818	ESTs	1.53
	331128	R51361	Hs.23423	ESTs	1.53
	305177	AA663591		EST singleton (not in UniGene) with exon hit	1.53
10	337685			CH22_EM:AC000097.GENSCAN.77-1	1.53
	335290			CH22_FGENES.527_3	1.53
	308896	AI858667		EST singleton (not in UniGene) with exon hit	1.53
	307944	AI418246		EST singleton (not in UniGene) with exon hit	1.53
	300867	AW340374	Hs.121033	neural precursor cell expressed; developmentally down-regulated 1	1.53
15	335320			CH22_FGENES.534_7	1.53
	329841			CH.14_p2 gjl6672062	1.53
	317916	AI565071	Hs.159983	ESTs	1.53
	332901			CH22_FGENES.36_2	1.53
	305413	AA724659		EST singleton (not in UniGene) with exon hit	1.53
20	316707	AI016387	Hs.184406	ESTs	1.53
	313693	AW469180	Hs.170651	ESTs	1.53
	316101	AA922236	Hs.221037	ESTs	1.53
	320796	AF038966	Hs.184543	secretory carrier membrane protein 1	1.53
	307451	AI248615		EST singleton (not in UniGene) with exon hit	1.53
25	323648	AI679968	Hs.152060	ESTs	1.53
	331482	N27515	Hs.40296	ESTs	1.53
	318059	AI023175	Hs.167022	ESTs	1.53
	325958			CH.16_hs gjl5867142	1.53
	315736	AA664265	Hs.230213	ESTs	1.53
30	314740	AW015667	Hs.119427	ESTs	1.52
	314117	AA224368	Hs.185164	ESTs	1.52
	301646	AA313954		EST cluster (not in UniGene) with exon hit	1.52
	338752			CH22_EM:AC005500.GENSCAN.513-10	1.52
	309314	AW009312		EST singleton (not in UniGene) with exon hit	1.52
35	301445	AI208364	Hs.128233	ESTs; Weakly similar to REGULATOR OF CHROMOSOME CONDENSATION [H.sapiens]	1.52
	308501	AI685263	Hs.201150	EST	1.52
	312330	AA635305	Hs.121574	ESTs	1.52
	318040	AI018150	Hs.148781	ESTs	1.52
40	336205			CH22_FGENES.719_10	1.52
	325701			CH.14_hs gjl5867028	1.52
	315009	AW189460	Hs.208358	ESTs	1.52
	303121	AW407585	Hs.27769	ESTs; Weakly similar to mCAC [M.musculus]	1.52
	309271	AI986221		EST singleton (not in UniGene) with exon hit	1.52
45	328385			CH.07_hs gjl5868395	1.52
	307700	AI318545		EST singleton (not in UniGene) with exon hit	1.52
	314591	AW103292	Hs.245328	ESTs	1.52
	304484	AA432067	Hs.258373	ESTs	1.52
	304382	AA232873		EST singleton (not in UniGene) with exon hit	1.52
50	304232	W52674		EST singleton (not in UniGene) with exon hit	1.52
	309853	AW298169	Hs.57553	tousled-like kinase 2	1.52
	312504	AW207346	Hs.143202	ESTs	1.52
	313134	N63406	Hs.258697	ESTs	1.52
	330391	AF015950	Hs.115256	telomerase reverse transcriptase	1.52
55	314342	AI873046	Hs.258775	ESTs	1.51
	305977	AA887293		EST singleton (not in UniGene) with exon hit	1.51
	301165	N85789	Hs.224155	ESTs; Weakly similar to PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE [H.sapiens]	1.51
	300613	AI932294	Hs.249604	ESTs; Weakly similar to B-CELL LYMPHOMA 6 PROTEIN [H.sapiens]	1.51
60	324124	AI554212	Hs.185664	ESTs; Weakly similar to SERINE/THREONINE-PROTEIN KINASE NRK2 [H.sapiens]	1.51
	308037	AI458207	Hs.174181	ESTs	1.51
	323909	AI043148	Hs.186257	ESTs	1.51
	315464	AW139500	Hs.116135	ESTs	1.51
	306700	AI022056		EST singleton (not in UniGene) with exon hit	1.51
65	337976			CH22_EM:AC005500.GENSCAN.107-1	1.51
	306855	AI083982		EST singleton (not in UniGene) with exon hit	1.51
	311045	AI568399	Hs.174746	ESTs	1.51
	315010	AA531082	Hs.240049	ESTs	1.51
	310205	AW025248	Hs.202445	ESTs	1.51
	310759	AW135924	Hs.224883	ESTs	1.51

	310954	AW449044	Hs.171298	ESTs	1.51
	312019	T77046	Hs.188750	ESTs	1.51
	334773			CH22_FGENES.430_5	1.51
5	332043	AA490831	Hs.125058	ESTs	1.51
	322950	AA296219		EST cluster (not in UniGene)	1.51
	337920			CH22_EM:AC005500.GENSCAN.67-3	1.51
	328993			CH.09_hs gj5868538	1.51
	309245	AI972447		EST singleton (not in UniGene) with exon hit	1.51
10	312172	AI222168	Hs.191168	ESTs	1.51
	304039	T47349		EST singleton (not in UniGene) with exon hit	1.5
	301329	AI149653	Hs.190496	ESTs	1.5
	313376	AI949246	Hs.200381	ESTs	1.5
	324248	AW504918		EST cluster (not in UniGene)	1.5
15	308771	AI809301		EST singleton (not in UniGene) with exon hit	1.5
	334935			CH22_FGENES.464_3	1.5
	319764	AA019827		EST cluster (not in UniGene)	1.5
	318519	T27135		EST cluster (not in UniGene)	1.5
	332807			CH22_FGENES.7_9	1.5
20	322310	AF086376		EST cluster (not in UniGene)	1.5
	324557	AA489166	Hs.156933	ESTs	1.5
	332118	AA609585	Hs.162689	EST	1.5
	319539	R09027		EST cluster (not in UniGene)	1.5
	313149	AW291092	Hs.201058	ESTs	1.5
25	329722			CH.14_p2 gj6065785	1.5
	323514	AA861209		EST cluster (not in UniGene)	1.5
	308078	AI472621		EST singleton (not in UniGene) with exon hit	1.5
	337965			CH22_EM:AC005500.GENSCAN.100-10	1.5
	335905			CH22_FGENES.635_13	1.5

TABLE 14A shows the accession numbers for those primekeys lacking unigeneID's for Table 14. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
15	Pkey	CAT number	Accession
	322064	234514_1	BE261397 Z78343 BE176419 AA383657 N90640 AA334052 AW955761 BE536232 AA374087 AA584776
20	321409	197898_1	N71838 AA282003 T54072 AA761419 H92966 AI831371 AI095435 AI690247 R99331 AW964110 AA975590 AA346128 H94196 C03864
	322092	46678_1	AF085833 R69689 AW341677 AA923375 BE327566 AW630415 R69601 AW615339
	321452	212379_2	AW962489 H64300 AA329527
	313603	199797_1	AA284333 AW468119 AA284334 AA810992
25	320856	36098_1	AB040928 T94673 AI289313 AI536039 Z44366 BE141499 D60116 D61488 D59945 AA419503 R28090 R72986 H03255 AI189112 AI912312 AW511018 AI401349 AW470144 C14624 AI335797 Z40300 AI014456 D60269 D60115 T16722 AI370673 D60270
	322139	46806_1	H53744 AF075088 H53797
	321500	552826_1	BE004271 AI248023 AI022157 H71999
30	313733	441212_1	AA766346 AA809877 AA836116 AW469598 AW977404
	322215	47002_1	AF088005 N51816 N51731
	322235	47070_1	AF086106 AI193589 AW665594 N71795 AA722627 AW665373 AI300251
	321632	286374_1	AW812795 AA419617 H87827 AW299775 AW382168 AW382133 BE171659 AW392392 BE171641 AA541393
	313833	120893_1	AA766825 AA811180 AA085906 AI762946 AW977820
35	322310	47376_1	AF086376 W77804 W72689 AA837735
	322313	47386_1	AF086386 W77947 W72708
	322322	47434_1	AF086431 AA886756 AI557237
	322331	47467_1	AF086467 W81444 W81445
	322345	47537_1	W95298 AF086529 AI912180 AW294159 AI458747 W94782
	322347	47545_1	AF086538 W95969 AI631911 W95835
40	322370	187612_1	AA330095 W25112 AA249401
	321739	43998_1	AL080280 T73124 H02689 AL080281
	321781	1511778_1	D78667 D78871 C18258
	314570	280469_1	AA904776 AA405696 AA405962
45	300129	635249_1	AW028820 AI219068
	322452	497108_2	AI147202 W56755 W56710
	321861	1651920_1	N79341 N99082 N47551
	323140	159551_1	AA180467 AA449184 AA464831 AA505048
	322520	38916_1	T55958 T57205 AF147346
50	321914	85114_1	AA011603 N58604 N58611
	322571	22297_1	NM_016102 AF156271 AA781868 AW152318 AW770403 AA909463 AA482996 AA758672
	322574	39412_1	AF156548 AA639797 AI675267 AI825497 AI823355
	314753	311451_1	AA463262 AA463615 AW160405 AW407583
	300370	3910_2	AW136181 AA581939 AK001221 AA694538 AA424043 AI016272 AA098960 AA884473 AI356180 BE391633 AA437086 AI277866 AA098827 AA992680 BE172624 AA424101 AA320776 AW962967 N77431 AW858960 AW858897 T85649 AA357743 AI827817 AI905672
55	322601	577912_1	AI082395 W92924 BE048524 AW005302 AI084474 AI369330 AI827710 AW135506 AW298694
	322613	34330_1	AW160507 NM_013367 AF191338 AA384939 AI445790 AA730309 BE397003 BE267753 AI979163 N50386 AW583671 AW583608 BE074466 BE074479 BE074471 AW976283 AA604393 AW162122 W73648 AI823475 N75898 W73713 AW470099 AW513236 AW025055 AW613115 AI923379 W58081 AW664525 AW196795 AI143619 AI565152 AA025406 AA505846 AI685494 AA829964 N59156 N59163 R15442 AA826919 AI610221 AI200120 AA603279 AW150822 AI189513 AI807122 AI016368 AI335868 AW583389 AI193892 AI956157 AI628879 AW591589 AW583446 AI955406 AW148396 AI340255 AI867942 AA748525 AA876991 Z38516 AI874002 AI869474 N63100 AA429094 AA082443 AW105663 AA693880 AW517398 AI768507 BE220851 AW978538 AA831489 BE219300 BE327455 AL134620 R36741 R17996 AL031709 AI249061 AA907658 AI420444
60	316055	409389_1	
	323316	981458_1	
	300492	25768_1	
65			

316141	423880_2	AW303457 AA972713 AA724265
323371	117336_2	N45114 N51465 BE087338 AI083551 AL135118 BE395609
307700	30923_11	BE280998 BE254670 BE294951 BE564979 AW405364 AA069256 AA129837 AI559667 BE281405 AW410850 BE041153
5		AI254811 AW301340 AI613335 AW301411 AI609469 AI611607 AI611616 AI377623 AI335509 AI613544 BE043165 AI371663
		AI340452 AI612066 AW072890 AI254558 AI349884 AI370095 AI613383 AI611946 AI613353 AI307414 AI318229 AI612685
		AW305327 AW268924 AI370063 AI349292 BE049068 AI369098 AW274098 AI344845 AW075187 AI053401 AI345220
		BE138515 AI613386 AI583302 AW301955 AI349661 AI307432 AI054168 AI223913 AI612081 AI348942 AI334539 AI309366
		AI370098 AI252360 AW086316 AW268911 AW073482 AI379802 AI224284 AI053661 AI334538 AI309369 AI309588 AI310023
10		AI492709 AI335418 AI053999 AI366989 AW073478 AI247058 AI249584 AI305875 AI308585 AW071272 AI271487 AI340719
		AI366995 AI223673 AW271066 AI611936 AW071296 AI270796 AI254385 AI251393 AI252562 AW268236 AI254858
		AW071317 AI309102 AI609897 AW268971 AI583267 AI792484 AW075168 BE138443 AI254126 AI309822 AI310872
		AI611953 AI251054 AW276658 AI335405 AW075039 AI311768 AI612028 AW271895 AI612005 AI312240 AW271082
		AI371642 AI334879 AI310194 AI310772 AI345419 AI334675 AI223914 AI284707 AI284813 AI349140 AI254853 AI313094
15		AI310170 AI309499 AI312476 AI376484 AI335467 AI340802 AI309815 AI310168 AI611446 AI345824 BE327775 AI318545
		F17185 AW614950
	308362 792518_1	AW998989 AI613519
	307783 697809_1	AI347274 AW844024
	301161 427238_1	AA731518 AA765714
	324094 270098_1	BE395109 AW663898 AW237041 AI492154 BE046906 AI651285 AI983290 AW002590 AI201040 F32424 AA992272
20		AW271836
	309023 4737_1	AF180681 NM_015313 AA229509 AA225792 AA216413 AI888045 BE005205 AB002380 T55518 BE276097 AW380669
		BE142836 AW370976 AA479384 R96425 AI680999 AA595138 H54582 AI022709 T55440 AI041769 AA861144 AW392028
25		AA479287 AA824634 AI638446 H54691 R96382 AA770352 AI640467 AW293491 AA779138 R28298 AA970562 C15590
		R84455 AA020769 AL036394 H05566 BE548861 AA301207 AW959414 AI284253 AA043173 W52429 BE544571 R24852
		Z42603 F13120 R24340 R24326 T75305 H70110 N56255 AA334210 F11453 AW947285 H80345 AA298992 AW380931
		AI267175 Z45421 AW380981 W86113 AA663590 AA167577 BE566760 BE169166 AA449904 AA459205 N31126 W03564
		N31208 AW993277 N44765 AW605275 D61449 W68572 AA258190 D60496 AW992964 U46277 H04097 AA370360
		AW957211 AA159775 AI631243 H83367 H21671 D61077 AW392712 N21112 H98522 N45298 N83629 AI393509 AW022043
30		AA744886 AI580482 AA723286 AI22244 AI23984 D62804 AI088349 AA587890 AI144172 N33275 BE074397 H03399
		D62578 AI056639 AI829918 AA579584 AI089460 AI350124 W68573 AI580828 H98897 AI570468 H83715 W86114 AA923123
		D57446 AA043174 AW337721 AI266551 AI140017 AW022356 D79855 D79650 D79393 D60495 AA788666 AA693443
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	309815	AW292760
	309839	AW296076
30	309849	AW297444
	309906	AW339340
	302705 31765_1	U09060 U09061
	304037	T26438
	304039	T47349
35	304236	W93278
	304257	AA053294
	304382	AA232873
	304405	AA282572
	304561	AA489792
40	304569	AA490934
	304787	AA582678
	304921	AA603092
	327819 c_5_hs	
	304968	AA614308
	306382	AA968967
45	331263 47479_1	AW780192 AA015718 W02571
	332252 1663967_1	N63882 T91174

TABLE 14B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 14. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
15	332807	Dunham, I. et al.	Plus	297686-297808
	332808	Dunham, I. et al.	Plus	298277-298360
	332812	Dunham, I. et al.	Plus	309688-310561
20	332901	Dunham, I. et al.	Plus	1841954-1842090
	333149	Dunham, I. et al.	Plus	3574317-3574413
	333916	Dunham, I. et al.	Plus	8298994-8299169
	334026	Dunham, I. et al.	Plus	9196549-9196681
	334061	Dunham, I. et al.	Plus	9686941-9687077
	334073	Dunham, I. et al.	Plus	9792201-9792374
25	334150	Dunham, I. et al.	Plus	10529221-10529854
	334379	Dunham, I. et al.	Plus	13908356-13908467
	334719	Dunham, I. et al.	Plus	15778859-15779026
	334773	Dunham, I. et al.	Plus	16235169-16235328
	334893	Dunham, I. et al.	Plus	19302753-19302881
30	334935	Dunham, I. et al.	Plus	20108247-20108373
	335146	Dunham, I. et al.	Plus	21491292-21491457
	335320	Dunham, I. et al.	Plus	22542132-22542246
	335568	Dunham, I. et al.	Plus	24935021-24935655
	335586	Dunham, I. et al.	Plus	24990333-24990497
35	335601	Dunham, I. et al.	Plus	25044923-25045157
	336036	Dunham, I. et al.	Plus	29019796-29019877
	336123	Dunham, I. et al.	Plus	30051089-30051186
	336268	Dunham, I. et al.	Plus	31997555-31998040
	337173	Dunham, I. et al.	Plus	23624127-23624224
40	337460	Dunham, I. et al.	Plus	32536159-32536395
	337685	Dunham, I. et al.	Plus	3547161-3547245
	337736	Dunham, I. et al.	Plus	3850500-3850643
	337780	Dunham, I. et al.	Plus	4113793-4113990
	337965	Dunham, I. et al.	Plus	7034267-7034392
45	337976	Dunham, I. et al.	Plus	7166011-7166119
	338030	Dunham, I. et al.	Plus	8072708-8072827
	338112	Dunham, I. et al.	Plus	10391398-10391600
	338165	Dunham, I. et al.	Plus	12205719-12205875
	338178	Dunham, I. et al.	Plus	12800037-12800181
50	338427	Dunham, I. et al.	Plus	19685043-19685354
	338506	Dunham, I. et al.	Plus	21221871-21221953
	338794	Dunham, I. et al.	Plus	27114697-27114763
	338910	Dunham, I. et al.	Plus	28795375-28795551
	339047	Dunham, I. et al.	Plus	30760793-30760968
55	332864	Dunham, I. et al.	Minus	1390386-1390296
	332933	Dunham, I. et al.	Minus	2035790-2035681
	333193	Dunham, I. et al.	Minus	3832993-3832494
	333712	Dunham, I. et al.	Minus	7286177-7286073
	333940	Dunham, I. et al.	Minus	8523830-8523671
60	333942	Dunham, I. et al.	Minus	8552629-8552330
	334287	Dunham, I. et al.	Minus	13294116-13293871
	334387	Dunham, I. et al.	Minus	13946021-13945781
	334487	Dunham, I. et al.	Minus	14432191-14432132
	334913	Dunham, I. et al.	Minus	19463909-19463815
65	335109	Dunham, I. et al.	Minus	21325792-21325667
	335250	Dunham, I. et al.	Minus	21952922-21952826

	335288	Dunham, I. et.al.	Minus	22304275-22303770
	335290	Dunham, I. et.al.	Minus	22309950-22309891
	335549	Dunham, I. et.al.	Minus	24666203-24666128
5	335862	Dunham, I. et.al.	Minus	26690300-26690125
	335864	Dunham, I. et.al.	Minus	26694537-26694382
	335905	Dunham, I. et.al.	Minus	26988888-26988719
	336205	Dunham, I. et.al.	Minus	30477456-30477311
	336276	Dunham, I. et.al.	Minus	32093320-32093181
10	336433	Dunham, I. et.al.	Minus	34067540-34067425
	336605	Dunham, I. et.al.	Minus	15616509-15616358
	336616	Dunham, I. et.al.	Minus	26021027-26020848
	336679	Dunham, I. et.al.	Minus	2035790-2035681
	337043	Dunham, I. et.al.	Minus	17407330-17407251
15	337272	Dunham, I. et.al.	Minus	28241476-28241307
	337357	Dunham, I. et.al.	Minus	30906179-30906109
	337393	Dunham, I. et.al.	Minus	31471747-31471569
	337497	Dunham, I. et.al.	Minus	33371317-33371258
	337646	Dunham, I. et.al.	Minus	2648689-2648632
20	337920	Dunham, I. et.al.	Minus	6051648-6051510
	338083	Dunham, I. et.al.	Minus	9318438-9318301
	338220	Dunham, I. et.al.	Minus	14166440-14166104
	338752	Dunham, I. et.al.	Minus	26421374-26421135
	338763	Dunham, I. et.al.	Minus	26628148-26628009
25	338983	Dunham, I. et.al.	Minus	29908865-29908702
	339209	Dunham, I. et.al.	Minus	32492953-32492593
	325240	5866848	Minus	32301-32650
	329532	3983505	Plus	42937-43014
	329522	3983507	Minus	35265-35458
30	329519	3983510	Plus	18407-18597
	329511	3983514	Plus	20965-21325
	325326	5866875	Plus	47726-48024
	325303	5866908	Minus	73556-73630
	325389	5866921	Plus	239672-239759
35	325417	5866925	Minus	110635-110745
	325450	5866941	Minus	435379-435552
	325452	5866941	Minus	704103-704202
	325498	5866967	Plus	173372-173930
	325587	6682462	Plus	126724-126967
40	325602	5866994	Plus	79122-79251
	325701	5867028	Minus	72936-73046
	325780	6381953	Plus	63634-63873
	329722	6065785	Minus	112713-112992
	329728	6065785	Minus	207544-207741
45	329666	6272129	Plus	98307-98446
	329815	6624888	Minus	68431-68720
	329841	6672062	Minus	40181-40331
	325824	5867048	Minus	42450-42833
	325866	5867076	Minus	94358-94628
50	325902	5867101	Minus	127729-127842
	325958	5867142	Plus	53437-53550
	326014	5867160	Minus	10358-10447
	329941	6165199	Minus	34319-34411
	330002	6623983	Plus	46097-46158
55	326154	5867170	Minus	7103-7179
	326023	5867245	Plus	171799-171896
	326278	5867269	Plus	75250-75903
	330036	6042048	Plus	117120-117216
	326547	5867307	Minus	623677-623870
60	326495	5867423	Plus	11843-11930
	326507	5867435	Minus	13038-13111
	326505	5867435	Minus	8818-8949
	326506	5867435	Minus	9368-9509
	326530	5867441	Minus	303000-303122
	326508	6682496	Plus	78904-79112
65	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
	326858	6552462	Minus	69337-69670
	326983	5867657	Minus	16023-16581
	327014	5867664	Plus	1017630-1017788

	326930	6456782	Plus	606950-607705
	326920	6456782	Minus	42425-42519
	327058	6531965	Plus	2384268-2384835
5	327061	6531965	Minus	3486389-3486673
	327075	6531965	Plus	4041318-4041431
	327120	6531970	Minus	6-1088
	330126	6093735	Plus	82458-82623
	327157	5866841	Minus	4408-4746
10	327183	5867442	Plus	84317-84531
	327192	5867445	Minus	194652-194764
	327288	5867481	Plus	48583-48773
	327469	5867772	Plus	145549-145708
	327489	6004459	Minus	57796-58015
15	327526	6381882	Minus	97010-97123
	327574	5867818	Plus	68767-69126
	327665	5867839	Plus	141736-141900
	327752	5867949	Plus	93721-94421
	327819	5867968	Minus	92202-92717
20	327796	5867982	Plus	85267-85405
	330260	6671884	Plus	45203-45269
	330282	6671910	Plus	3982-4114
	328078	5868008	Plus	72807-72865
	328121	5868031	Plus	153782-153850
25	328190	5868077	Plus	21082-21165
	328227	5868105	Minus	21082-21242
	327871	5868131	Minus	88889-89221
	328018	5902482	Minus	542547-543133
	328624	5868246	Minus	120666-120836
	328744	5868290	Plus	138639-138722
30	328799	5868316	Minus	80771-80923
	328291	5868363	Minus	144244-144434
	328329	5868375	Plus	191709-192239
	328369	5868388	Plus	75371-75583
35	328385	5868395	Plus	369952-370155
	328397	5868397	Plus	344967-345063
	328412	5868405	Plus	86427-86519
	328538	5868485	Plus	3814-4243
	328656	6004473	Plus	792616-792729
40	328638	6004473	Plus	294618-294903
	328903	5868514	Plus	23625-24468
	328960	6456775	Plus	38547-38837
	330320	5932415	Minus	54458-54697
	328993	5868536	Plus	49160-50084
45	329081	5868602	Plus	93368-93510
	329089	5868614	Plus	25805-26923
	329109	5868626	Plus	102168-102273
	329192	5868716	Plus	166936-167020
	329218	5868726	Minus	71408-71707
50	329224	5868728	Plus	27422-27664
	329246	5868732	Minus	250541-250792
	329415	5868874	Plus	1011438-1011818
	329454	5868887	Plus	51342-51593

TABLE 15: 169 GENES WITH SEQUENCE INFORMATION DEPICTED IN TABLE 16

Table 15 depicts UnigeneID, UnigeneTitle, Primekey, Predicted Cellular Localization, and Exemplar Accession for all of the sequences in Table 16. The information in Table 15 is linked by EosCode to Table 16.

	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
10	Unigene Title:	Unigene gene title				
	EosCode:	Internal Eos name				
	Localization:	Predicted cellular localization of gene product				
<hr/>						
15	Pkey	ExAccn	UnigeneID	Unigene Title	EosCode	Localization
	100394	D84276	Hs.66052	CD38 antigen (p45)	PBC1	plasma membrane
	100452	D87742	Hs.241552	KIAA0268 protein	PAB7	not determined
	101249	L33881	Hs.1904	protein kinase C, ι iso	OAA1	cytoplasmic
20	101485	M24736		selectin E (endothelial adhesion molecule)	ACC5	plasma membrane
	101514	M28214	Hs.123072	RAB3B, member RAS oncogene family	PFJ2	cytoplasmic
	101851	M94250	Hs.82045	midkine (neurite growth-promoting factor)	LBH9	secreted
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	PDG3	
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	PFJ4	plasma membrane
25	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	LEM9	cytoplasmic
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	LBG2	plasma membrane
	103709	AA037316	Hs.13804	hypothetical protein dJ462O23.2	PDO6	
	104080	AA402971	Hs.57771	kallikrein 11	PBA6	secreted
	104144	AA447439	Hs.183390	hypothetical protein FLJ13590	PDM3	
30	104691	AA011176	Hs.37744	Homo sapiens beta-1 adrenergic receptor	PAV1	plasma membrane
	105370	AA236476	Hs.22791	transmembrane protein with EGF-like and	PDM9	plasma membrane
	106149	AA424881	Hs.256301	hypothetical protein MGC13170	PDO8	
	106579	AA456135	Hs.23023	ESTs	PAA4	plasma membrane
	107102	AA609723	Hs.30652	KIAA1344 protein	PAA3	not determined
35	107217	D51095		DKFZP586E1621 protein	PDG8	
	108153	AA054237	Hs.40808	ESTs	PBF1	plasma membrane
	109014	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	PDG7	
	109112	AA169379	Hs.257924	hypothetical protein FLJ13782	BCU4	not determined
	109890	H04649	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	PDG4	
40	110151	H18836	Hs.31608	hypothetical protein FLJ20041	PAV9	plasma membrane
	112971	T17185	Hs.83883	transmembrane, prostate androgen induced	CHA1	not determined
	113021	T23855	Hs.129836	KIAA1028 protein	PDO3	
	114908	AA236545	Hs.54973	cadherin-like protein VR20	PFJ6	plasma membrane
	114965	AA250737	Hs.72472	ESTs	BCY2	mitochondrial
45	116393	AA599463		hypothetical protein MGC2648	PDV3	secreted
	116416	AA609219	Hs.39982	ESTs	OAB6	
	117698	N41002	Hs.45107	ESTs	PDT9	ER
	117984	N51919	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	PAJ5	not determined
	118985	N94303	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	PDM8	
50	119018	N95796	Hs.278695	Homo sapiens prostate mRNA, complete cds		-PAB2 plasma membrane
	119126	R45175	Hs.117183	ESTs	PBF8	
	120992	AA398246	Hs.97594	KIAA1210 protein	PDG5	
	121710	AA419011		prostate androgen-regulated transcript 1	PDV5	
	121913	AA428062		ESTs; protease inhibitor 15 (PI15)	BCU7	vesicular
55	122041	AA431407	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT		PAZ1 not determined
	122593	AA453310	Hs.128749	alpha-methylacyl-CoA racemase	PDO1	
	123209	AA489711	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S		PAA2 plasma membrane
	124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	PAV4	plasma membrane
	126399	AA128075		transmembrane, prostate androgen induced	PDY4	
60	126645	AJ167942	Hs.61635	six transmembrane epithelial antigen of	PAA5	plasma membrane
	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	PDO5	plasma membrane
	127537	AA569531	Hs.162859	ESTs	PAA6	not determined
	128790	AA291725	Hs.105700	secreted frizzled-related protein 4	BCX2	secreted
	129109	AA491295	Hs.108708	calcium/calmodulin-dependent protein kin	PFJ7	
65	129184	W26769	Hs.109201	CGI-86 protein	PAV6	vesicular
	129389	AA621604		spondin 2, extracellular matrix protein	CJA5	not determined

	129404	AA172056	ESTs	PAB4	
	129534	R73640	Hs.11260 hypothetical protein FLJ11264	PAJ3	secreted
	130760	AA128997	Hs.18953 phosphodiesterase 9A	PEE6	nuclear
	131425	AA219134	Hs.26691 ESTs	PBA7	
5	132964	AA031360	ESTs	PAA7	plasma membrane
	132967	AA032221	Hs.61635 six transmembrane epithelial antigen of	PM17	plasma membrane
	133179	U81599	Hs.66731 homeo box B13	PFJ5	nuclear
	133330	U42360	Hs.71119 Putative prostate cancer tumor suppressor	PDM1	plasma membrane
	133520	X74331	Hs.74519 primase, polypeptide 2A (58kD)	PDM2	
10	133724	U07919	Hs.75746 aldehyde dehydrogenase 1 family, member		PDT1 mitochondrial
	133724	U07919	Hs.75746 aldehyde dehydrogenase 1 family, member		PDT1 mitochondrial
	133944	AA045870	Hs.7780 Homo sapiens mRNA; cDNA DKFZp564A072 (fr		PAB9 cytoplasmic
	134110	U41060	Hs.79136 LIV-1 protein, estrogen regulated	BCR4	plasma membrane
	301805	AI800004	Hs.142846 hypothetical protein	PEU4	nuclear
15	302005	AI869666	Hs.123119 MAD (mothers against decapentaplegic, Dr	PBJ6	cytoplasmic
	302881	AA508353	Hs.105314 relaxin 1 (H1)	PBH3	secreted
	303506	AA340605	Hs.105887 ESTs, Weakly similar to Homolog of rat Z	PEG4	
	303699	D30891	Hs.19525 hypothetical protein FLJ22794	PBM4	not determined
	303753	AW503733	Hs.9414 KIAA1488 protein	PBY3	not determined
20	308050	AI460004	Hs.31608 hypothetical protein FLJ20041	PEU5	plasma membrane
	310382	AI734009	Hs.127699 KIAA1603 protein	PCQ8	
	310431	AI420227	Hs.149358 ESTs, Weakly similar to A46010 X-linked	PBH1	plasma membrane
	310573	AW292180	Hs.156142 ESTs	PEN3	plasma membrane
	310598	AI338013	Hs.140546 ESTs	PCW3	
25	310816	AI973051	Hs.224965 ESTs	PET5	
	311596	AI682088	Hs.79375 holocarboxylase synthetase (biotin-prop	PBH8	
	313676	AA861697	Hs.120591 ESTs	PBY2	
	314121	AI732100	Hs.187619 ESTs	PBY1	
	314691	AW207206	Hs.136319 ESTs	BFF8	not determined
30	314785	AI538226	Hs.32976 guanine nucleotide binding protein 4	CB07	cytoplasmic
	314907	AI672225	Hs.222886 ESTs, Weakly similar to TRHY_HUMAN TRICH	PBM2	not determined
	315051	AW292425	ESTs	PBM9	
	315052	AA876910	Hs.134427 ESTs	PBJ7	plasma membrane
	316442	AA760894	Hs.153023 ESTs	PBJ9	
35	317548	AI654187	Hs.195704 ESTs	PBQ6	
	317869	AW295184	Hs.129142 deoxyribonuclease II beta	PBQ7	
	318524	AW291511	Hs.159066 hypothetical protein FLJ10188	PBJ1	cytoplasmic
	319191	AF071538	prostate epithelium-specific Els transcr	PEN1	
	319763	AA460775	Hs.6295 ESTs, Weakly similar to T17248 hypotheti	PEO7	
40	320324	AF071202	Hs.139336 ATP-binding cassette, sub-family C (CFTR	PBH5	plasma membrane
	320561	NM_006953	Hs.159330 uroplakin 3	PEL9	plasma membrane
	320796	AF038966	Hs.31218 secretory carrier membrane protein 1	PBY4	not determined
	321441	AW297633	Hs.118498 Homo sapiens LUCA-15 protein mRNA, splic	PBY8	not determined
	322303	W07459	Hs.157601 ESTs	CBF9	secreted
45	322782	AA056060	Hs.202577 Homo sapiens cDNA FLJ12166 fis, clone MA	PCQ7	PBQ1 not determined
	322818	AW043782	Hs.293616 ESTs		plasma membrane
	323226	AF055019	Hs.21906 Homo sapiens clone 24670 mRNA sequence		PCI2 not determined
	323287	AA639902	Hs.104215 ESTs, Moderately similar to SPCN_HUMAN S		PBJ5
	324295	AI146686	Hs.143691 ESTs	PBQ9	not determined
50	324430	AA464018	Hs.184598 Homo sapiens cDNA: FLJ23241 fis, clone C		PBY6 not determined
	324603	AW016378	Hs.292934 ESTs	PBM3	
	324617	AA508552	Hs.195839 ESTs, Weakly similar to I38022 hypotheti	PBH4	cytoplasmic
	324626	AI685464	gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	PCW6	
	324658	AI694767	Hs.129179 Homo sapiens cDNA FLJ13581 fis, clone PL	PBJ4	plasma membrane
55	324718	AI557019	Hs.116467 small nuclear protein PRAC	CBK1	nuclear
	330211			PBJ2	not determined
	330546	U31382	Hs.299867 guanine nucleotide binding protein 4	PEW1	cytoplasmic
	330762	AA449677	Hs.15251 hypothetical protein	PBW1	not determined
	330790	T48536	Hs.122764 TMPRSS2, transmembrane protease, serine		PEL3 plasma membrane
60	330892	AA149579	Hs.91202 ESTs	PBQ4	plasma membrane
	331099	R36671	Hs.14846 Homo sapiens mRNA; cDNA DKFZp564D016 (fr		PCQ1 cytoplasmic
	331490	N32912	Hs.291039 ESTs	PCI4	nuclear
	331889	AA431407	Hs.98802 ESTs, Moderately similar to T14342 NSD1	PBH7	not determined
	332247	N58172	gb:za21f09.s1 Soares fetal liver spleen	PBQ5	nuclear
65	332396	AA340504	gb:hw31a09.x1 NCI_CGAP_Kid11 Homo sapien		PBJ8 not determined
	332697	T94885	transgelin 2	PBQ8	secreted
	332798			PBH2	nuclear
	334447			PBY9	not determined
	338255			PBY7	not determined

	401424			PFG2	mitochondrial
	407122	H20276	Hs.31742	ESTs	PEW7
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	PEZ3
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	PEY1
5	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	PFG1
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog	PEW3
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	PEZ9
	413125	BE244589	Hs.75207	glyoxalase I	PFJ3
	413623	AA825721	Hs.246973	ESTs	OBH6
10	414422	AA147224	Hs.337232	Homeo box A13	PFC6
	415263	AA948033	Hs.130853	ESTs	PEZ5
	417153	X57010	Hs.81343	*collagen, type II, alpha 1 (primary ost	PFJ1
	418601	AA279490	Hs.86368	calmegin	PFA1
	418848	AI820961	Hs.193465	ESTs	PEY4
15	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	OBH2
	419839	U24577	Hs.93304	*phospholipase A2, group VII (platelet-a	PFH9
	421887	AW161450	Hs.109201	CGI-86 protein	PFH2
	422083	NM_001141	Hs.111256	*arachidonate 15-lipoxygenase, second ty	PFH5
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	PFA3
20	425071	NM_013989	Hs.154424	*delodinsase, iodothyronine, type II"	PFH6
	425710	AF030880		solute carrier family, member 4	PFH4
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	PFH1
	428819	AL135623	Hs.193914	KIAA0575 gene product	PFH6
	429900	AA460421	Hs.30875	ESTs	PEZ7
25	429918	AW873986	Hs.119383	ESTs	PEY5
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	PEZ4
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	PFG6
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	PEZ1
	431992	NM_002742	Hs.2891	protein kinase C, mu	PFH4
30	432189	AA527841		gb:nh30cd4.s1 NCL_CGAP_Pr3 Homo sapiens	PFA2
	432244	AI669973	Hs.200574	ESTs	PEW8
	432437	W07088	Hs.293685	ESTs	PFG3
	432966	AA650114	Hs.325198	ESTs	PEY3
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B26096 line-1 pr	PEW5
35	440260	AI972867	Hs.7130	copine IV	PEW6
	440901	AA909358	Hs.128612	ESTs	PFC8
	445424	AB028945		cortactin SH3 domain-binding protein	PEZ6
	446320	AF126245	Hs.14791	*acyl-Coenzyme A dehydrogenase family, m	PFH7
	447210	AF035269		phosphatidylserine-specific phospholipas	PFH8
40	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding OD	PEZ8
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	PEZ2
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	PFH2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	PFJ8
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	PFG9
45	452039	AI922988		ESTs	PFH8
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	PFG4
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	PFC5
	452946	X95425	Hs.31092	EphA5	PFH3

TABLE 15A shows the accession numbers for those primekeys lacking a unigeneID in Table 15. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
116393	131543_1	AI972402 AI634409 AI523716 AI799749 W44518 AI424438 AI688513 AI971048 AI686324 AW013854 AA588483 AA528111 AI627428 AI582200 AI669296 AI826926 AI620526 AI669958 AI972458 AI924500 AA512903 W44517 AA335363 AW238997 BE300165 BE250665 AA284195 AA523420 W52834 AI471970 AI952824 AW003820 AW009463 AA669796 AA114966 AI653342 AA115038 AI342150 AI092100 AI968211 W51994 AI804005 AI201420 AI123210 AI738405 AI674964 AI970341 AW027500 AI493316 AI333193 AI139353 AA599463 AI656163 AI804200 AI365321 AI990213 AI657011 AA650025 AI968810 AI341978 AA599839 AW592602 AA644289 AI468578 AI565265 AI565228 BE221535 AW973052 AA296520 AL021940 M30640 NM_000450 M24736 M61894 AL047443 H39560 AI694691 AA916787 AI214796 AA939085 AI150616 AA412553 AA412545 AI051015 T27654 AA694430 AA088767 AF224278 AA128075 AL035541 AA027926 AI761441 AI972096 AW071693 AI742327 AI377498 AI804815 AI640802 AI885001 AI921394 AA595115 N71820 AI921217 AW007283 AI467828 AI369306 AA917446 AI493698 AA088701 AA126899 AI936228 AW204238 AI039567 AI925027 BE138909 AW452945 AW135998 AA310984 AA027860 AW073519 AI537597 AA953976 AI521341 AW273569 AW050740 AA536113 AA559064 AI474392 AW135709 AA535181 AW572959 AA570597 AI905464 AI677810 AI587642 AW975102 AA424310 AA482527 N64192 AA658276 AW889117 AA486591 AW889172 AI381990 AI381991 AI673419 AI990950 AA487031 AI272934 AI150565 AA229168 AW316722 AI142707 BE222396 AA614168 AA122026 AW338227 AA632457 AI968726 AW369662 AA512956 AA541675 AA451748 AI250993 BE146418 AA122025 AI362575 AI805082 AW263421 AI432462 AA135870 AA031360 AA031604 AA298475 AA298464 NM_012445 AB027466 BE407510 BE047605 AA047125 AW084003 AA149494 AA149490 AA292528 AA570505 AA526186 AW006250 AW007762 AI341557 AI799666 AI972710 AI377966 AI962810 AI084783 AI458032 AI190971 AW148913 AA372354 AW970032 AW007426 AA650188 AI123203 AI122890 AI280975 W73595 W73495 AI863238 AA374109 AA603986 AW149089 AW957523 AI307748 AI921067 AI336463 F24537 AI380460 AI367500 AI189309 AI814701 AI766921 AW572106 AA037024 AW072576 AA578293 AI288103 AA235464 AW450642 AA574230 AW294024 AI589229 AI580733 AW512227 AA877009 AI660255 AW188597 AA558228 AI572782 AA658397 AI274628 AI866359 AA864573 AI264439 AA621604 AW515493 AW243333 Z39737 AI567038 AA573997 AA573559 AW236431 AI652870 AI684973 AA034505 AA047126 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172238 AW953397 AA355086 AL080235 AA031750 D81382 AI480231 AI095947 AI560953 BE010721 AI870290 AA374945 AA125792 D51527 D51556 AI685541 D51559 AW117286 AA195741 AI675138 AW593439 AI201885 T30590 AW952100 D51095 AA523864 W70043 AA987586 AI421515 AI205532 AA127069 AI337367 D51595 AI453785 AW075677 AW088359 C14287 C14284 AF163474 NM_016590 AF163475 AI761105 AI770098 AA410580 AA411616 AI590343 AI739050 AL050198 AI862645 AA419104 AA513809 AA333032 AI816915 AW139625 AA640889 AI311391 AI627693 AW135514 AA419011 AI269149 AI245259 AI970008 AI970017 AW139445 AA569503 AI761072 AI766179 AI759995 AI300776 AI870129 AW150770 AA226501 AA226220 AI249368 AI742316 AA428062 AA442089 AI864189 BE349478 AI803475 AI584049 BE552085 AI088609 AI264197 AI886144 AI129474 AI307145 BE181300 AW058403 AI696838 AW748598 AA442196 AI216428 102398 entrez_U42359U42359 .315051 347217_1 AW292425 BE467167 AI702953 BE550961 BE222309 AI299348 AI693336 AA541708 324626 336411_1 AI685464 AW971336 AA513587 AA525142 319191 16065_1 NM_012391 AF071538 AB031549 AI685592 AI745526 AA662204 AW130657 AA662164 AW971121 AI668916 AA513274 AI991223 AI979170 AW298436 AA639821 AI859010 AW513942 AI687669 AA662521 AA548598 AI345056 AI305374 BE043418 AI432856 AI334840 AI379796 AI492693 AI307915 BE042082 AI307834 AI307858 AI309488 BE042210 AI435670 AI371605 AI862491 AI284563 AI306872 AI255044 AI254601 AI251236 AI473073 AI473042 AI432760 AI435664 AI336826 AI289365 AI369096 AI862274 AI334871 AI349863 AI250405 AI377617 AI309895 AI313017 AI862291 AI311936 AI378718 AI305722 AI306769 AI308888 AI334565 AI862296 AI344230 AI435685 AI344087 AI378696 AI311209 AI435775 AI310611 AI311154 AI432289 AI431561 AI492681 AI432867 AI335288 AI492796 AI432769 AI310299 AI432273 AI379820 AI275319 AI435753 AI609441 AI432767 AI369100 AI311420 AI349974 AI247157 AI334677 AI270910 AI224320 AI305608 AI334489 AI377152 AI350012 AI370088 AI335053 AI306781 AI306750 AI334849 AI334874 AI340380 AI307876 AI305974 AI305972 AI311521 AI334872 AI862509 AI311498 AI335051 AI289684 AI310859 AI311862 AI862483 AI492775 AI307906 AI492708 AI289693 AI340373 AI307910 AI311359 AI435653 AI334865 AI311492 AI492809 AI492690 AI431576 AI862268 AI311879 AI308435 AI492792 AI862512 AI275321 AI431568 AI431564 AI307885 AI307926 AI435692 AI435778 AI310182 AI308894 AI492707 AI492713 AI308560 AI307829 AI343234 AI580598 AW472786 AI340918 AI310243 AI309368 AI307920 AI289665

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AI306777 AW086318 AW086292 AW086378 AI310027 AI275293 AI369082 AI340900 AI306749 AI371558 AW086287 BE043803
AI306793 AI306272 AI287948 AI270917 AI284816 AI336813 AI284546 AI308044 AI275290 AI270872 AI306795 AI289687 AI223570
AI305303 AI289677 AI287742 AI275284 AI306812 AI336701 AI371554 AI378719 AI344988 AI223631 AI335141 AI343222 AI284568
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AI432897 AI473043 AI432871 AI436536 AI473157 AI349715 AI432777 AI473016 AI473158 AI340369 AI307941 AI432773 AI377146
AI492791 AI270950 AI305342 AI284604 AI306269 AI284811 AI270811 AI289347 AI334869 AI334852 AI311759 AI250382 AI309520
AI289550 AI305721 AI340870 AI270901 AI308575 AI307904 AI340715 AI270941 AI309808 AI246867 AI473014 AI307039 AI289360
AI473069 AI492786 AI344013 AI305876 AI436510 AI340742 AI473028 AI307891 BE041871 BE041268 BE042340 BE041946
BE041783 AI306173 AI201948 AI926972 AI275769
338255 CH22_6856FG_LINK_EM:AC00
330211 c_5_p2
332798 CH22_14FG_6_5_LINK_C4G1.G
334447 CH22_1746FG_387_7_LINK_EM
332247 372969_1
332396 20265_1
332697 13699_1
425710 25529_1
432189 342819_1
445424 6391_1
447210 7119_1
449625 8113_1
452039 89513_1
AA669097 AA513815 AA026798 AA676526 AA704429 AA704269 AW118292 AA579216 N58172
AW579842 BE156562 BE156690 BE156489 BE081033 AK001559 BE149402 M85387 AW367811 AW367798 R17370 AI908947
AA382932 R58449 H18732 AA371231 AW962899 AA713530 AW892946 R53463 H11063 AW068542 Z40761 BE176212 BE176155
W23952 W92188 AW374883 AA303497 AW954769 AA036808 BE168063 AW382073 AW382085 AL041475 H80748 AI078161
BE463983 AI805213 AI761264 W94885 N94502 AI623772 AI419532 AI810302 AI634190 AW002516 AW150777 AI352312 AI367474
AW204807 AI675502 AI337026 AW134715 BE328451 AI123157 AI560020 AI300745 AI608631 AI248873 AA742484 AW051635
H18646 AI245045 AA507111 AI640510 AI925594 AA115747 AA143035 AA151106
X51405 NM_001873 T11322 AL118886 BE328175 AW136009 BE467445 AW470313 AA774852 BE504139 AW501046 AA082792
AW389231 AA370044 R36841 AA371457 C04813 R25791 R25556 AW895854 AW903819 AW895671 AW895677 BE159723
AW895664 AW895597 AW895595 AW895665 AW888518 AI903724 F06081 F08503 AL119462 AW895730 AW888516 R26511
R26489 AA334126 AA327626 N85713 AW895998 AA223622 F05468 AA370749 W05590 M78202 AA371073 AW498607 R15017
T16991 AA001282 AA001138 AA551566 AA330159 AI922855 AA383512 AA029603 D82246 D82171 T94933 H56545 AA348060
AA176888 R96764 AW451817 AA385766 AA452618 AI690057 AA988822 BE549928 AA150901 W57992 AW899925 C05281
AA932042 AA370980 AW962877 W04741 AA369982 AW385948 AA922466 N75882 AI422070 AI361256 AI680224 D57122 T94885
R53266 R46713 T19071 AW796277 AA325333 F04719 F02334 AA358146 AA626597 AA358304 AW028099 AL119570 D57290
D58273 D57796 N48555 AI361969 AA329457 D57225 AW024046 AA982606 AW022118 AW021538 AA935845 H89870 H56546
AW961219 AA453239 AW837541 N45521 BE218029 AA318877 AA327740 AW961809 T92139 D53216 D52365 D53363 D53312
D53116 AI547267 AA679935 AW026552 AW026418 AW190507 AI927710 AW244108 D50848 AW054991 AW021063 AW022511
AA493436 AI365636 BE464751 AW149384 AA102442 AW771368 AI818251 AI126368 D51049 AI421542 AI559467 AW079779
AW021048 AW023969 AW044214 AI458264 AA027274 AI620254 AW028917 BE219511 AA326242 N67561 AI971273 AA878328
D57131 AA770662 AI309299 AI796767 AA613338 W58076 AI566287 AI445573 AI980260 AA001919 AW339259 AI492610 AI492611
R97692 AI301425 AA722603 D58361 AI350323 AA973928 AI431263 AA516126 AA865467 AI925177 N39443 AA001943 AI289371
AI082412 AA665090 AA583433 H89871 AA977231 AI362219 AI056096 AI270446 N67524 N22103 AW614224 AA744054 AW243622
AI613188 AI929173 AI350243 AI362138 AA744004 AA176661 D56787 AI955625 AI393109 AI094769 AI479728 AI423107 AI955617
AI034036 AI582196 AW264534 AI418961 AA570761 AI343538 AA650341 AA992503 AA770004 AL039666 AI862675 AW190335
AA510274 AW418627 BE467472 D56786 T28749 AI217610 AI359556 T23523 AL040189 AA846222 AA651636 D51280 AI888986
AI521167 AI340177 AW612815 AI625285 AA621607 AA177059 AA229768 AA829788 AI749682 AW190631 N75299 AA230089
AI915632 BE069542 AA890020 AA528397 AA995390 BE503860 AA570812 AW339396 AI197986 AI203725 AI282379 AA670375
AA461513 F01728 AW243599 C00856 N75567 R95995 AA150932 R95981 AA648060 AA933800 AA927073 AA101126 AA864190
T93566 BE167472
AF030880 NM_000441 AC002467 AA385554 H23053 AW891838 AI139968 AA653057 AI695233
AA527941 AI810608 AI620190 AA635266
AB028945 T77648 F13328 AL157605 Z46212 AA304736 F11855 T66098 T30174 AW954164 AW176301 AW748243 AA456428
AI369958 AA938565 AW959613 Z42008 AA994779 AI683909 F11019 F10926 AI769597 AI752550 T65015 AI884314 AA643954
Z41838 AW020147 AI038822 AW571822 AA289781 AA894928 AF131790 BE005411 AI902476 AW082695 AA464384 R42750
AW902301 AA464273 R05837 Z38294 H41098 AL134507 M86079
AF035269 AF035268 NM_015900 T96213 U37591 AA156832 AA299371 AI084325 H95977 AI765967 BE221465 AA156726 AI869563
AW024539 AI436791 AI949451 AA843093 AI452756 AA824232 AI306667 T96131 AW207447 AW243556 AW957032 AI084332
H95978 U30998
NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370
AW779760 N48674 AI375997 RA5432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526
T61415 AA331486
AI922988 H05475 AA021608 AW169947 AA913750 Z41614 AW800012

TABLE 15B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 15. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
334447	Dunham, I. et al.	Plus	14308764-14308824
332798	Dunham, I. et al.	Minus	232147-231974
338255	Dunham, I. et al.	Minus	15242294-15242231
330211	6013592	Plus	59158-59215
401424	8176894	Plus	24223-24428

TABLE 11 AND SEQUENCE LISTING

SEQ ID NO:1 BCU4 DNA SEQUENCE

5 Nucleic Acid Accession #: NM_024915
Coding sequence: 13-1890 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

10 ATTTGGATCAA ACATGTCACA AGAGTCGGAC AATAATAAAA GACTAGTGGC CTTAGTGCCC 60
ATGCCCAGTG ACCCTCCATT CAATACCCGA AGAGCCTACA CCAGTGAGGA TGAAGCCTGG 120
AAGTCATACT TGGAGAATCC CCTGACAGCA GCCACCAAGG CCATGATGAT CATTAAATGGT 180
GATGAGGACA GTGCTGCTGC CCTCGGCTGT CTCTATGACT ACTACAAGGT TCCTCGAGAC 240
AAGAGGGTGC TGCTGTAAAG CAAAGCAAGT GACAGCCAAG AAGACCAGGA GAAAAGAAAC 300
15 TGCCCTTGCCA CCAGTGAAGC CCAGAGTAAT TTGAGTGGAG GAGAAAACCG AGTGCAAGTC 360
CTAAAGACTG TTCCAGTGAA CCTTCCCTTA AATCAAGATC ACCTGGAGAA TTCCAAGCGG 420
GAACAGTACA GCATCAGCTT CCCCAGAGC TCTGCCATCA TCCCGGTGTC GGGAAATCACG 480
GTGGTGAAGG CTGAAGATT CACACCAGTT TTCATGGCCC CACCTGTGCA CTATCCCCGG 540
GGAGATGGGG AAGAGCAAGC AGTGGTTATC TTTGAACAGA CTCAGTATGA CGTGCCCTCG 600
20 TGCCGACCCC ACAGCGCCTA TCTCAAAGAC GACCAGCGCA GCACTCCGGA CAGCACATAC 660
AGCGAGAGCT TCAAGGACGC AGCCACAGAG AAATTTCGGA GTGCTTCAGT TGGGGCTGAG 720
GAGTACATGT ATGATCAGAC ATCAAGTGGC ACATTTCACT ACACCTGGA AGCCACCAAA 780
TCTCTCCGTC AGAAGCAGGG GGAGGGCCCC ATGACCTACC TCAACAAAGG ACAGTTCTAT 840
GCCATAACAC TCAGCGAGAC CGGAGACAAC AAATGCTTCC GACACCCCAT CAGCAAAGTC 900
25 AGGAGTGTGG TGATGTGGT CTTCACTGAA GACAAAAACA GAGATGAACA GCTCAAATAC 960
TGGAAATACT GGCATCTCG GCAGCATACG GCGAAGCAGA GGGTCTTGA CATTGCCGAT 1020
TACAAGGAGA GCTTTAATAC GATTGGAAGC ATTGAAGAGA TTGCATATAA TGCTGTTTCC 1080
TTTACCTGGG ACGTGAATGA AGAGGCGAAG ATTTTCATCA CCGTGAATTG CTTGAGCACA 1140
GATTCTCTCT CCAAAAAAGG GGTGAAAGGA CTTCCTTTGA TGATTAGAT TGACACATAC 1200
30 AGTTATAACA ATCGTAGCAA TAAACCCATT CATAGAGCTT ATTGCCAGAT CAAGGTCTTC 1260
TGTGACAAAG GAGCAGAAAG AAAAATCCGA GATGAAGAGC AGAAGCAGAA CAGGAAGAAG 1320
GGGAAGGGCC AGGCCTCCCA AACTCAATGC AACAGCTCCT CTGATGGGAA GTTGGCTGCC 1380
ATACCTTTAC AGAAGAAGAG TGACATCAC TACTTCAAAA CCATGCCCTGA TCTCCACTCA 1440
CAGCCAGTTC TCTTCATACC TGATGTTTAC TTTGCAAAAC TGCAGAGGAC CGGACAGGTG 1500
35 TATTACAAAC CGATAGTGA ACGAGAAGGT GGCAGTGTCC TTGTTAAACG GATGTTCCGG 1560
CCCATGGAAG AGGAGTTTGG TCCGGTGCCT TCAAAGCAGA TGAAGAAGA AGGGACAAAG 1620
CGAGTGCTCT TGACGTGAG GAAGGAGACT GACGATGTGT TCGATGCATT GATGTTGAAG 1680
TTTACCTGGG ACGTGAATGA AGAGGAGCG ATATCTGAGA AATATGGGCT GCCCGTGGAG 1740
AAGATAGCAA AGCTTTACAA GAAAAGCAAA AAAGGCATCT TGGTGAACAT GGATGACAAC 1800
40 ATCATCGAGC ATCTAGTCAA CGAGGACACC TTCATCTCA ACATGGAGAG CATGGTGGAG 1860
GGCTTCAAGG TCACGCTCAT GGAATCTAG CCCTGGGTTT GGCATCCCTT TTGGCTGGAG 1920
CTCTCAGTGC GTTCTCTCCT GAGAGAGACA GAAGCCCCAG CCCCAGAAAC TGGAGACCCA 1980
TCTCCCCCAT CTGTTACAAG ACCGTGCTGG GAGTGGGGC AAGGGACAGG 2040
CCCCACAGTC GGTGTGCTTG GCCCATCCAC TGGCACCTAC CACGGAGCCG AAGCCTGAGC 2100
45 CCCTCAGGAA GGTGCCCTAG GCCTGTTGGA TTCTATTTA TTGCCACCT TTTCTGGAG 2160
CCCAAGTCCA GGGCCGCCAG GACTCTGCAG GTCAGTCTA GCTCCAGATG AGACCGTCCA 2220
GCGTTCCTCC TTCAAGAGAA ACATCTATCC CGAAGAGCCT AAAAAATTC CATCCCTTCT 2280
TTCTCACACG TGCATATCTA TATCTCCGA GTGGCTGGAC AAAATGAGCT ACGTCTGGGT 2340
GCAGTAGTTA TAGGTGGGGC AAGAGGTGGA TGCCCACTTT CTGGTCAGAC ACCTTTAGGT 2400
TGCTCTGGGG AAGGCTGTCT TGCTAAATAC CTCCAGGTTT CCAGCAAGT GGCCACCAGG 2460
50 CCTGTACAG GAAGACATTC AGTCACCGTG TAATTAGTAA CACAGAAAGT CTGCCTGTCT 2520
GCATTGTACA TAGTGTATT AATATTGTAA TAATATATT TACCTGTGGT ATGTGGGCAT 2580
GTTTACTGCC ACTGGCCTAG AGGAGACACA GACCTGGAGA CCGTTTAAAT GGGGGTTTTT 2640
GCCTCTGTGC CTGTTCAAGA GACTTGCAGG GCTAGGTAGA GGGCCTTTGG GATGTTAAGG 2700
TGACTGCAGC TGATGCCAAG ATGGACTCTG CAATGGGCAT ACCTGGGGGC TCGTTCCTG 2760
55 TCCCCAGAGG AAGCCCCCTC TCCTTCTCCA TGGGCATGAC TCTCTTCA GGCCACCAG 2820
TTTATCTCAC AATGATGTGT TTTGCCGTAC TTTCCCTTTG CGCTGTCTCG TGGGAAAGGT 2880
CATCTGTCT GAGACCCAG CTCCTTCTCC AGCTTTGGCT GCGGGCATGG CTTGAGCTTT 2940
CTGGAGAGCC TGTGACGGG GTTGCCATC AGGCCCCGTG GGCTGGGTCT GCTGCAGAGC 3000
60 TCCTTGCTA TCAGGAGAAT CCTGGACACT GTACTGTGCC TCCAGTTTA CAAACACGCC 3060
CTTCATCTCA AGTGGCCCTT TAAAAGGCCT GCTGCCATGT GAGAGCTGTG AACAGCTCAG 3120
CTCTGAGTCG GCAGACTGGG GCTTCTCTCT GGGCCACCAG ATGGAAAGGG GGTATTGTTT 3180
GCCTCACTCC TGGATGCTGC GTTTAAGGA AGTGAGTGAG AAAGAATGTG CCAAGATACC 3240
TGGCTCTGTG GAAACACGCC TCAGGAGGGA AACTGGGAGA GAGAAGCTGT GGTCTCTCTG 3300
TACATGCCCT GGGAGCTGGA AGAGAAAAAC ACTCCCTTAA ACAATCGCAA AATGATGAAC 3360
65 CATCATGGGC CACTGTCTCT TTTGAGGGGA CAGGTTTAGG GGTGTGCTT CGCCCTTGTG 3420
GGCTGAAGCA CTAGCTTTTT GGTAGCTAGA CACATCTGTC ACCCAAAGGT TCTTACAAA 3480
GGCCAGATT TGTTTGTTAA GCATTTGAC TCTTACCTGG AGGCCCGCTC TCTAAGGGCT 3540
TCTGCGCTC CCACCTCATC TGTCCTGAG ATGCAGAGCA GGATGGAGGG TCTGCTTCTA 3600
GCTCAGCTGT TCTCTCTGA GGTGCGGAG GAATTGAAT GAATGGGACA GAGGGCAGGT 3660
70 GCTGTGGCCA AGAAGATCTC CGAGCAGCAG TGACGGGGCA CTTGTCTGTG TGCTCTCTG 3720
GCATGTTAAC CTTTCTGTGG GGCCAAAGGT TTGCATCGTG GATCCAGCTG TGCTCCAGTC 3780
TGTCCTCTCC TCTCCACTC TGACTGCCAC GCCCCGAC AGCAGCTTGG GGACCTCCA 3840
GGGTACTAAT GGGGCTCTGT TCTGAGATGG ACAATTTCAG TGTGGAAT ACATGTTGTA 3900
75 CATGCACTT CCAATGCTCC TAGGGTAGG AATAGTTTCA AACATGATTG GCAGACATAA 3960
CAACGGGAAA TACTCGGACT GGGGCATAGG ACTCCAGAGT AGGAAAAAGA CAAAAGATT 4020
GGCAGCCTGA CACAGGCAAC CTACCCCTCT CTCTCCAGCC TCATTATGAA ACTGTTTGT 4080
TGCCAGTCTC GCCTAAGGC AGAAGATGAA TTGAAGATGC TGTGATGTT TCCTAAGTCC 4140
TTGAGCAATC ATGGTGTGTA CAATTGCCAC AAGGATATG AGGCCAGTGC CACCAGAGG 4200

TGGTGCCAAG TGCCACATCC CTTCGGATCC ATTCCTCTCT GTATCCTCGG AGCACCCCAG 4260
 TTTGCCCTTTG ATGTGTCGCG TGTGTATGTT AGCTGAACTT TGATGAGCAA AATTTCCTGA 4320
 GCGAAACACT CCAAAGAGAT AGGAAAACCT GCCGCCTCTT CTTTTTGTG CCTTAATCAA 4380
 ACTCAATAA GCTTAAAAA AATCCATGGA AGATCATGGA CATGTGAAAT GAGCATTTTT 4440
 TCTTTTCTT TTTTITTTT TTTTITTAAC AAAGTCTGAA CTGAACAGAA CAAGACTTTT 4500
 TCCTCATACA TCTCCAAATT GTTTAAACTT ACTTTATGAG TGTITGTTA GAAGTTCCGA 4560
 CCAACAGAAA AATGCAGTCA GATGTCATCT TGGAAATGGT TTCTAAAAAG GTAAGGCATG 4620
 TCCCTGCCCA GAAACTTAGG AAGCATGAAA TAAATCAAAT GTTTATTTTC CTCTTATTT 4680
 AAAATCATGC TAATGCAACA GAAATAGAGG GTTTGTGCCA AATGCTATGA ACGGCCCTTT 4740
 CTTAAAGACA AGCAAGGGAG ATTGATATAT GTACAATTG CTCTCATGTT TTT

SEQ ID NO:2 BCU4 Protein sequence:
 Protein Accession #: NP_079191.1

1 11 21 31 41 51
 MSQESDNNKR LVALVPMPSD PPFNTRRAYT SEDEAWKSYL ENPLTAATKA MMIINGDEDS 60
 AAALGLLYDY YKVPDRKRL SVSKASDSQE DQEKRNCLGT SEAQSNLSGG ENRVQVLKTV 120
 PVNLSLNQDH LENSKEQYS ISFPSSAII PVSGITVVKA EDFTPVFMAP PVHYPRGDGE 180
 EQRVVFIEQT QYDVPSLATH SAYLKDDQRS TPDSTYSESF KDAATEKFRS ASVGAEEMY 240
 DQTSSTGTFQY TLEATKSLRQ KQGEFPMTYL NKGQFYAITL SETGDNKCFR HPISKVRSVV 300
 MVVFSDEKNR DEQLKYWKY W HSRQHTAKQR VLDIADYKES FNTIGNIEEI AYNVASFWD 360
 VNEEAKIFT VNCLSTDFSS QKGVKGLPLM IQIDTYSYNN RSNKPIHAY CQIKVFCDDG 420
 AERKIRDEEQ KQNRKNGKGQ ASQTQCNSSS DGKLAAPLQ KKSIDITYFKT MPDLHSQPV 480
 FIPDVHIFANL QRTGQVYNT DDEREGGSVL VKRMFRPMEE EFGVPVSKQM KEEGTKRVL 540
 YVRKETDDVF DALMLKSPV MGLMEAISEK YGLPVEKIAK LYKSKKGIL VNMDNIEH 600
 YSNEDITFILN MESMVEGFKV TLMEI

SEQ ID NO:3 BCU7 DNA SEQUENCE VARIANT 1:

Nucleic Acid Accession #: AA428062
 Coding sequence: 1-777 (entire sequence represents open reading frame)

1 11 21 31 41 51
 ATGATAGCAA TCTCTGCCGT CAGCAGTGCA CTCCTGTCTCT CCCTTCTCTG TGAAGCAAGT 60
 ACCGTGCTCC TACTCAATTC CACTGACTCA TCCCGGCCAA CCAATAATT CACTGATATT 120
 GAAGCAGCTC TGAAGACACA ATTAGATTCA GCGGATATCC CCAAGCCAG GCGGAAGCGC 180
 TACATTTCGC AGAATGACAT GATCGCCATT CTTGATTATC ATAATCAAGT TCGGGGCAAA 240
 GTGTTCCAC CGGCAGCAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300
 GCAGAGGCTT GGGCGGCTAC TTGCATTGG GACCATGGAC CTCTTACTT ACTGAGATT 360
 TTGGGCCAAA ATCTATCTGT ACGCACTGGA AGATATCGCT CTATCTCCA GTTGGTCAAG 420
 CCATGTTATG ATGAAGTAA AGATTATGCT TTTCCATATC CCCAGGATTG CAACCCAGA 480
 TGTCTTATGA GATGTTTGG TCCCATGTGC ACACATTATA CGCAGATGGT TTGGGCCACT 540
 TCCAATCGGA TAGGATGCC AATTCATGCT TGCCAAAAA TGAATGTTG GGGATCTGTG 600
 TGGCGACGTG CAGTTTACTT GGTATGCAAC TATGCCCAA AGGGCAATTG GATTGGAGAA 660
 GCACCATATA AAGTAGGGGT ACCATGTTCA TCTTGCTCTC CAAGTTATGG GGGATCTTGT 720
 ACTGACAATC TGTGTTTTC AGGAGTTACG TCAAACTACC TGTACTGGTT TAAATAA

SEQ ID NO:4 BCU7 DNA SEQUENCE VARIANT 2:

Nucleic Acid Accession #: AA428062
 Coding sequence: 1-777 (entire sequence represents open reading frame)

1 11 21 31 41 51
 ATGATAGCAA TCTCTGCCGT CAGCAGTGCA CTCCTGTCTCT CCCTTCTCTG TGAAGCAAGT 60
 ACCGTGCTCC TACTCAATTC CACTGACTCA TCCCGGCCAA CCAATAATT CACTGATATT 120
 GAAGCAGCTC TGAAGACACA ATTAGATTCA GCGGATATCC CCAAGCCAG GCGGAAGCGC 180
 TACATTTCGC AGAATGACAT GATCGCCATT CTTGATTATC ATAATCAAGT TCGGGGCAAA 240
 GTGTTCCAC CGGCAGCAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300
 GCAGAGGCTT GGGCGGCTAC TTGCATTGG GACCATGGAC CTCTTACTT ACTGAGATT 360
 TTGGGCCAAA ATCTATCTGT ACGCACTGGA AGATATCGCT CTATCTCCA GTTGGTCAAG 420
 CCATGTTATG ATGAAGTAA AGATTATGCT TTTCCATATC CCCAGGATTG CAACCCAGA 480
 TGTCTTATGA GATGTTTGG TCCCATGTGC ACACATTATA CGCAGATGGT TTGGGCCACT 540
 TCCAATCGGA TAGGATGCC AATTCATGCT TGCCAAAAA TGAATGTTG GGGATCTGTG 600
 TGGCGACGTG CAGTTTACTT GGTATGCAAC TATGCCCAA AGGGCAATTG GATTGGAGAA 660
 GCACCATATA AAGTAGGGGT ACCATGTTCA TCTTGCTCTC CAAGTTATGG GGGATCTTGT 720
 ACTGACAATC TGTGTTTTC AGGAGTTACG TCAAACTACC TGTACTGGTT TAAATAA

SEQ ID NO:5 BCU7 Protein sequence Variant 1:
 Protein Accession #: none

1 11 21 31 41 51
 MIAISAVSSA LLPSLLCEAS TVVLLNSTDS SPPTNNFTDI EAALKAQLDS ADIPKARRKR 60

YISQNDMIAI LDYHNQVRGK VFPPAANMEY MVWDENLAKS AEAWAATCIW DHGPSYLLRF 120
 LGQNLVSRVG RYRSILQLVK PWYDEVKDYA FPYPQDCNPR CPMRCFGPMC THYTQHWAT 180
 SNRIGCAIHA QONMNVWGSV WRRAVYLCVN YAPKGNWIGE APYKVGVPSC SCPPSYGGSC 240
 TDNLCPGVT SNLYWFK

SEQ ID NO:6 BCX2 Protein sequence Variant 2:
 Protein Accession #: none

1 11 21 31 41 51
 MIAISAVSSA LLPSLLCEAS TVVLLNSTDS SPPTNNFTDI EAALKAQLDS ADIPKARRKR 60
 YISQNDMIAI LDYHNQVRGK VFPPAANMEY MVWDENLAKS AEAWAATCIW DHGPSYLLRF 120
 LGQNLVSRVG RYRSILQLVK PWYDEVKDYA FPYPQDCNPR CPMRCFGPMC THYTQHWAT 180
 SNRIGCAIHT QONMNVWGSV WRRAVYLCVN YAPKGNWIGE APYKVGVPSC SCPPSYGGSC 240
 TDNLCPGVT SNLYWFK

SEQ ID NO:7 BCX2 DNA SEQUENCE

Nucleic Acid Accession #: NM_003014
 Coding sequence: 238-1278 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGCGGGTTTCG CGGCCCGAAG GCTGAGAGCT GCGCGTGCTC GTGCCCTGTG TGCCAGACGG 60
 CGGAGCTCCG CGGCCGGACC CCGCGGCCCC GCTTGTCTGC CGACTGGAGT TTGGGGGAAG 120
 AAATCTCTCT CGGCCCCAGA AGATTCTTTC CTCGGCGAAG GGACAGCGAA AGATGAGGGT 180
 GGCAGGAAGA GAAGGGCGCTT TCTGTCTGCC GGGGTCGCAG CGCAGAGGGG CAGTGCCATG 240
 TTCTCTCTCA TCTAGTGGC GCTGTGCTG TGGCTGCACC TGCGCGTGGG CGTGCAGCGG 300
 GCGCCCTGCG AGCGGGTGG CATCCCTATG TGCCGGCACA TGCCCTGGAA CATCACGCGG 360
 ATGCCCAACC ACCTGCACCA CAGCAGCGAG GAGAACGCCA TCCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGGACGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTTCTG TGCCATGTAC 480
 GCGCCCATTT GCACCTTGA GTTCTGTGAC GACCCATCA AGCCGTGCAA GTCGGTGTGC 540
 CAACGCGCGC GCGACGACTG CGAGCCCTC ATGAAGATGT ACAACACAG CTGGCCCGAA 600
 AGCCTGGCCT GCGACGAGCT GCTGTCTAT GACCGTGCGG TGTGCATTTC GCTGAAGCC 660
 ATCGTCACGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720
 CAGGAAAGGC CTCTGTATGT TGAATGTAAA CGCCTAAGCC CCGATCGGTG CAAGTGTAAG 780
 AAGGTGAAGC CAACCTTTGGC AACGTATCTC AGCAAAAACT ACAGCTATGT TATTCATGCC 840
 AAAATAAAAG CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAA 900
 GAGATCTTCA AGTCTCATC ACCCATCCCT CGAACTCAAG TCCCGTCAAT TACAATTCT 960
 TCTTGCCAGT GTCCACACAT CCTGCCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1020
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATGCA TAAGCTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140
 AAGAAAACAG CCGGGCGCAC CAGTCGTAGT AATCCCCCA AACCAAGGG AAAGCCTCCT 1200
 GCTCCCAAC CAGCCAGTCC CAAGAAGAAC ATTAATACTA GGAGTGCCA GAAGAGAACA 1260
 AACCAGAAA GAGTGTGAGC TAAGTAGTTT CCAAGCGGA GACTCCGAC TCCCTTACAG 1320
 GATGAGGCTG GGCATTGCTT GGCACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCTTAACA 1380
 ACTACTGCA GTGCTCTTCA TAGACACATC TTGCAGCATT TTCTTAAGG CTATGCTTCA 1440
 GTTTTCTTCT GTAAGCCATC ACAAGCCATA GTGGTAGGTT TGCCCTTTGG TACAGAAGGT 1500
 GAGTTAAAGC TGGTGGAAAA GGCTTATGTC ATTGCATTCA GAGTAACCTG TGTGCATACT 1560
 CTAGAAGAGT AGGGAATAAT ATGCTTGTTA CAATTCGACC TAATATGTGC ATTGTAAAA 1620
 AAATGCCATA TTCAAAACAA AACACGTAAT TTTTATACAG TATGTTTAT TACCTTTTGA 1680
 TATCTGTGT TGCAATGTTA GTGATGTTTT AAAATGTGAT GAAATATAA TGTTTTAAAG 1740
 AAGGAACAGT AGTGAATGA ATGTTAAAG ATCTTATGT GTTATGGTC TGCAGAAGGA 1800
 TTTTGTGAT GAAAGGGAT TTTTGAATA ATAGAGAAG TAGCATATGG AAAATTATA 1860
 TGTGTTTTT TACCAATGAC TTCAGTTTCT GTTTTAGCT AGAACTTAA AAACAAAAAT 1920
 AATAATAAAG AAAATAAAT AAAAAGGAGA GGCAGACAAT GTCTGGATT CTGTTTTTTG 1980
 GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCAACAC CCTCTTAAGC AGCACCAGAA 2040
 ACAGTGAGTT TGCTGTGACC ATTAGGAGTT AGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100
 ATTTTATACC CACAAGAGAG GTATGTCACT CATCTTACT CCCAGGACAT CCACCTGAG 2160
 AATAATTGA CAAGCTTAAA AATGGCCTC ATGTGAGTGC CAAATTTTGT TTTTCTTCAT 2220
 TTAAATATTT TCTTTGCTTA AATACATGTG AGAGGAGTTA AATAATAATG TACAGAGAGG 2280
 AAAGTTGAGT TCCACCTG AAATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340
 AAAAAGAACT TATTGCAGC ATTTTATCAA CAAATTTTCA ATTTGTGGAC AATTGGAGGC 2400
 ATTTATTTTA AAAACAATTT TATTTGCTT TTGCTAACA CAGTAAGCAT GTATTTTATA 2460
 AGGCATTCAA TAAATGCACA ACGCCAAAAG GAAATAAAAT CCTATCTAAT CCTACTCTCC 2520
 ACTACACAGA GGTAATCACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580
 GCACITTATA AATGATTTGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
 CTGCTCTCTT TGCTTGGCCC TTTATTGAGA TAAGTTTTC TGTCAAGAAA GCAGAAACCA 2700
 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCACT TACTCAACAA ACTGTTGTGC 2760
 TATTGGATAC TTAGTGGTT TCTCACTGA CAATACTGAA TAAACATCTC ACCGGAATTC

SEQ ID NO:8 BCX2 Protein sequence:
 Protein Accession #: NP_003005.1

1 11 21 31 41 51
 MFLSILVALC LWLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60

5 YEELVDVNCs AVLRFFFCAM YAPICTLEFL HDPIKPKSV QQRARDCEP LMKMYNHSWP 120
 ESLACDELVP YDRGVCSPE AIVTDLPEDV KWIDITPDMV VQERPLDVDC KRLSPDRCKC 180
 KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVV DV KEIFKSSSPI PRTQVPLJTN 240
 SSCQCPHILP HQDVLMCYE WRSRMMILEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD 300
 KKKTAGRTSR SNPPKPKGKP PAPKPASPKK NIKTRSAQKR TNPKR V

SEQ ID NO:9 CBK1 DNA SEQUENCE

10 Nucleic Acid Accession #: NM_032391
 Coding sequence: 129-302 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
 | | | | |
 GTCTTCCTCT TCCTAGCCTA AGGCGTGCAA ACAGAGCGCC ACTGGGAGGC TGAACCTTT 60
 AGGCCGATGC TTGCTTGCAA GGTGAGGCAA GCTGGATCTT GGTCCCCACC TTTGACAGAGA 120
 GAACAGCGAT GTTGTGCGCC CATTTCTCAG ATCAAGGACC GGGCCATCTT ACTACCTCCA 180
 AGAGTGCTTT TCTCTCTAAT AAGAAAACAT CTACTTTGAA ACATCTACTG GGCAGACCA 240
 GGAGTGATGG CTCAGCTGT AATTCTGGAA TTTCGGGAGG CCGAGGCAGG AAGATTCTCT 300
 20 GAGCACAGGA GTTCAGACC AGCCTGGGCA ATGTAGCAAG ACGCTGTCTC TATTTATACA 360
 ATAAATTTT TTTAAAAAG G

25 SEQ ID NO:10 CBK1 Protein sequence:
 Protein Accession #: NP_115767

30 1 11 21 31 41 51
 | | | | |
 MLCAHFSQDG PAHLTTSKSA FLSNKKSTL KHLGETRSD GSACNSGISG GRGRKIP

SEQ ID NO:11 CHA1 DNA SEQUENCE

35 Nucleic Acid Accession #: NM_020182
 Coding sequence: 96-854 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 | | | | |
 TCCTTGGGTT CGGCTGAAAG CGCCTGGGGG TTCGTGGCCA TGATCCCCGA GCTGCTGGAG 60
 AACTGAAGGC GGACAGTCTC CTGCGAAACC AGGCAATGGC GGAGCTGGAG TTTGTTCAGA 120
 TCATCATCAT GTTGGTGGTG ATGATGGTGA TGGTGGTGGT GATCAGCTGC CTGCTGAGCC 180
 ACTACAAGCT GTCTGCACGG TCTTTCATCA GCCGGCAGC CCAGGGGCGG AGGAGAGAAG 240
 ATGCCCTGTC CTCAGAAGGA TGCTGTGGC CTTCGGAGAG CACAGTGTA GGCACACGAA 300
 45 TCCAGAGCC GCAGGTCTAC GCCCGGCTC GCGCCACCGA CCGCTGGCC GTGCCGCCCT 360
 TCGCCACGG GAGCGCTTC CACGCTTCC AGCCACCTA TCGTACCTG CAGCAGAGA 420
 TCGACCTGCC ACCCACCATC TCGCTGTGAG ACGGGGAGGA GCGCCACCC TACCAGGGCC 480
 CCTGCACCTT CCAGCTTCGG GACCCGAGC AGCAGCTGGA ACTGAACCGG GAGTCGCTGC 540
 GCGCACCCCC AAACAGAAC ATCTTCGACA GTGACCTGAT GGATAGTGCC AGGCTGGGCG 600
 50 GCCCTGGCC CCCCAGCAGT AACTCGGGCA TCAGCGCCAC GTGCTACGGC AGCGCGGGC 660
 GCATGGAGGG GCGCCGCCCC ACCTACAGCG AGGTTCATCGG CCACCTACCG GGGTCTCTCT 720
 TCCAGACCA GCAGAGCAGT GGGCCGCCCT CCTTGTGGA GGGGACCCG CTCACACCA 780
 CACACATCGC GCCCTTAGAG AGCGCAGCCA TCTGGAGCAA AGAGAAGGAT AAACAGAAAG 840
 GACACCTCT CTAGGGTCCC CAGGGGGGCC GGGCTGGGGC TGCGTAGGTG AAAAGGCAGA 900
 55 ACACCTCTCT CTCTTAGAA GAGGAGTGAG AGGAAGCGG GGGGCGCAGC AACGCATCGT 960
 GTGCCCTCC CCTCCACCT CCTGTGTAT AAATATTAC ATGTGATGTC TGGTCTGAAT 1020
 GCACAAGCTA AGAGAGCTTG CAAAAAAG AAGAAAAAG AAAAAAAG ACCACGTTTC 1080
 TTTGTGAGC TGTGCTTGA AGGCAAAAG AAAAAATTT CTACAGTAAA AAAAAAAG 1140
 A

60 SEQ ID NO:12 CHA1 Protein sequence:
 Protein Accession #: NP_064567

65 1 11 21 31 41 51
 | | | | |
 MAELFVQII IIVVMMVMV VVITCLLSHY KLSARSPISR HSQRRREDA LSSEGCLWPS 60
 ESTVSGNGIP EPQVYAPRP TORLAVPPFA QRERFHRFP TYPYLOHEID LPPTISLSDG 120
 70 EEPYPYQGP TLQLRDPEQ LELNRESVRA PPNRTIFDSD LMSARLGGP CPPSSNSGIS 180
 ATCYSGSGRM EGPPTTYSEV IGHYPGSSFQ HQSSGPPSL LEGTRLHPTH IAPLESAAIW 240
 SKEKDKQKH PL

SEQ ID NO:13 CJA5 DNA SEQUENCE

75 Nucleic Acid Accession #: NM_012445
 Coding sequence: 276-1271 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
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GCACGAGGGA AGAGGGTGAT CCGACCCGGG GAAGGTCGCT GGGCAGGGCG AGTTGGGAAA 60
GCGGCAGGCC CCGCCGCCCC CGCAGCCCTT TCTCCTCCTT TCTCCACGCT CCTATCTGCC 120
TCTCCTGGA GGCAGGCCCG TGCAGCATCG AAGACAGGAG GAACTGGAGC CTCTATGGCC 180
GGCCCGGGGC GCGGCGCTCG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG GGACCCGACC 240
GCTGCCGGCC GCGCTCCCGC TGCTCCTGCC GGGTGATGGA AAACCCACAG CCGCCCGCCG 300
CCCTGGGCAA GGCCCTCTGC GCTCTCCTCC TGGCCACTCT CCGCGCCGCC GGCAGCCCTC 360
TTGGGGGAGA GTCCATCTGT TCCGCCAGAG CCCCAGCCAA ATACAGCATC ACCTTCACGG 420
GCAAGTGAGC CAGACAGGCC TTCCCAAGC AGTACCCCTT GTTCCGCCCC CCTGCGCAGT 480
GGTCTTTCGT AGTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCAGT 540
ACGTCACTAA CCGGCTGCGC GACTTTGCGG AGCGCGGCGA GGCTGGGCG CTGATGAAGG 600
AGATCGAGGC GCGGGGGGAG GCGCTGCAGA GCGTGCACGC GGTGTTCCTG GCGCCCGCCG 660
TCCCCAGCGG CACCGGGGAG ACCTCGCGCG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG 720
TCTCGTTTGT GGTGCGCATC GTGCCAGGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG 780
ACCTGTGCGA CGGGGACCGT TGGCGGGAAC AGCGGGCGCT GGACCTGTAC CCTACGACG 840
CCGGGACGGA CAGCGGCTTC ACCTTCTCCT CCCCCAACTT CGCCACCATC CCGCAGGACA 900
CGGTGACGGA GATAACGTCC TCCTCTCCCA GCCACCCGCG CAACTCCTTC TACTACCCGC 960
GGCTGAAGGC CCGGCTCCTC ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA 1020
GGCCCTTCAT CCTCCCGCC CAGTCTCTGC CAGCAGGGA CAATGAGATT GTAGACAGCG 1080
CCTCAGTTCC AGAAAGCGCG CTGGACTGCG AGGTCTCCTT TGCTGTCTC TGGGACTGT 1140
GCGGAGGCCA CTGTGGGAGG CTCGGGACCA AGAGCAGGAC TCGCTACGTC CCGGTCCAGC 1200
CCGCCAACAA CCGGAGCCCC TGCCCGAGGC TCGAAGAAGA GGCTGAGTGC GTCCCTGATA 1260
ACTGCGTCTA AGACAGAGGC CCGCAGCCCC CTGGGGCCCC CGGAGCCATG GGGTGTGCGG 1320
GGCTCCTGTG CAGGCTCATG CTCGAGCGCG CCGAGGCACA GGGGGTTTCG CGCTGTCTCT 1380
GACCGCGGTG AGCCCGCCCG GACCATCTCT GCACTGAAGG GCCCTCTGTT GGCCGCGACG 1440
GGCATTGGGA AACAGCCTCC TCCTTTCCCA ACCTTGCTTC TTAGGGGCCC CCGTGTCCCG 1500
TCTGCTCTCA GCCTCCTCCT CTGCAAGGAT AAAGTCAATC CCAAGGCTCC AGTACTCTTA 1560
AATTATGTC TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGTCTTCAT CGTCCAGGGG 1620
CCTGGCTCCC AGTGGTTCG AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGCCCA 1680
CTCTCCCGAG GCGGCATCCA AGCGGGGGCC ACTTGAGAGT TGAATAAATG GGGCGGTTTC 1740
GGAAGCGTCA GTGTTTCCAT GTTATGGATC TCTCTGCGTT TGAATAAAGA CTATCTCTGT 1800
TGCTCAC

35
SEQ ID NO:14 CJA5 Protein sequence:
Protein Accession #: NP_036577

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1 11 21 31 41 51
| | | | |
MENPSPAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAPFKQY 60
PLFRPPAQWS SLLGAAHSSD YSMWRKNQYV SNGLRDFAEER GEAWALMKEI EAAGEALQSV 120
HAVFSAPAVP SGTGQTSAL EVQRRLSLVS FVVRIVPSPD WFGVDSLDL CDGDRWREQA 180
ALDLYPYDAG TDSGFTTSSP NFATIPQDTV TEITSSSPSH PANSFYPRRL KALFPPIARVT 240
LVRLRQSPRA FIPPAFVLPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTSK 300
RTRYVRVQPA NNGSPCELE EEAECVPDNC V

SEQ ID NO:15 LBH9 DNA SEQUENCE

50
Nucleic Acid Accession #: NM_002391
Coding sequence: 26-457 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCCTCC TCACCTCCT 60
CGCCCTGCTG GCGCTCACCT CCGCGGTGCG CAAAAGAGAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGGAGC GAGTGCGCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
CGCGGTGGGT TTCCGCGAGG GCACCTGCGG GGCCAGACC CAGCGCATCC GGTGAGGGT 240
GCCCTGCAAC TGGAAGAAGG AGTTTGAGGC CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
TGCGTGTGAT GGGGGCAGC GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGACCCCCA AGACCAAGC 420
AAAGGCCAAA GCCAAGAAGG GGAAGGGAAA GGAAGTACAG CCAAGCCTGG ATGCCAAGGA 480
GCCCTGGTG TCACATGGGG CCTGGCCACG CCTCCTCTCT CCCAGGCCCG AGATGTGACC 540
CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCTT TGTCTCTCTC 600
ACTCCCCAGC CCCACCCCTA AGTGGCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTCTCTCC CCACAATTCC 720
ATTACTAAGA AACACATCAA ATAACTGAC TTTTCCCCC CAATAAAGC TCTTCTTTT 780
TAATAT

70
SEQ ID NO:16 LBH9 Protein sequence:
Protein Accession #: NP_002382

75

1 11 21 31 41 51
| | | | |
MQHRGFLLLT LLALLALTS VAKKKDKVKK GPGSECAEW AWGPTPSSK DGVGFREGT 60
CGAQTQRIKC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
RVTKPCTPKT KAKAKAKGK GKD

SEQ ID NO:17 LEM9 DNA SEQUENCE

Nucleic Acid Accession #: NM_005244

Coding sequence: 1-1617 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGTTAGAAC TAGTGATCTC ACCCAGCCTC ACTGTAAACA GCGATTGTCT GGATAAACTG 60
AAGTTTAACC GTGCTGACGC TGCTGTGTGG ACTCTGAGTG ACAGACAAGG CATCACCAAA 120
TCGGCCCCCC TGAGAGTGTC CCAGCTCTTC TCCAGATCTT GCCCAGTGT CCTCCCCCG 180
CAGCCTTCCA CAGCCATGGC AGCCTACGGC CAGACGCAGT ACAGTGCGGG GATCCAGCAG 240
GCTACCCCTT ATACAGCTTA CCCACCTCCA GCACAAGCCT ATGGAATCCC TTCTACAGC 300
ATCAAGACAG AAGACAGCTT GAACCATTCC CTGGCCAGA GTGGATTCTT CAGCTATGGC 360
TCCAGCTTCA GCACCTCACC CACTGGACAG AGCCCATACA CCTACCAGAT GCACGGCACA 420
ACAGGGTTCT ATCAAGGAGG AAATGGACTG GGCAACGCAG CCGGTTTCGG GAGTGTGCAC 480
CAGGACTATC CTTCCTACCC CGGCTTCCCC CAGAGCCAGT ACCCCAGTA TTACGGCTCA 540
TCCTACAACC CTCCTACGTT CCGGGCAGC AGCATCTGCC CTTCGCCCTT CTCCACGTCC 600
ACCTACGTCC TCCAGGAGGC ATCTCACAAC GTCCCCAACC AGAGTTCCGA GTCACTTGCT 660
GGTGAATACA ACACACACAA TGGACCTTCC ACACCAGCGA AAGAGGGAGA CACAGACAGG 720
CCGACCCGGG CCTCCGACGG GAAGCTCCGA GGCCGGTCTA AGAGGAGCAG TGACCCGTCC 780
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GCCTTCCGCT ACCGGCGGGT GAAGGAGATG TACAATACCT ACAAGAACA CGTTGGTGGG 1200
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SEQ ID NO:18 LEM9 Protein sequence:

Protein Accession #: NP_005235

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SYNPPYPVPS SICPSPLSTS TVVLQEAHNV VFNQSSBSLA GEYNTHNGPS TPAKEGDTDR 240
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SVRIGLHMEB MIFNLADTHL FPNLDECDQ IHVDVSSDD NGQDLSTYNF SADGFHSSAP 360
GANLCLGSGV HGGVDMWRKL AFYRVRVKEM YNTYKNNVGG LIGTPKRETW LQLRAELEAL 420
TDLWLTHSLK ALNLINSRPN CVNVLVTTTQ LIPALAKVLL YGLGSVFPIE NIYSATKTGK 480
ESCFERIMQR FGRKAVVVVI GDGVEEEQGA KKHNMFFWRI SCHADLEALR HALELEYL

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SEQ ID NO:19 OAA1 DNA SEQUENCE

Nucleic Acid Accession #: NM_002740

Coding sequence: 178-1968 (underlined sequences correspond to start and stop codons)

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ATGAAAGTTG TGA AAAAAGA GCTTGTTAAT GATGATGAGG ATATTGATTG GGTACAGACA 1080
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TTTCAGACAG AAAGCAGATT GTTCTTTGTT ATAGAGTATG TAAATGGAGG AGACCTAATG 1200
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5 ATCAGTCTAG CATTAAATTA TCTTCATGAG CGAGGGATAA TTTATAGAGA TTTGAAACTG 1320
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20 SEQ ID NO:20 QAA1 Protein sequence:
 Protein Accession #: NP_002731

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 CGRHSLPQEP VMPMDQSSMH SDHAQTVIPY NPSSHESLDQ VGEKEAMNT RESGKASSSL 240
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 30 SNHFFLVGLH SCFQTESRLF FVIEYVNGGD LMFHMQRQRK LPEEHARFYS AEISLALNYL 360
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 35 DNFDQSFTNE PVQLTPDDDD IVRKIDQSEF EGFYINPLL MSAEECV

SEQ ID NO:21 OBH2 DNA SEQUENCE

Nucleic Acid Accession #: L05628
 Coding sequence: 197-4792 (underlined sequences correspond to start and stop codons)

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50 SEQ ID NO:22 QBH2 Protein sequence:
 Protein Accession #: AAB46616

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 80 ARALLRKTRI LVLDEATAAV DLETDDLQIS TIRTQPEDCT VLTIAHRLAT IMDYTRVIVL 1500
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SEQ ID NO:23 PAA2 DNA SEQUENCE

Nucleic Acid Accession #: NM_013309

Coding sequence: 1-1290 (underlined sequences correspond to start and stop codons)

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SEQ ID NO:24 PAA2 Protein sequence:

Protein Accession #: NP_037441

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VLSAMISVLL VYILMGFLLY EAVQRTIHMN YEINGDIMLI TAAVGVAVNV IMGFLNLSG 240
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SEQ ID NO:25 PAA3 DNA SEQUENCE

Nucleic Acid Accession #: AB037765

Coding sequence: 375-2798 (underlined sequences correspond to start and stop codons)

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GAAAAGAAAA GGATTGTATG AAAGCATATT TATTCAGGG CAACATATTG CTCAGAGAA 660
TCCCTACTGA CACCTTGTGT GATGTGAATG CCATTGTGCG CCATGTCTC TTTGCTCTTC 720
TTTTTAGTGA AGTGAATAT ATTACCAACC TGAAGAAGCT TCAGAACATA GAAAATGCTC 780
TGAAGGAAA AGCAATATT ATATTCTCAT ATGTAAGAGC CATTTGAATA CCAGAGCACA 840
GAGCAGTCAT GGAAGCCGGT TTTGTGTATG GCACTACATA CCAATTTGTC TTAACACAG 900
AAATTGCCCT TTTGAAAGT ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT 960
TTCAATTGTA ACATAGTCTT GACTTGACCC AGCAATGTAG AAGAACACTA ATGGAACAG 1020
CATTTACTAC ACTGAACATT CACCTGTTTA TTAAGACAAAT GAAAGCACT CTGTGACTG 1080
AAGTTGCTGA AGATCTCAA CAAGTTTCAA CTGTCCATCT CCAACTGGCG TTACCACTGG 1140
TTTTTATGTT TAGCCAACAG GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTTG 1200
CTTGGCGTCT TCTGGGAAAA GCAGGAGTTC TACTCTTGTT AAGGGACTCT TTGGAAGTAA 1260
ACATTCTTCA AGATGCTAAT GTGGTCTTCA AAAGAGCAGA AGAGGGAGTT CCAATGGAAT 1320
TTTTGTATTT ACATGATGTT GATTTAATAA TATCTCATGT GGAATAAAT ATGCACATG 1380
AGGAATACA AGAAGATGAA GACAATGACA TGAAGGTGCC AGATATAGAT GTTCAGGATG 1440
ATGAAGTGGC AGAACTGTT TTCAGAGATA GGAAGAGAAA ATTACCTTTG GAACCTACAG 1500

```

5 TGGAACTAAC AGAAGAAACA TTTAATGCAA CAGTGATGGC TTCTGACAGC ATAGTACTCT 1560
 TCTATGCTGG TTGGCAAGCA GTATCCATGG CATTTTGTGA ATCCTATATT GATGTGGCAG 1620
 TTAAACTGAA AGGCACATCT ACTATGCTTC TTACTAGAAAT AAACGTGTGA GATTTGGTCTG 1680
 10 ATGTATGTAC TAAGCAAAAT GTTACTGAAT TTCTATCAT AAAGATGTAC AAGAAAGGCG 1740
 AGAACCCAGT ATCTTATGCT GGAATGTTAG GAACCAAGA TCTCCTAAAA TTTATCCAGC 1800
 TCAACAGGAT TTATATATCA GTGAATATAA CATCGATCCA AGAAGCAGAA GAATATTTAA 1860
 GTGGGGAATT ATATAAAGAC CTCATCTTGT ATTCAGTGTG GTCAGTATTG GGACTATTTA 1920
 GTCCAAACCAT GAAACAGACA AAAGAAGATT TTAGTGAAGC AGGAAACTAC CTAAGAGGAT 1980
 ATGTTATCAC TGAATTTTAT TCTGAAGAAG ATGTTTGTCT ACTGTCAACC AAATATGCTG 2040
 CAAGTCTTCC AGCCCTGCTG CTGCGCAGAC ACACAGAAGG CAAAATAGAG AGCATCCAC 2100
 TAGCTAGCAC ACATGCACAA GACATAGTTC AAATAATAAC AGATGCACTA CTGGAATATG 2160
 TTCCGGAAAT CACTGTGGAA AATCTTCCCA GTTATTTCAG ACTTCAGAAA CCATTATTGA 2220
 TTTTGTTCAG TGATGGCACT GTAAATCCCT AATATAAAAA AGCAATATTG ACATGGGTAA 2280
 15 AGCAGAAATA CTGTGATCCA TTTACTCCAT GCTGGTTAAA TCTAAAGAAT ACTCCAGTGG 2340
 GGAGAGGAAT CTGCGGGACA TATTTTGATC CTCTGCCTCC CCTTCTCTTT CTGTGTTTGG 2400
 TGAATCTGCA TTCAAGTGGC CAAGTATTTG CATTTCCCTC AGACCAGGCT ATAATTGAAG 2460
 AAAACCTTGT ATGTGCGCTG AAGAAATTAG AAGCAGGACT AGAAATCAT ATCACAATTT 2520
 TACCTGTCTA AGAATGGAAA CCTCTCTTTC CAGCTTATGA TTTTCTAAGT ATGATAGATG 2580
 CCGCAACATC TGAACGTGGC ACTAGGAAAG TTCCCAAGTG TATGAAGAA ACAGATGTGC 2640
 20 AGGAGAATGA TAAGAAACAA CATGAAGATA AATCGGCACT CAGAAAAGAA CCGATTGAAA 2700
 CTCTGAGAAT AAAGCATTTG AATAGAAGTA ATGGTTTAA AGAAGCAGAA AAATCATTTA 2760
 GACGTGATAA AGAGTTAGGA TGCTCAAAAG TGAACATAAT TTATAGGGCT GTGGTTTCCA 2820
 AAATTTTPTT GGCATGATAG ACTTAATTTA TTCTCTTAAA GAATAATATT AAATCATTTT 2880
 AAGTTTGCAG ACTAGTGCCA TCCAATAGAA TTATAATATA AGTCACATAT TTTATTTAAA 2940
 25 ATTTTCTAGT AACTACATTA AACAAAGTAA AAGTGAGCAG GGCAAAATAA TTTTGATATT 3000
 ACTTTTCAAC CAGTAGTATA CCCAAATAG CGAAATATAG AAATTATTAA TGAGATATTT 3060
 TACATCTCTT TTTGTACCAA GTCTCTTAAA TGCAGTACAT ATTTTATACT TACTGCATT 3120
 CTACTTCCG AGTAGCCATA TTTCAGTGT TCATTGCCAC ATGTGGCCTG TGACTACTGT 3180
 ATTGGACAGT TCAGTACTAG ACAAAACATA GCATAATTAA CTTAGTTCTA GCCATGATTT 3240
 30 CTATTTGATG TAAATTTAAA CTCTAATCAC AGTTAACTCC ACAGTGCATT CATGCAGCTG 3300
 ACAGTTATAT TTGTTTATTT GGAGTCATGA TATTAATAAT AGCGTTTGTG AACCTCAGGG 3360
 GATATTTAGC AATTGTCGGG AGACATTTT GTATGCATGA CTAGGGCAGT TATTGACATT 3420
 TAGTGAGTAG AGGCCATGGA TCCTGCTAAA TAACCTGCAT TGGACAGCGC CCCACAACAA 3480
 35 AGAATTATCC TGCCCGAAAT GGTAGTCGTG CCAAGGCTGA GTAACCTTGT GTTAAAGTA 3540
 ACCTGTGGCA GACTAGGTTT CCAGAATTTT CTGGTTCCTG TCACGTATCA TGGTTGAAAA 3600
 AATTTTGGCT ATTAAGATA TGTATTAGAT GGCTTATACC TGATTATTAC CTGGATACAA 3660
 CTGTGATCTT TCTAATATTT TCAGAAAGTG ATGGGATAAC CCTAGAAGAG GACTCAGAA 3720
 GATATTATTA TTTTAAGTGA GTCTTAAAC CTCTCTTAT TTCTACAAGT TATATGGCTA 3780
 40 AATTCAGAT TGAACAGGGA TTACGATTC TGCCATCTCC TCATGGAAG AGAGGCTCCC 3840
 TCATCTGAAG CGTCTCTGAA ATCTACCCCT GCAAGCTTCA GACAAATCAG TTGATCTCCC 3900
 TGAGCCACAC GGCCTCATTC TGTGAGGAG GGAAGATTA GCCAAAGAGT TAAATTTTAT 3960
 TCCAAATCAC TTAGCTGTTA GACTGATCTG TTTGTAGCAG TTGTTTGTCT CATTTTGTCT 4020
 CTGTGATATT TTTGAGACAT TTGTGAGAA TATCTATTT GGTGCTCTAC TGTATTTTTC 4080
 45 TTTTAAATAT CTACTTGATA TCTTGTCTT TAAATTTTCT TCACATATGG TTTCCTGAT 4140
 ACAACTGATT TTTATAACTG AAATTTAAGG AATCTAACAG CTAAGTGCAT GTAAGTGCAT 4200
 MTATTTCTCT ATACATAGA CCGTTGCTA CTCTCAGCAC CCTCTCTTCA ATTTTPTTTC 4260
 CTGTAGCATG TTAGCTGTTA TTAAACTCAT TTTCATTTCG TTTTATPTCT AATATGGGAA 4320
 CAATGAGAGT GAATCTTAAA TATAGGTTGT AGTAATAAAA CATCATAGC CTAATATATA 4380
 50 GAAAATGCTA ATTAAGTACC AGCACAAGA AACATGAAAT TGCTTAGTCA TTGTACCTTT 4440
 GTCAGCAATT TTGACAGTCA TTAATGTTTG TCATAATTTT AAATAAAGTG TCTGGGTTTC 4500
 AGAATACCTT CAAAAAATAA AAAAAA

SEQ ID NO:26 PAA3 Protein sequence:

Protein Accession #: BAA92582

55 1 11 21 31 41 51
 | | | | |
 MFSGFNVFRV GISFVIMCIF YMPTVNSLPE LSPQKYFSTL QPGLLEELNEA VRFLQDYGIS 60
 VAKVNCVKEE ISRYCGREKD LMKAYLFKGN ILLREFPTDT LFDVNAIVAH VLFALLFSEV 120
 60 KYITNLEDLQ NIENALKGKA NIIPSYVRAI GIPEHRAVHE AGFVYGTITYQ FVLTTETIALL 180
 ESIGSEDVEY AHLVFFHCKL VLDLTQQCRR TLMEQPLTTL NIHLFIKTMK APLLTEVAED 240
 PQQVSTVHLQ LGLPLVPIVS QQATYEADRR TAENVAWRLL GKAGVLLLLR DSELVNIPQD 300
 ANVVFKAARE GVPEFLVLH DVDLIISHVE NNMHIEEIQE DEDNDMEGPD IDVQDDEVAE 360
 TVFRDRKRKL PLELTVELTE EFNATVNAS DSIVLFYAGW QAVSMAPLQS YIDVAVKLKG 420
 65 TSTMLLTRIN CADWSDVCTK QNVTEPPIIK MYKKGENFVS YAGHLGTKDL LKPIQLNRIS 480
 YFVNITSIQE ABEYLSGELY KDLILYSSVS VLGLFSPTHK TAKEDFSEAG NYLKGIVITG 540
 IYSEEDVLLL STKYAASLPA LLLARHTEGK IESIPLASTH AQDIVQIITD ALLEMPPEIT 600
 VENLPSYFRL QKPLLLFSD GTVNPQYKKA ILTIVKQKYL DSFTPCWNLN KNFVVGRIIL 660
 RAYFDPLPPL PLLVLVNLHS GGQVFPAPSD QAIIEENLVL WLKLEAGLE NHITLPAQE 720
 70 WKFPPLPAYDF LSMIDAATSQ RGRTRVPKCM KETDVQENDK EQHEDKSAVR KEPIETLRIK 780
 HWNRNSNWFKE AEKSFRRDKE LGCSKVN

SEQ ID NO:27 PAA5 DNA SEQUENCE

Nucleic Acid Accession #: NM_012449

Coding sequence: 66-1085 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 | | | | |
 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60
 80 AATTAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA 120

5 GGAGAAATTT AGAAGAAGAC GATTATTTCG ATAAGGACAC GGGAGAGACC AGCATGCTAA 180
 AAAGACCTGT GCTTTTGCAT TTGCACCAAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
 CAGAACTTGT GCACACACAG GAACTCTTTC CACAGTGGCA CTTGCCAATT AAAATAGCTG 300
 CTATTATAGC ATCTCTGACT TTTCTTTACA CTCCTCTGAG GGAAGTAATT CACCCTTTAG 360
 CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGTCTTGC 420
 CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480
 TCCAACCTCA TAATGGAACC AAGTATAAGA AGTTTCACCA TTGGTTGGAT AAGTGGATGT 540
 TAACAAGAAA GCAGTTTGGG CTTCTCAGTT TCTTTTITGC TGTACTGCAT GCAATTTATA 600
 10 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC 660
 AGGTCCAACA AAATAAAGAA GATGCCCTGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT 720
 ATGTGTCTCT GGGAAATGTG GGATGGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTG 780
 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACCT TATTAGAGAC AAGCTAGGAA 840
 TTGTTCCCTT TCTACTGGGC ACAATACACG CATTGATTTT TGCTTGGAAAT AAGTGGATAG 900
 15 ATATAAACA ATTTGTATGG TATACACCTC CAACCTTTAT GATAGCTGTT TTCCTTCCAA 960
 TTGTTGTCTT GATATTATAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA 1020
 AGATTAGACA TGGTGGGAAA GACGTCACCA AAATTAACAA AACTGAGATA TGTTCCTCAGT 1080
 TGTAGATTAT CTGTTTACAC ACATTTTGTG TCAATATTGA TATATTTTAT CACCAACATT 1140
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA

20 SEQ ID NO:28 PAA5 Protein sequence
 Protein Accession #: NP_036581

25 1 11 21 31 41 51
 MESRKDITNQ EELWKKPKRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDCPSE 60
 LQHTQELFPQ WHPFKIAAI IASLTFLYTL LREVIHPLAT SHQQVFPYKIP ILVINKVLPM 120
 VSTLLALVY LPGVIAIVQ LHNGTKYKRF PHWLDKWLMT RKQFGLLSFF FAVLHAIYSL 180
 SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
 30 VSDSLTWREP HYIQSKLGIV SLLGLTIAL IFAWNKWIDI KQFVWYTPPT FMAVFLPIV 300
 VLIFRSILFL PCLRKILKI RHGWEDVTRI NKTEICSQL

SEQ ID NO:29 PAA7 DNA SEQUENCE

Nucleic Acid Accession #: NM_030774
 Coding sequence: 1-963 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 ATGAGTTCCT GCAACTTCAC ACATGCCACC TTTGTGCTTA TTGGTATCCC AGGATTAGAG 60
 AAAGCCCATT TCTGGGTGGG CTTCCCTCTC CTTTCCATGT ATGTAGTGGC AATGTTTGA 120
 40 AACTGCATCG TGGTCTTCAT CGTAAGGACG GAACGCAGCC TGCACGCTCC GATGTACCTC 180
 TTTCTCTGCA TGCTTGACGC CATTGACCTG GCCTTATCCA CATCCACCAT GCCTAAGATC 240
 CTTGCCCTTT TCTGGTTTGA TTCCCGAGAG ATTAGCTTTG AGGCCTGTCT TACCAGATG 300
 TCTTTTATTC AGCCCTCTC AGCCATGAA TCCACCATCC TGCTGGCCAT GGCCTTTGAC 360
 CGTTATGTGG CCATCTGCCA CCCACTGCGC CATGCTGCAG TGCTCAACAA TACAGTAACA 420
 45 GCCCAGATTG TGGTCTGGG TGTGGTCCGC GGATCCCTCT TTTTTCCTCC ACTGCCTCTG 480
 CTGATCAAGC GGTGCGCTTT CTGCCACTCC AATGTCTCTC CGCACTCCTA TTGTGTCCAC 540
 CAGGATGTAA TGAAGTTGGC CTATGCAGAC ACTTTGCCCA ATGTGCTATA TGGTCTTACT 600
 GCCATTCTGC TGGTCATGGG CGTGGACGTA ATGTTCATCT CTTTGTCTTA TTTTCTGATA 660
 ATAGCAACCG TTCTGCAACT GCCTTCCAAG TCAGAGCGGG CCAAGGCCCT TGGAACTCTG 720
 50 GTGTACACCA TTGGTGTGGT ACTCGCCTTC TATGTGCCAC TTATTGGCCT CTCAGTGGTA 780
 CACCGCTTTG GAACAGCCTC TCATCCCATC GTGCGTGTG TCATGGGTGA CATCTACCTG 840
 CTGCTGCCTC CTGTCTACAA TCCCATCATC TATGGTGCCA AAACCAACAA GATCAGAACA 900
 CGGTGCTCGG CTATGTTCAA GATCAGCTGT GACAAGGACT TGCAGGCTGT GGGAGGCAAG 960
 TGACCCCTAA CACTACACTT CTCTTATCTT TTATTGGCTT GATAAACATA ATTATTCTTA 1020
 55 ACATAGCTTT ATTTCCAGTT GCCCATAAGC ACATCAGTAC TTTTCTCTGG CTGGAATAGT 1080
 AAATAAAGT ATGTTACATC TACCTAAAGG ACTATTATGT GGAATAATAC ATACTAATGA 1140
 AGTATTACAT GATTTAAGA CTACAATAAA ACCAAACATG CTTATAACAT TAAGAAAAAC 1200
 AATAAAGATA CATGATTGAA ACCAAGTTGA AAAATAGCAT ATGCCCTTGA GGAATGTGTC 1260
 60 TCAAATTAAT AATGATTTAG TGTGTCTCCT ACTTTCTCTC TCTTTTCTCT TTCTTTTCTT 1320
 TTTATTATGG TTAGCTGTCA CATACAACTT TTTTTTTTTT TGAGATGGGG TCTCGCTCTG 1380
 TCACCAGGCT GGAGTGCACT GGCCTGATCT CGGCTCACTG CAACCTCCAC ATCCCATGTT 1440
 GAAGTAATTC TTCTGCCTCA GCCTCCCGAG TAGCTGGGAC TAGAGGAACG TGCCACCATG 1500
 ACTGGCTAAT TTCTGTATT TTTTAGTAGA GACAGAGTTT CACCATGTTG GCCAGGATGG 1560
 65 TCTCGATCTC CTGACCTTGT GATCCACCCG CCTCAGCTTC CCAAGTGTGT GGGATTACAG 1620
 GTGTGAACCA CTGTGCCCGG CCTGTGTACA ACTTTTAAAA TAGGGAATAT GATAGCTTCG 1680
 CATGGTGGTG TGCACCTATA GCCCCACTG CCTGGAAGGC TGAGGTGGGA GAATCGCTTG 1740
 AGTCCAGGAG TTGAGGTTTA CAGTGATCCA CGATCGTACC ACTACACTCC AGCCTGGGCA 1800
 ACAGAGCAAG ACCCTGTCTC AAAGCATAAA ATGGAATAAC ATATCAAATG AAACAGGGAA 1860
 AATGAAGCTG ACAATTTATG GAAGCCAGGG CTGTGCACAG TCTCTACTGT TATTATGCAT 1920
 70 TACCTGGGAA TTAGATATAA CCCTTAATAA TARTGCCAAT GAACATCTCA TGTGTGCTCA 1980
 CAATGTCTCG GCACTATTAT AAGTGCTTCA CAGGTTTAT GTGTCTCTCG TAACCTTTATG 2040
 GAGTAGGTAC CATTGTGTCT TCTTTATTAT AAGTGAGAGA AATGAAGTTT ATATTATCAA 2100
 GGGGACTAAA GTACACCGGC TTGTGGGCAC TGTGCCAAGA TTTAAATTA AATTGTATGG 2160
 TTGAATACAG TTACTTAATG ACCATGTTAT ATTGCTTCCT GTGTAAACAT TGCCATTAT 2220
 75 TTCTCAGCT GTACAAATCC TCTGTTTCTC CTCTGTTACA CACTAACATC AATGGCTTTG 2280
 TACTTGTGAT GAGAGATAAC CTTCGCCCTAG TTGTGGGCAA CACATGCAGA ATAATCCTGT 2340
 TTTACAGCT CATTTCGTGA TCTTATGCT TGCTTTTCTC CAGATTACAG GAGAATGTTG 2400
 TTGTCTATTT GTCTCTTACA TCTCCTTGAT CATGTCTTCA TTTTAAATG TGCTCTGTAC 2460
 80 CTGTCAAAAA TTTTGAATGT ACACCACATG CTATTGTCTG AACTTGAGTA TAAGATAAAA 2520
 TAAAAATTTA TTTTAAATTT T

SEQ ID NO:30 PAA7 PROTEIN SEQUENCE

Protein Accession #: NP_110401

5 1 11 21 31 41 51
 | | | | |
 MSSCNFTHAT FVLIGIPGLE KAHFWVGPPL LSMYVVMFPG NCIVVPIVRT ERSIHAPMYL 60
 FLCMLAIDL ALSTSTMPKI LALFWFDSRE ISPEACLQHM PFIHALSAIE STILLAMAPD 120
 RYVAICHPLR HAALNNNTVT AQIGIVAVVR GSLPFPPLPL LIKRLAFCHS NVLSHSYCVH 180
 10 QDVMKLAYAD TLPNVVYGLT ALLVMGVVDV MFISLSYFLI IRTVLQLPSK SERAKAFGTC 240
 VSHIGVVLAF YVPLIGLSVV HRFGNLSLHPI VRVVMGDIYL LLPPVINPII YGAKTKQIRT 300
 RVLAMPKISC DKDLQAVGGK

SEQ ID NO:31 PAV6 DNA SEQUENCE

Nucleic Acid Accession #: XM_050837

Coding sequence: 1-1020 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 20 ATGAACTGGG AGCTGCTGCT GTGGCTGCTG GTGCTGTGCG CGCTGCTCCT GCTCTTGGTG 60
 CAGCTGCTGC GCTTCTTGAG GCCTGACGGC GACCTGACGC TACTATGGGC CGAGTGGCAG 120
 GGACGACGCC CAGAATGGGA GCTGACTGAT ATGGTGGTGT GGGTGACTGG AGCCTCGAGT 180
 GGAATTGGTG AGGAGCTGGC TTACCACTTG TCTAACTAG GAGTTTCTCT TGTGCTGTCA 240
 25 GCCAGAAAGAG TGCATGAGCT GGAAGGGGTG AAAAGAAGAT GCCTAGAGAA TGCCAATTTA 300
 AAAGAAAAAG ATATACTTGT TTTGCCCTTT GACCTGACCG ACACCTGGTTC CCATGAAGCG 360
 GCTACCAAAG CTGTTCTCCA GGAGTTTGGT AGAATCGACA TTCTGGTCAA CAATGGTGGA 420
 ATGTCCAGC GTTCTCTGTG CATGGATACC AGCTTGGATG TCTACAGAAA GCTAATAGAG 480
 CTTAACTACT TAGGGACGGT GTCCTTGACA AAATGTGTTT TGCCCTACAT GATCGAGAGG 540
 30 AAGCAAGGAA AGATTGTATC TGTGAATAGC ATCCTGGGTA TCATATCTGT ACCTCTTTCC 600
 ATTGGATACT GTGCTAGCAA GCATGCTCTC CGGGGTTTTT TTAATGGCCT TCGAACAGAA 660
 CTTGCCACAT ACCCAGTAT AATAGTTTCT AACATTTGCC CAGGACCTGT GCAATCAAAT 720
 ATTTGTGAGA ATTCCTAGC TGGAGAAATC ACAAGACTA TAGGCAATAA TGGAGACCAG 780
 TCCCAACAGA TGACAACCA TCGTTGTGTG CGGCTGATGT TAATCAGCAT GGCCAATGAT 840
 35 TTGAAAGAAG TTTGGATCTC AGAACAACCT TTCTTGTAG TAACATATTT GTGCCAATAC 900
 ATGCCAACCT GGGCTGGTG GATAACCAAC AAGATGGGGA AGAAAAGGAT TGAGAACTTT 960
 AAGATGGTG TGGATGCAGA CTCCTCTTAT TTTAAATCT TTAAGACAAA ACATGACTGA

SEQ ID NO:32 PAV6 Protein sequence

Protein Accession #: XP_050837

40 1 11 21 31 41 51
 | | | | |
 MNWELLMLL VLCALLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD HVVWVTGASS 60
 GIGEEAYQL SKLGVSLVLS ARRVHELERV KRRCLENGNL KEKDILVLP DLTDTGSHEA 120
 45 ATKAVLQEFQ RIDILVNNGG MSQSLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHMIER 180
 KQKIVTVNS ILGIISVPLS IGYCASKHAL RGFFNGLRTE LATYPGLIIVS NICPGFVQSN 240
 IVENSLAGEV TKTTGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISQEP PLLVTYLYWQY 300
 MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD

SEQ ID NO:33 PBA6 DNA SEQUENCE

Nucleic Acid Accession #: NM_006853

Coding sequence: 26-874 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 | | | | |
 AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC 60
 ATCGGGCAGA GGTCTCAGC CAGCCAAAGGA ACCTGGGGCC CGCTCTCTCC CCTCCAGGC 120
 CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180
 60 CAGGATCATC AAGGGGTTCC AGTGCAAGCC TCACTCCAG CCTGGCAGG CAGCCCTGTT 240
 CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAAC 300
 AGCCCACTGS CTCAGCCCC GCTACATAGT TCACCTGGGG CAGCACAAAC TCCAGAAGGA 360
 GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCTTTC CCCCACCCCG GCTTCAACAA 420
 CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
 65 CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCTCA CGCTGTGTCA CTGCTGGCAC 540
 CAGCTGCCTC ATTTCCGGCT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCCCTACAC 600
 CTTGCGATGC GCCAACATCA CCATCATTTGA GCACCAAGAG TGTGAGAACG CCTACCCCGG 660
 CAACATCACA GACACCATGG TGTGTCCAG CGTGCAGGAA GGGGGCAAGG ACTCTGCCA 720
 GGGTGACTCG GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCTGGGG 780
 70 CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATG 840
 GGACTGTGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
 ACCCTCTATT TCCACTTGGT GTTTGGTTCC GTTACTCTCT GTTAATAAGA AACCTAATG 960
 CAAGACCCCT TACGAACATT CTTTGGGCCT CTTGACTTAC AGGAGATGCT GTCACTTAAT 1020
 AATCAACCTG GGGTTCGAAA TCAGTGAAGC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080
 75 GACTCTGGGA ATGACAACAC CTGGTTTGTG CTCGTGTGTA TCCCCAGCCC CAAAGACAGC 1140
 TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

SEQ ID NO:34 PBA6 PROTEIN SEQUENCE

Protein Accession #: NP_006844

1 11 21 31 41 51
 5 MRILQLILLA LATGLVGGET RIIGFECKP HSQFWQAALF EKTRLLCGAT LIAPRWLLTA 60
 AHCLKPRYIV HLGQHNLOKE EGCEOTRTAT ESFPHPGFNN SLPNKDHRND IMLVRMASPV 120
 SITWAVRPLT LSSRCVTAQT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCNAYPG 180
 NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVYTKVKYV 240
 DWIQETMKN

10 Nucleic Acid Accession #: NM_001775 SEQ ID NO:35 PBC1 DNA SEQUENCE
 Coding sequence: 70-972 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 15 CTAAAGCTCT CTGCTGCCT AGCCTCCTGC CGGCTCATC TTCGCCAGC CAACCCCGCC 60
 TGGAGCCCTA TGGCCAACTG CGAGTTTACG CCGGTGTCCG GGGACAAACC CTGCTGCCGG 120
 CTCTCTAGGA GAGCCCAACT CTGCTTTGGC GTCAATATCC TGGTCTGTAT CCTCGTCGTG 180
 GTGCTCGCGG TGGTCGTCCC GAGGTGGCGC CAGACGTGGA GCGGTCCGGG CACCACCAAG 240
 20 CGCTTTCCCG AGACCTCTCT GCGCGGATGC GTCAAGTACA CTGAAATTCA TCCTGAGATG 300
 AGACATGTAG ACTGCCAAAG TGTATGGGAT GCTTTCAAGG GTGCAITTTAT TTCAAAACAT 360
 CCTTGCACAA TTACTGAAGA AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA 420
 CCTTGCACAA AGATTCTTCT TTGGAGCAGA ATAAAGATC TGGCCCATCA GTTCACACAG 480
 GTCCAGCGGG ACATGTTTCA CCTGGAGGAC ACCTGCTAG GCTACCTTGC TGATGACCTC 540
 25 ACATGGTGTG GTGAATTCAC CACTTCCAAA ATAACTATC AATCTTGCCC AGACTGGAGA 600
 AAGGACTGCA GCAACAACCC TGTTCAGTA TTCTGAAAA CGGTTTCCCG CAGGTTTGCA 660
 GAAGCTGCCCT GTGATGTGTT CCATGTGATG CTCAATGGAT CCGCAGTAA AATCTTTGAC 720
 AAAAAACAGCA CTTTGGGAG TGTGGAAGTC CATAATTTCG AACCCAGAGAA GGTTCAGACA 780
 CTAGAGGCTT GGGTGATACA TGGTGAAGA GAAGATTCCA GAGACTTATG CCAGGATCCC 840
 30 ACCATAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAT 900
 ATCTACAGAC CTGACAAGTT TCTTCAGTGT GTGAAAAATC CTGAGGATTC ATCTTGACA 960
 TCTGAGATCT GAGCCAGTCG CTGTGTTGT TTTAGCTCCT TGACTCCTTG TGGTTTATGT 1020
 CATCATACAT GACTCAGCAT ACCTGCTGTT GCAGAGCTGA AGATTTTGGG GGGTCTCTCA 1080
 CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTTCCCAA AGTCTTAAAA TAACCTATAT 1140
 35 CATCAGCATA CCTTTATTGT GATCTATCAA TAGTCAAGAA AAATTATTGT ATAAGATTAG 1200
 AATGAAAAAT GTATGTTAAG TTACTTCCTT TAG

SEQ ID NO:36 PBC1 Protein sequence
 Protein Accession #: NP_001766

1 11 21 31 41 51
 40 MANCFSPVVS GDKPCRLSR RAQLCLGVSI LVLILVVVLA VVPRWRQTW SGPQTTRFP 60
 ETVLARCVKY TEIHPERHVR DCQSVWDAFK GAFISKHPCN ITEEDYQPLM KLGTVTPCN 120
 45 KILLWSRIKD LAHQFTQVQR DMFTLEDTL L GYLADDLTWC GEPNTSKINY QSCPDRKDC 180
 SNNPVSFVFW TVSRFAEAAA CDVVHVLNNG SRSKIFDKNS TFGSVEVHNL QPEKVQTLA 240
 WVIHGREDSD RDLCDPTIK ELESIIKSRN IQFSCRNIR PDKFLQCVKN PEDSSCTSEI

50 Nucleic Acid Accession #: XM_017718 SEQ ID NO:37 PBH1 DNA SEQUENCE
 Coding sequence: 1-3315 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 55 ATGTCCTTTC GGGCAGCCAG GCTCAGCATG AGGAACAGAA GGAATGACAC TCTGGACAGC 60
 ACCCGGACCC TGTACTCCAG CCGTCTCCGG AGCAGAGACT TGTCTTACAG TGAAGCGAC 120
 TTGGTGAATT TTATTCAAGC AATTTTAAAG AAACGAGAAT GTGCTTCTTT TACCAAGAT 180
 TCCAAGGCCA CGGAGAATGT GTGCAAGTGT GGCTATGCCC AGAGCCAGCA CATGGAAGGC 240
 60 ACCCAGATCA ACCAAAGTGA GAAATGGAAC TACAAGAAAC ACACCAAGGA ATTTCTTACC 300
 GAGCGCTTTG GGGATATTCA GTTTGAGACA CTGGGAAGA AAGGGAAGTA TATACGCTTG 360
 TCCTGCGACA CGGACGCGGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGARA 420
 ACACCAACCC TGGTCATTTC TGTGACCGGG GCGCCAAGA ACTTCGCCCT GAAGCCGCGC 480
 ATGCGCAAGA TCTTCAGCCG GCTCATCTAC ATCGCGCAGT CCAAAGGTGC TTGGATTCTC 540
 65 ACGGAGGCA CCATTATGCG CCGTATGAAG TACATCGGGG AGGTGGTGAG AGATAACACC 600
 ATCAGCAGGA GTTCAGAGGA GAATATTGTG GCCATTGGCA TAGCAGCTTG GGCATGGTC 660
 TCCAACCGGG ACACCTCAT CAGGAATTGC GATGCTGAGG GCTATTTTTC AGCCAGTAC 720
 CTTATGGATG ACTTCACAAG AGATCCACTG TATATCTTGG ACAACAACCA CACACATTTG 780
 CTGCTCGTGG ACAATGGCTG TCATGGACAT CCCACTGTG AAGCAAAGCT CCGGAATCAG 840
 70 CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGA CAAGATCCCC 900
 ATTGTGTGTT TTGCCCAAGG AGGTGGAAGA GAGACTTGA AAGCCATCAA TACCTCCATC 960
 AAAAAATAAA TTCTTGTGTT GGTGTGGGAA GGCTCGGGCC AGATCGCTGA TGTGATCGCT 1020
 AGCTTGTGG AGGTGGAGGA TGCCCTGACA TCTTCTGCGG TCAAGGAGAA GCTGTTGCGC 1080
 TTTTACCACC GCACGGTGTG CCGGCTGCCCT GAGGAGGAGA CTGAGAGTTG GATCAAATGG 1140
 75 CTCAAGAAA TTCTCGAATG TTCTCACTTA TTAACAGTTA TTAATAAGTA AGAAGCTGGG 1200
 GATGAAATG TGAGCAATGC CATCTCTAC GCTCTATACA AAGCCTTCAG CACCAGTGAG 1260
 CAAGACAAGG ATAACCTGAA TGGGCAGCTG AAGCTTCTGC TGGAGTGGAA CCAGCTGGAC 1320
 TTAGCAATG ATGAGATTTT CACCARTGAC CGCGATGGG AGTCTGCTGA CCTTCAAGAA 1380
 80 GTCATGTTTA CGGCTCTCAT AAAGGACAGA CCCAAGTTTG TCCGCCCTCT TCTGGAGAAT 1440
 GGCTTGAACC TACGGAAGTT TCTCACCCAT GATGTCTCA CTGAACCTCT CTCCAACCA 1500
 TTCAGCACGC TTGTGTACCG GAATCTGAG ATCGCCAAGA ATTCCTATAA TGATGCCCTC 1560

CTCACGTTTG TCTGGAAGCT GGTTCGGAAC TTCCGAAGAG GCTTCCGGAA GGAAGACAGA 1620
 AATGCCCGGG ACCGAGATGGA CATAGAACTC CACGACCTGT CTCCATTATC TCGGCACCCC 1680
 CTGCAAGCTC TCTTCATCTG GGCATCTCTT CAGAATAAGA AGGAACCTCT CAAAGTCATT 1740
 TGGGAGCAGA CCAGGGGCTG CACTCTGGCA GCCCTGGGAG CCAGCAAGCT TCTGAAGACT 1800
 CTGGCCAAAG TGAAGAACGA CATCAATGCT GCTGGGGAGT CCGAGGAGCT GGCTAATGAG 1860
 TACGAGACCC GGGCTGTTGA GCTGTTCACT GAGTGTACCA GCAGCGATGA AGACTTGGCA 1920
 GAACAGCTGC TGGTCTATTG CTGTGAAGCT TGGGGTGGAA GCAACTGTCT GGAGCTGGCG 1980
 GTGGAGGCCA CAGACCAGCA TTTCATCGCC CAGCCTGGGG TCCAGAATTG TCTTTCTAAG 2040
 CAATGGTATG CAGAGATTTC CCGAGACACC AAGAACTGGA AGATTATCCT GTGTCTGTTT 2100
 ATTATACCTT TGTGGGCTG TGGCTTTGTA TCATTTAGGA AGAAACCTGT CGACAAGCAC 2160
 AAGAAGCTG TTTGCTACTA TGTGGCGTTC TTCACCTCCC CCTTCGTGGT CTCTCCTGG 2220
 AATGTGGTCT TCTACATCCG CTTCCTCCTG CTGTTTGCTT ACGTCTGTCT CATGGATTTC 2280
 CATTCGGTGC CACACCCCCC CGAGCTGGTC CTGTACTCGC TGGTCTTTGT CCTCTCTGT 2340
 GATGAAGTGA GACAGTGGTA CGTAAATGGG GTGAATTATT TTAAGTACCT GTGGAATGTG 2400
 ATGGACACGC TGGGGCTTTT TTAATTCATA GCAGGAATTG TATTTCGGCT CCACTCTTCT 2460
 AATAAAGCT CTCTGTATTG TGGACGAGTC ATTTCTGTCT TGAAGTACAT TATTTTCACT 2520
 CTAAGATTGA TCCACATTTT TACTGTAAGC AGAACTTAG GACCCAAGAT TATAATGCTG 2580
 CAGAGGATGC TGATCGATGT GTTCTTCTTC CTGTCTCTCT TTGCGGTGTG GATGGTGGCC 2640
 TTTGGGCTGG CCAGGCAAGG GATCCTTAGG CAGAATGAGC AGCGCTGGAG GTGGATATTC 2700
 CGTTCCGCTG TCTACGAGCC CTACCTGGCC ATGTTGCGCC AGGTGCCCGG TGACGTGGAT 2760
 GGTACACCTF ATGACTTTGC CCACTGCACC TTCACTGGGA ATGAGTCCAA GCCACTGTGT 2820
 GTGGAGCTGG ATGAGCACAA CCTGCCCCGG TTCCCGGAGT GGATCACCAT CCCCTGTGTG 2880
 TGCATCTACA TGTATCCAC CAACATCCCT CTGGTCAACC TGCTGGTCCG CATGTTTGGC 2940
 TACACCGTGA GCACCGTCCA GGAGAACAAT GACCAGTCTC GGAAGTTCCA GAGGTACTTC 3000
 CTGGTGCAGG AGTACTGACG CCGCTCAAT ATCCCTTCC CCTTCATCTC CTTCGCTTAC 3060
 TTCTACATCT TGTGAAGAA GTGCTTCAAG TGTGTCTGCA AGGAGAAAAA CATGGAGTCT 3120
 TCTGTCTGCT GTTTCAAAAA TGAAGACAAT GAGACTCTGG CATGGGAGGG TGTATGAAG 3180
 GAAACCTACC TTGTCAAGAT CAACACAAAA GCCAACGACA CCTCAGAGGA AATGAGGCAT 3240
 CGATTAGAC AACTGGATAC AAGCTTAAT GATCTCAAGG GTCTTCTGAA AGAGATTGCT 3300
 AATAAATCA AATGA

SEQ ID NO:38 PBH1 Protein sequence

Protein Accession #: XP_017718

1 11 21 31 41 51
 MSFRAARLSM RNRNRDLDLS TRTLYSSASR STDLSYSED LVNFIQANFK KRCVFFTKD 60
 SKATENVCKC GYAQSQHMEG TQINQSEKWN YKHKTEFPT DAFGDIQFET LGRKKGYIRL 120
 SCDTDAEILY ELLTQWHHLK TPNLVISVTG GAKNFALKPR MRKIFSRLLI IAQSKGAWIL 180
 TGGTHYGLMK YIGEVVRDNT ISRSSEENIV AIGIAAWGMV SNRDLTIRNC DAEGYFLAQP 240
 LMDDFTRDPL YILDNNHNLH LLVDNGCHGH PTVEAKLRNQ LEKYISERTI QDSNYGGKIP 300
 IVCFAGGGGK ETLKAINTSI KNKIPCVVVE GSGQIADVIA SLVEVEDALT SSAVKEKLV 360
 FLPRTVSRPL EETESWIKW LKEILECSHL LTVIKMEEAG DEIVSNAISY ALYKAFSTSE 420
 QDKDNWNGQL KLLLENNQLD LANDEIFTND RRWESADLQE VMFTALIKDR PKFVRLFLEN 480
 GLNLRKFLTH DVLTELFNSH FSTLVYRNLO IAKNSYNDAL LTFVWKIVAN FRRGRFRKEDR 540
 NGRDEMDIEL HDVSPITRHP LQALFIWAIL QNKKELSKVI WEQTRGCTLA ALGASKLLKT 600
 LAKVNDINA AGESEELANE YETRAVELFT ECYSSDEDLA EQLLVYSCEA WGGSNCLELA 660
 VEATDQHFIA QPGVQNFSLK QWYGEISRDT KNWKIILCLF IIPLVGCGFV SFRKKPVDKH 720
 KLLWYVAF FTSPPVVFWS NVVFYIAFL LFAVLLMDF HSPVPPPELV LYSLVFVLF 780
 DEVRQWYVNG VNYFTDLWNV MDTLGLFYFI AGIVFRLHSS NKSSLYSGRV IFCLDYIIFT 840
 LRLIHIFTVS RNLGPKIIML QRHLIDVFFP LFLFAVMHVA FGVARQGI LR QNEQRWRWIP 900
 RSVIYEPYLA MFGQVPSVDV GTTYDFAHCT FTGNESKPLC VELDEHNLPR FPEWITIPLV 960
 CIYMLSTNLL LVNLLVAMFG YTVGTQVQEN DQVWKFQRYF LVQEYCSRLN IPFPFIVPAY 1020
 FYMVKKCFK CCKEKNMES SVCCPKNEDN ETLAWEGVMK ENYLVKINTK ANDTSEMRH 1080
 RFRQLDTKLN DLKGLLKEIA NKIK

SEQ ID NO:39 PBH3 DNA SEQUENCE

Nucleic Acid Accession #: XM_011804

Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGCCTCGCC TGTCTTGTG CCACCTGCTA GAATCTCTGT TACTACTGAA CCAATTTTCC 60
 AGAGCAGTCC CGGCCAAATG GAAGGACGAT GTTATTAAAT TATCGGCGCG CGAATTAGTT 120
 CGCGCGCAGA TTGCCATTG CCGCATGAGC ACCTGGAGCA AAGGCTCTCT GAGCCAGGAA 180
 GATGCTCTCT AGACACCTAG ACCAGTGCCA GAAATGTGAC CATCTTCAT CAACAAAGAT 240
 ACAGAACTA TAATTATCAT GTTGGAATTC ATTGCTAATT TGCCACCGGA GCTGAAGGCA 300
 GCCCTATCTG AGAGGCAACC ATCATTAACA GAGCTACAGC AGTATGTACC TGCAATTAAG 360
 GATTCCAACT TTAGCTTTGA AGAATTTAAG AAACCTATTC GCAATAGCCA AAGTGAAGCC 420
 GCAGACAGCA ATCTTTCAGA ATTAAATATC TTAGGCTTGG ATACTCATTC TCAAAAAAG 480
 AGACGACCTC ACGTGGCACT GTTTGAGAAA TGTTCCTTAA TTGGTTGTAC CAAAAGGTCT 540
 CTGTCTAAAT ATTGCTGA

SEQ ID NO:40 PBH3 PROTEIN SEQUENCE

Protein Accession #: NP_008842

1 11 21 31 41 51
 MPRLFLHLL EFCLLNQFS RAVAAKWKDD VIKLCGRRLV RAQIAICGHS TWSKRSLSQE 60

DAPQTPRPVA EIVPSFINKD TETIIIMLEF IANLPPELKA ALSERQPSLP ELQYVPALK 120
 DSNLSFEEFK KLIRNRQSEA ADSNPSELKY LGLDTHSQK RRPYVALPEK CCLIGCTKRS 180
 LAKYC

5

SEQ ID NO:41 PBH5 DNA SEQUENCE

Nucleic Acid Accession #: NM_005845

Coding sequence: 1-3978 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
 | | | | | |
 ATGCTGCCCG TGTACCAGGA GGTGAAGCCC AACCCGCTGC AGGACGCGAA CCTCTGCTCA 60
 CGCGTGTCT TCTGGTGGCT CAATCCCTTG TTTAAATTTG GCCATAAACG GAGATTAGAG 120
 GAAGATGATA TGTATTTCAGT GCTGCCAGAA GACCGCTCAC AGCACCTTGG AGAGGAGTTG 180
 CAAGGCTTCT GGGATAAAGA AGTTTTAAGA GCTGAGAATG ACGCACAGAA GCCTTCTTTA 240
 15 ACAAGAGCAA TCATAAAGTG TTAAGTGAAG TCTTATTTAG TTTTGGGAAT TTTTACGTTA 300
 ATTGAGGAAA GTGCCAAAGT AATCCAGCCC ATATTTTGGG GAAAAATTAT TAATTATTTT 360
 GAAAAATTAT ATCCCAATGA TTCTGTGGCT TTGAACACAG CGTACGCCCTA TGCCACGGTG 420
 CTGACTTTT GCACGCTCAT TTTGGCTATA CTGATCACT TATATTTTTA TCACGTTTCA 480
 TGTGCTGGGA TGAGGTTACG AGTAGCCATG TGCCATATGA TTTATCGGAA GCGACTTCGT 540
 20 CTTAGTAACA TGCCCATGGG GAAGACAACC ACAGGCCAGA TAGTCAATCT GCTGTCCAAT 600
 GATGTGAACA AGTTTGATCA GGTGACAGTG TTCTTACACT TCCTGTGGGC AGGACCACATG 660
 CAGGCGATCG CAGTGACTGC CCTACTCTGG ATGGAGATAG GAATATCTGT CCTTGTGGG 720
 ATGGCAGTTC TAATCATCTT CCTGCCCTTG CAAAGCTGTT TGGGGAAGTT GTTCTCATCA 780
 25 CTGAGGAGTA AAAGTCAAC TTTACCGAT GCCAGGATCA GGACCATGAA TGAAGTTATA 840
 ACTGTTATAA GGATAATAAA AATGTACGCC TGGGAAAAGT CATTTTCAAA TCTTATTACC 900
 AATTGTAGAA AGAAGGAGAT TTCCAAGATT CTGAGAAGTT CCTGCTCAG GGGGATGAAT 960
 TTGGCTTCGT TTTTCAGTGC AAGCAAAATC ATCGTGTGTT TGACCTTCAC CACCTACGTG 1020
 CTCTCTGGCA GTGTGATCAC AGCCAGCCGC GTGTCTGTGG CAGTGACGCT GTATGGGGCT 1080
 30 GTGCGGCTGA CGGTACCTCT TTCTTCCCTC TCAGCCATTC AGAGGGTGTG AGAGGCAATC 1140
 GTCAGCATCC GAAGAATCCA GACCTTTTTC CTACTTGATG AGATATCACA GCGCAACCGT 1200
 CAGCTGCCGT CAGATGGTAA AAAGATGGTG CATGTGCAGG ATTTTACTGC TTTTGGGAT 1260
 AAGGCATCAG AGACCCCAAC TCTACAAGGC CTTTCTTTTA CTGTACAGCC TGGCGAATGT 1320
 TTAGCTGTGG TCGGCCCTGT GGGAGCAGGG AAGTCATCAC TGTAAAGTGC CGTGCTCGGG 1380
 35 GAATTGGCCC CAAGTCACGG GCTGCTCAGC GTGCATGAA GAATTGCCTA TGTGTCTCAG 1440
 CAGCCCTGGG TGTTCCTGGG AACTCTGAGG AGTAATATTT TATTTGGGAA GAAATACGAA 1500
 AAGGAACGAT ATGAAAAGT CATAAAGGCT TGTGCTCTGA AAAAGGATTT ACAGCTGTGT 1560
 GAGGATGTG ATCTGACTGT GATAGGAGAT CGGGGAACCA CGCTGAGTGG AGGGCAGAAA 1620
 GCACGGGTAA ACCTTGCAAG AGCAGTGTAT CAAGATGCTG ACATCTATCT CCTGACGAT 1680
 40 CCTCTCAGTG CAGTAGATGC GGAAGTTAGC AGACACTTGT TCGAACTGTG TATTTGTCAA 1740
 ATTTTGCATC AGAAGATCAC AATTTTAGTG ACTCATCAGT TGCAGTACCT CAAAGCTGCA 1800
 AGTCAGATTC TGATATTGAA AGATGGTAAA ATGGTGCGA AGGGGACTTA CACTGAGTTC 1860
 CTAAATATCT GTATAGATTT TGGCTCCCTT TTAAGAAGG ATAATGAGGA AAGTGAACAA 1920
 CCTCAGTTC CAGGAACCTC CACACTAAGG AATCGTACCT TCTCAGATTC TTCGGTTTGG 1980
 45 TCTCAACAAT CTTCTAGACC CTCTTGAAA GATGGTGTCT TGGAGAGCCA AGATACAGAG 2040
 AATGTCCATG TGTACTATTC AGAGGAGAAC CGTTCTGAAG GAAAAGTTGG TTTTCAAGCC 2100
 TATAAGATT ACTTCAGAGC TGGTGTCTAC TGGATGTCT TCATTTCCTT TATTTCTCTA 2160
 AACACTGTG CTGAGGTGCT CTATGTGCTT CAAGATTGGT GGCTTTTATA CTGGGCAAAC 2220
 AAACAAAGTA TGCTAAATGT CACTGTAAAT GGAGGAGGAA ATGTAAACCA GAAGCTAGAT 2280
 50 CTTAACTGGT ACTTAGGAAT TTATTCAGT TTAACGTAG CTACCGTCTT TTTTGGCATA 2340
 GCAAGATCTC TATTTGTATT CTACGTCTTT GTTAACCTTT CACAACTTT GCACAAACAA 2400
 ATGTTTGAGT CAATTCGAA AGCTCCGGTA TTAATCTTTG ATAGAAATCC AATAGGAAGA 2460
 ATTTTAAATC GTTTCTCCAA AGACATTGGA CACTTGGATG ATTTGTCTGC GCTGACGTTT 2520
 TTAGATTTC TCCAGACATT GCTACAAGTG GTTGGTGTGG TCTGTGTGGC TGTGGCCGTG 2580
 55 ATTCCTTGGA TCGCAATACC CTTGGTTCCT CTTGGAATCA TTTTCATTTT TCTTCGGCGA 2640
 TATTTTTTGG AAACGTCAAG AGATGTGAAG CGCTTGAAT CTACAACCTG GAGTCCAGTG 2700
 TTTTCCACT TGTCACTCTC TCTCCAGGGG CTCTGGACCA TCCGGGCATA CAAAGCAGAA 2760
 GAGAGGTGTC AGGAAGTGTG TGATGCACAC CAGGATTTAC ATTCAGAGGC TTGGTTCTTG 2820
 TTTTGTGCAA CGTCCCGCTG GTTCGCCGTC CGCTGGATG CCATCTGTGC CATGTTTGTG 2880
 60 ATCATCGTTG CCTTTGGGTC CTTGATTTCT GCAAAAACCT TGGATGCCGG GCAGGTTGGT 2940
 TTGGCACTGT CCTATGCCCT CACGCTCATG GGGATGTTTC AGTGGTGTGT TCGACAAAGT 3000
 GCTGAAGTTG AGAATATGAT GATCTCAGTA GAAAGGGTCA TTGAATACAC AGACCTTGAA 3060
 AAAGAAGCAC CTTGGGAATA TCAGAAACGC CCACCACCAG CCTGGCCCA TGAAGGAGTG 3120
 ATAATCTTTG ACAATGTGAA CTTATGTATC AGTCCAGGTG GGCCTCTGGT ACTGAAGCAT 3180
 65 CTGACAGCAC TCATTAATTC ACAAGAAAAG GTTGGCATTG TGGGAAGAAC CCGAGCTGGA 3240
 AAAAGTTCCC TCATCTCAGC CCTTTTGA TGTGAGAAC CCGAAGGTAA AATTGGGATT 3300
 GATAAGATCT TGACAACTGA AATTGGACTT CACGATTTAA GGAAGAAAAT GTCAATCATA 3360
 CCTCAGAAC CTGTTTGTGT CACTGGAACA ATGAGGAAAA ACCTGGATCC CTTTAAATGAG 3420
 70 CACACGGATG AGGAACGTGT GAATGCCTTA CAAGAGGTAC AACTTAAAGA AACCATTGAA 3480
 GATCTTCTCT GTAAATGGA TACTGAATTA GCAGAACTAG GATCCAATTT TAGTGTGGA 3540
 CAAAGACAACT TGTGTGCTCT TGCCAGGGCA ATTCTCAGGA AAAATCAGAT ATTGATTATT 3600
 GATGAAGCGA CGGCAAAATG GGATCCAAGA ACTGATGAGT TAATACAAAA AAAAATCCGG 3660
 GAGAAATTTG CCCACTGCAC CGTGCTAAC ATTGCACACA GATTGAACAC CATTAATTGAC 3720
 AGCGACAAGA TAATGGTTTT AGATTCAAGA AGACTGAAAG AATATGATGA GCCGTATGTT 3780
 75 TTGCTCCAAA ATAAAGAGAG CCTATTTTAC AAGATGGTGC AACAACCTGG CAAGGCAGAA 3840
 CGCGTGGCCC TCAGTGAAC AGCAAAACAG GTATACTTCA AAAGAAATTA TCCACATATT 3900
 GGTCAACATG ACCACATGGT TACAAACACT TCCAATGGAC AGCCCTCGAC CTTAACTATT 3960
 TTCGAGACAG CACTGTGA

SEQ ID NO:42 PBH5 PROTEIN SEQUENCE

Protein Accession #: NP_005836

5 1 11 21 31 41 51
 | | | | |
 MLFVYQEVKP NPLQDANLCS RVFFWLNPL FKIGHKRRLE EDDMYSVLPE DRSQHLGEEL 60
 QGFWDKEVLR AENDAQKPSL TRAIKCYWK SYLVLGIFTL IEESAKVIQF IFLGKIINYF 120
 ENYDPMDSVA LNTAYAYATV LTFCTLILAI LHHLYFYHVQ CAGMRLRVAM CHMIYRKALR 180
 LSNHAMGKTT TGQIVNLLSN DVNKFQDQTV FLHFLWAGPL QAIATVALLW MEIGISCLAG 240
 10 MAVLIILLPL QSCFGKLPSS LRSKTATFTD ARIRTMNEVI TGIRIIKMYA WEKSFSNLIT 300
 NLRKKEISKI LRSSCLRGMN LASPPSASKI IVFVTFTTYV LLGSVITASR VFFAVTLYGA 360
 VRLTVTLFFP SAIERVSEAI VSIRRIQTFL LLDEISQRNR QLPSDGKKQV HVQDFTAFWD 420
 KASETPTLQG LSFTVVRPEGL LAVVGPVGAG KSSLLSAVLG ELAPSHGLVS VHGRLAYVSQ 480
 15 QPWVFSGTLR SNILFGKKYE KERYEKVIKA CALKKDLQLL EDGDLTVIGD RGTTLSGGQK 540
 ARVNLARAVY QDADIYLLDD PLSAVDAEVS RHLFELCICQ ILHEKITILV THQLQYLKAA 600
 SQILILKDGK MVQKGTYTEF LKSGIDFGSL LKKDNEESEQ PVPVGTPTLR NRTFSESSVW 660
 SQQSRSRSLK DGALESQDTE NVFVTLSEEN RSEGVGFQA YKNYFRAGAH WIVFIFLILL 720
 NTAQAVAYVL QDMWLSYWAN KQSHLVNTVN GGGNVTEKLD LNWYLGYSY LTVATVLPFI 780
 20 ARSLLVFVYL VNSSQPLHNK MFESILKAPV LFFDRNPGR ILNRFSRDIG HLDLPLPTP 840
 LDFIQTLLQV VGVVSVAVAV IPWIAIPLVP LGIIFIFLRR YFLETSRDVK RLESTTRSPV 900
 FSHLSSSLQG LWTIRAYKAE ERCQELFDAH QDLHSEAWFL FLTTSRWFV RLDIAICAMFV 960
 IIVAFSGSLK ALKTLDAGQV LALSALYTLM GMFQWCVRS AEVENMMISV ERVIEYTDLE 1020
 KEAFWEYQKR PPTAPWPHGV IIFDNVNFMY SPGGPLVLKH LTALIKSQEK VGIUGRTGAG 1080
 25 KSSLISALFR LSEPEKRIWI DKILTTEIGL HDLRKMSII PQEPVLFTGT MRKNDLPFNE 1140
 HTDEELWNL QEVQLKETIE DLPGKMDTEL AESGSNFSVG QRQLVCLARA ILRKNQILII 1200
 DEATANVDPR TDELIOKKIR EKFAHCTVLT IAHRLNTIID SDKIMVLDSC RLKEYDEPYV 1260
 LLQNKESLFY KMVQQLGKAE AALATETAKQ VYFKRNYPHI GHTDHMTNT SNGQPSTLTI 1320
 FETAL

SEQ ID NO:43 PBQ7 DNA SEQUENCE

Nucleic Acid Accession #: NM_021233

Coding sequence: 34-1119 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 | | | | |
 ATGGGGAAG TGCTCTGCTG TGGCATGAAA TAAATGAAAC AGAAAAATGAT GGCAAGACTG 60
 CTAAGAACAT CCTTGTCTTT GCTCTCTCTT GGCCTCTTTG GGGTGTCTGG GGCAGCAACA 120
 ATTTCTATGA GAATGAAGA AGGGAAGCT GTGACTGGT TTAATTTTAA TAAGTTACCT 180
 40 AAAAGACAAA ACAAGGAAAG TGGAGAGACT GGGTTAGAGT ACCTGTACCT AGACTCTACA 240
 ACTAGAGACT GGAGGAGAG TGAGCAACTA ATGAATGACA CCAAGAGTGT TTTGGGAAGG 300
 ACATTACAAC AGCTATATGA AGCATATGCC TCTAAGAGTA ACAACACAGC CTATCTAATA 360
 TACAATGATG GAGTCCCTAA ACCTGTGAAT TACAGTAGAA AGTATGGACA CACCAAGGT 420
 TTACTGCTGT GGAACAGAGT TCAAGGGTTC TGGCTGATTC ATTCCATCCC TCAGTTTCTC 480
 45 CCAATTCGGG AAGAAGGCTA TGATTATCCA CCCACAGGGA GACGAAATGG ACAAGTGGC 540
 ATCTGCATAA CTTCAGTA CAACAGTAT GAGGCAATAG ATTCTCAGCT CTGGTCTGCG 600
 AACCCCAACG TCTATAGCTG CTCCATCCCA GCCACCTTTC ACCAGGAGCT CATTCACATG 660
 CCCCAGCTGT GCACGAGGCG CAGCTCATCA GAGATTCTCT GCAGGCTCCT CACCACACTT 720
 CAGTGCCTGT AGGACACAAA ATTCTCCAT TTTGCAAAAT CGGATTTCTT TCTTGACGAC 780
 50 ATCTTTGCGA CCTGGATGGC TCAACGGCTG AAGACACACT TGTTAACAGA AACCTGGCAG 840
 CGAAAAGAC AAGAGCTTCC TTCAAATGCG TCCCTTCCTT ACCATGTCTA CAATATAAAA 900
 GCAATTAAAT TATCACGACA CTCTTATTTC AGTTCTTATC AAGATCACGC CAAGTGGTGT 960
 ATTTCCCAAA AGGGCACCAA AAATCGCTGG ACATGTATTG GAGACCTAAA TCGGAGTCCA 1020
 CACCAAGCTC TCAGAAAGTG AGGATTCAAT TGTACCCAGA ATTGGCAAA TACCAAGCA 1080
 55 TTTCAGGAT TAGTATTATA CTATGAAAGC TGTAAGTAAA CTTGGTGAAA GGACACAGGT

SEQ ID NO:44 PBQ7 Protein sequence

Protein Accession #: NP_067056

60 1 11 21 31 41 51
 | | | | |
 MMARLLRTSF ALLFLGLFGV LGAATISCRN EEGRAVDWFT FYKLPKRQNK ESGETGLEYL 60
 YLDSTTRSWR KSEQLMNDTK SVLGRTLQQL YEAYASKSNN TAYLIYNDGV PKPVNYSRKY 120
 GHTKGLLLNN RVQGFNLHNS IPQFPPIPEE GYDVPPTGRR NQSGGICITF KYNQYEAIDS 180
 65 QLLVCNPNVY SCSIPATFHQ ELIHPQLCT RASSSEIPGR LLTTLQSAQG QKFLHFAKSD 240
 SFLLDIFAAW MAQLKTHLL TETWQRKQRE LPSNCSLPYH VYNIAKILS RHSYFSSYQD 300
 HAKWCISQKG TKNRWTCIGD LNRSPHQAFR SGGFICTQNW QIYQAFQGLV LYYESCK

SEQ ID NO:45 PCQ8 DNA SEQUENCE

Nucleic Acid Accession #: XM_030453

Coding sequence: 89-1273 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 | | | | |
 CGGTGCCCCT GGGTGAATA TCCCTACGTA ATTTAACCAA GCGGACTTTA ATGCCACTGT 60
 GCAGTTCATC CAAAACCACT TGGATGACAT GGATGTCAAA AAGGGTGCTC CTGGGACCAC 120
 CATCCCTAC ATGATAGGAG AGATTCAATA TGGAGGCAGA GTCACAGAC ACTATGATAA 180
 GAGATTGTTG AACACATTTG CTAAGGTTTG GTTCAGTGAA AATATGTTG GACCAGATT 240
 CAGTTTITAC CAAGGATACA ATATTCAAA ATGCAGCACA GTGGATAACT ATCTTCAGTA 300
 TATCCAGAGT TTGCTGCCT ATGACAGCCC TGAGGTGTTT GGGCTGCACC CCAATGCTGA 360

5 CATCACCCTAC CAGAGCAAGC TGGCCAAGGA CGTGTGGAC ACCATCTCTAG GCATCCAACC 420
 CAAGGACACC TCTGGTGGAG GGGATGAGAC CCGGGAGGCG GTGGTGGCCC GGCTGGCTGA 480
 TGATATGCTG GAGAAGCTGC CCCCAGACTA TGTCCTCTTT GAAGTAAAAG AGAGGCTGCA 540
 GAAGATGGGG CCATTCCAGC CTATGAACAT TTCTCTCAGG CAGGAAATAG ACAGAATGCA 600
 AAGGGTACTC AGCCTTGCTC GCAGCACCTC CACTGAGCTG AAACCTTGCTA TTGATGGCAC 660
 CATCATCATG AGCGAAAATC TGCAAGATGC ATTGGATTGC ATGTTTGATG CTAGAATCCC 720
 TGCTTGGTGG AAAAAAGCTT CTGGGTCTTT TAGTACACTG GGTTCCTGGT TTACTGAATC 780
 10 TATAGAAAGA AACAGCCAGT TTACCTCGTG GGTTTTCAAT GGCCGACCTC ACTGCTTTTG 840
 GATGACGGGT TTTTAACTC CCCAGGGATT TTTAACTGCA ATGCGACAGG AATAACTCG 900
 GGCCAACAAA GGCTGGGCTC TGGACAATAT GGTGCTTTGC AATGAAGTCA CCAATGGAT 960
 GAAGGACGAC ATTTCCTACC CTCCACAGA GGGTGTCTAT GTCTATGGCT TATATCTTGA 1020
 AGGTGCTGGC TGGACAAGA GGAACATGAA ACTCATTGAA TCAAGGCCAA AAGTCTCTT 1080
 TGAGTGTATG CCTGTCTATA GGAATTTATG AGAAAACAT ACTTTACGAG ATCCTCGGTT 1140
 15 TTAATCTCTG CCCATCTATA AGAAGCCAGT TCGAACGGAC TTGAACCTACA TTGCGCTGT 1200
 GGATCTCAGG ACAGCCACGA CCCCTGAACA CTGGGTGCTC CGTGGGGTTG CCCTTCTGTG 1260
 TGATGTCAAG TAACATGTGG GGAGTGTCCC CACCAATGCG TTTGGAAAAT GCAAGATCTA 1320
 AATTATTTGA ACCCTTATTT CTGTATGACT GCTGGACAGT GTATGTTAGG TCGTTTATGC 1380
 AATTAATGAG CTGCATAGGT TTTCCTCACT CCTTAATGAG ATGCTTATAT TTTACTTGT 1440
 20 TCATCATGCT TACCAATGCT CTGAGTTTGT TGAAAATGTT ATTTAGTGAT ATAAAAGTAA 1500
 ATTTACAGCA TCCTAATGAA GTGTGGCCCT CAAATCCACA GTAGTATATT TTCTTCTTAC 1560
 TTGCTCTCGA AGACTGACTG TGATTATAAC AGCAAAATATA TTTGCATGTG GACAAAGATT 1620
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SEQ ID NO: 46 PCQ8 Protein sequence
 Protein Accession #: BAB15543

1 11 21 31 41 51
 40 MDVKKGVSWT TIRYMIGEIQ YGGRVDDYD KRLNTPAKV WFSNMFGPD FSFYQYINIP 60
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 TREAVVARLA DDMLEKLFPD YVFEVKERL QKMGPFQPMN IFLRQEDRM QRVLSLVRST 180
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 WVENGRPHCF WMTGFENPQG FLTAMRQELT RANKGWALDN MVLCEVETKW MKDDISTPPT 300
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SEQ ID NO: 47 PDG5 DNA SEQUENCE

Nucleic Acid Accession #: AB033036
 Coding sequence: 68-3349 (underlined sequences correspond to start and stop codons)

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SEQ ID NO: 48 PDG5 Protein sequence
 Protein Accession #: BAA86524

1 11 21 31 41 51
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5	RCLSQALEEP	EDAIEVFTESS	SYVEKYNTSD	DCSSSEEDLP	LRHPAQALGK	PKNQEVSSA	300
	SNNTPEEQND	FMQQLPSRCP	SQIMNPTVO	QQVPTSSVGT	SIKQSDSVEP	IPPRHPQFW	360
	VNPKVEQEV	SSPKSMAVEE	SISMKPLPPK	LLCQPLMNP	VQNMFSGSE	DIAPERVISV	420
	EPLLPYSPQ	SLTDPQIRQI	SESTAVEEGT	YVEPLPPRCL	SQPSPERPKFL	DSMSTSAEWS	480
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10	LSSNFERRAI	EADISGSLP	PQYATQFLKR	SKVQEMTSL	EKMAVEGTSN	KSPIPRRPTQ	600
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	MLPMKHPLQS	LGRPEDPQKV	FSYSERAPGK	CSSFKEQLSP	RQLSQALRKP	EYEQKVSFVS	720
	ASSPKWRNS	KKQLPPKHSS	QASDRSKPQP	QMSSKGFVNV	PVKQSSGEKH	LPSSSPFQQQ	780
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	DNFTQLASVP	SGPISSSVGR	GHKIRSTSQG	LLDAAGNLTK	ISYVADKQOS	RPKSESMAKK	960
	QPACKTPGKP	AGQQSDYAVS	EPVWITMAKQ	KQKSFKAHIS	VKELKTKSNA	GADAETKEPK	1020
	YEGAGSANEN	QPKKMTSSV	HKQEKTAQMK	PPKPTKSVGF	EAQKILQVPA	MEKETKRSST	1080
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SEQ ID NO:49 PAB7 DNA SEQUENCE

Nucleic Acid Accession #: D87742

Coding sequence: 208-3582 (underlined sequences correspond to start and stop codons)

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	GATGTTAATC	TGCAAGTCCC	TGACAGAGCA	GTTTATAGGGA	CCATTCATCC	AGATCCAGAA	180
	ATTGAAGAAA	GCAAGCAAGA	AAC TAGTATG	ATTTTGATA	GTGAAAAAAC	AAGTGAGACT	240
30	GCTGCCAAG	GGGTCAACAC	AGGAGGCAGG	GAACCAATA	CAATGGTGGG	AAAAGAACGC	300
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	CTCTCAAAAG	AGGACCATGG	GAACACAGAG	AAGTACATGG	GCACAGAAAG	CCAGGGGTCT	540
35	GCTGCTCAG	AACCTGAAGA	TGACTCGTTC	CACTGGACTC	CACATACAAG	TGTAGAGCCA	600
	GGGCATAGTG	ACAAGAGGGA	GGACTTACTT	ATCATAAGCA	GCTTCTTTAA	AGAACAACAG	660
	TCCTTTCACG	GGTTCAGAAA	GTACTTTAAT	GTCCATGAGC	TGGAAGCCTT	GCTACAAGAA	720
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	CTAGATAAGG	CTTTCGCTGC	TTCTGAGTCA	CAAAATCTGA	GCATAGCAGA	AAAAATGCTT	840
40	GATACTCGTG	TGGCTGAAAA	TAGAGATCTG	GGAAATGAACG	AAAAATAACAT	ATTTGAAGAG	900
	GCTGCAGTGC	TTGATGACAT	TCAAGACCTC	ATCTATTTTG	TCAGGTACAA	GCACTCCACA	960
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	GTTAATATGG	CTCCAAAAGG	GCCCCCTCCT	TTCCACAGGAG	TCCCTCTCAT	GAGCAACCCC	3180
	ATGGGAGGCT	GTGTACCACT	ACCCATTGCA	TATGGACCAC	CACCTCAGCT	CTGCGGACCT	3240
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ACAACTGAAG ATAGATAGTT TAGAAGATA AGGACCTTTG AAAGAAGACA ACTCTGTCAA 5160
AGTTCAATAA GAATATAAAA ATCTTTCAGG AAAAGAGAA TCAATCTATA TGTCTCTCCG 5220
TTTAATATCA AGAATAGAAG AAATTAAGAG GAAACTCCA CAGAAGAGCA TAGGCCACTT 5280
TTAGCCATGT AAAAATAAGA TTAAGTCACA AATACAACCT TTGAATTTAC CTGTCAATAT 5340
35 CTCTTTAGAG CACAAAACAA TGCTGAAGTT AATATAAATT CTAATTTTAA ATGTCAATTA 5400
AGTGTAGATT ATGCCATCTA GGAAGGTAAG TAGGAAAGGT AAATTAATAT TATTTTAA 5460
ATTTCAAATA TTAGAGTATT TTTCCCTCT AAAGCCTTTT TTGGTGATTA TTTGTATCT 5520
GACATAATTG AGAACTGCT AAGCTGTAAA GATTCCAGTG TAGCTTCTCT GAGAAGTTGT 5580
GAGCCAGTCC ATAAGTCTCT CCTCATATCC ATCTGATGTC ACCATTCTCT GAGCAAAACC 5640
40 CAAAGCAGGG TGCCAAATAG CAGATGGCAT AGGGAGTATC ATCCCTCAGC CAAATCACTT 5700
TTCCATCTCT AAAGTTTATC CTATTTTGA AGTCAATCTC AACTAATGTG GTCTGGATT 5760
AGTTGCTAAA ATTTGCTTAT TTATTTATGA AGCAGCAATA TTCAGCCTGA AAGCATTCT 5820
GCCATAGTTG TTGTAGTTAT ATCGCAATG GCTGATTTT TTCAATGGAA AGTAAATTTA 5880
45 AGTAATTCGT GGGATGTGGT ATATTCTGTG TCAACTTCAA GATAATCACT CATTTTCTCG 5940
TTATATTCAG GTCTGAATTA AAGTTAAGTT AATCAC

SEQ ID NO:50 PAB7 Protein sequence

Protein Accession #: BAA13448

50 1 11 21 31 41 51
| | | | | |
AFLSKVEEDD YPSEELLEDE NAINAKRSKE KNPGNQGRQF DVNLQVPDRA VLGTIHPDPE 60
IEESKQETSM ILDSEKTSST AAKGVMTGGR EPNTMVEKER FLADKKAQRP FERSDFSDSI 120
55 KIQTPELCEV FQNKDSYLYK NDNPEEHLKT SGLAGEPEGE LSKEDHGNTPE KYMGTESQGS 180
AAAEPEDDSF HWTFFHTSVEP GHSDKREDLL IISFFKEQQ SLQRFQKYFN VHELEALLQE 240
MSSKLKSAQQ ESLPYNMEKV LDKVFRASES QILSIAEKML DTRVAENRDL GMNENNIFEE 300
AAVLDDIQLD IYFVRYKHST AEETATLVMA PPLEEGLGGA MEEMQPLHED NFSREKTAE 360
60 NVQVPEEPETH LDQRVIGDTH ASEVSQKPNT EKDLDPGPVT TEDTPMDAID ANKQPETAEE 420
EPASVTPLEN AILLIYSFHF YLTKSLVATL PDDVQPGPDF YGLPWKPVFI TAPLGIASFA 480
IFLWRTLVVV KDRVYQVTEQ QISEKLKTIM KENTELVQKL SNYEQKIKES KKHVQETRRQ 540
NMILSDEAIK YDKIKITLEK NQEIILDTAK NLRVMESEER EQNVKNQDLI SENKKSIEKL 600
KDVISMNASE FSEVQIALNE AKLSEKVKES ECHRVQEENA RLKKKKEQLQ QEIEDMSKLH 660
AELSEQIKSF EKSQKDLIVA LTHKDDNINA LTNCITQLNL LECESESEGO NKGGNDSDEL 720
65 ANGEVGGDRN EKMKNQIKQM MDVSRQTQAI SVVEEDLKLL QLKLRASVST KCNLEDQVKK 780
LEDDRNLSQA AKAGLEDECK TLRQKVEILN ELYQQKEMAL QKKLSQEEYE RQEREHLISA 840
ADEKAVSAAE EVKTYKRRIE EMEDELQKTE RSFKNQIATH EKKAHENWLK ARAAERIAE 900
EKREANLRH KLELTLQKMA MLQEEPVIIV PMPGKPNQPN PPRRGLPSQN CSFGPSFVSG 960
70 GECSPPLTVE PVPRLSATL NRRDMPRSEF GSVDGPLPH RWSAEASGKP SPSPDPSGTA 1020
TMNSSSRGS SPTRLVDEGK VNMAKGPFPF PGVPLMSTP MGGPVPPPIR YGPPQLCGP 1080
FGPRPLPPFP GPGMRPFLGL REFAPGVFPF RRDPLHPRG FLPGHAPFRP LGLSGPREYF 1140
IPGTRLPPT HGPQYPPFP AVRDLPSGS RDEPPASQS TSQDCSQALK QSP

SEQ ID NO:51 PAB9 DNA SEQUENCE

Nucleic Acid Accession #: NM_006457

Coding sequence: 84-1874 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
| | | | | |
AGACTGAGGC GGAGGCAGCC CCGCGCCGCG CCGGACCCGA GCATATTCTA TTTTCTGTCA 60

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TTGGACTTTC AGCCATTAGA ACCATGAGCA ACTACAGTGT GTCAGTGGTT GGGCCAGCTC 120
 CTTGGGGTTT CCGGCTGCAG GCGGTAAGG ATTTCAACAT GCCTCTGACA ATCTCTAGTC 180
 TAAAAGATGG CGGCAAGGCA GCCCAGGCAA ATGTAAGAAT AGGCGATGTG GTTCTCAGCA 240
 TTGATGGAAT AAATGCACAA GGAATGACTC ATCTTGAAGC CCAGAATAAG ATTAAGGGTT 300
 GTACAGGCTC TTTGAATATG ACTTGCAAA GAGCATCTGC TGCACCCAAG CCTGAGCCGG 360
 TTCTGTPTCA AAAGGAGAAA CCTAAAGAAG TAGTTAAACC TGTGCCCATT ACATCTCCTG 420
 CTGTGTCCTA AGTCACTTCC ACAACAACA TGGCCTACAA TAAGGCACCA CGGCCTTTTG 480
 GTTCTGTGTC TTACACAAA GTACATCCA TCCCATCACC ATCTGTCTGC TTACCCAG 540
 CCCATGCGAC CACCTCATCA CATGCTTCCC CTTCACCGT GGTGCGGTC ACTCCTCCCC 600
 TGTTCGCTGC ATCTGGACTG CATGCTAATG CCAATCTTAG TGCTGACCAG TCTCCATCTG 660
 CACTGAGCGC TGGTAAAACT GCAGTTAATG TCCCACGGCA GCCCAGAGTC ACCAGCGTGT 720
 GTTCCGAGAC TTCTCAGGAG CTAGCAGAGG GACAGAGAAG AGGATCCAG GGTGACAGTA 780
 AACAGCAAAA TGGCCACCA AGAAAAACA TTGTGGAGCG CTATACAGAG TTTTATCATG 840
 TACCCACTCA CAGTGATGCC AGCAAGAAGA GACTGATTGA GGATACTGAA GACTGGCGTC 900
 CAAGAACTGG AACAACTCAG TCTCGCTCTT TCCGAATCCT TGCCACAGATC ACTGGGACTG 960
 AACATTGTAA AGAATCTGAA GCCGATAATA CAAAGAAGGC AAATAACTCT CAGGAGCCTT 1020
 CTCGCGAGTT GGCTTCTCTG GTAGCTTCCA CACGGAGCAT GCCCGAGAGC CTGGACAGCC 1080
 CAACCTCTGG CAGACAGGG GTTACCAGCC TCACAACTGC AGCTGCCCTC AAGCCTGTAG 1140
 GATCCACTGG CGTCTCAAG TCACCAAGCT GSCAACGGCC AAACCAAGGA GTACCTTCCA 1200
 CTGAAGAAT CTCAAACAGC GCTACTTACT CAGGATCAGT GGCACCAGCC AACTCAGCTT 1260
 TGGGACAAC CCAGCCAAGT GACCAGGACA CTTTAGTGCA AAGAGCTGAG CACATTCAG 1320
 CAGGGAACG AACTCCGATG TCGGCCCAT GTAAACAGGT CATCAGAGGA CCATTTCTAG 1380
 TGGCACTGGG GAAATCTTGG CACCAGAAG AATTCAACTG CGCTCACTGC AAAAATACAA 1440
 TTGGCTACAT TGGATTGTGA GAGGAGAAAG GAGCCCTGTA TTGTGAGCTG TGCTATGAGA 1500
 AATCTTTTGC CCCGTAATGT GGTGATGCC AAAGGAAGAT CCTTGGAGAA GTCATCAATG 1560
 CGTTGAACAA AACTTGGCAT GTTTCCTGTT TTGTGTGTGT AGCCTGTGGA AAGCCATTC 1620
 GGAACAATGT TTTTCACTTG GAGGATGGTG AACCTTACTG TGAGACTGAT TATTATGCC 1680
 TCTTTGGTAG TATATGCCAT GGATGTGAAT TTCCCATAGA AGCTGTGTAC ATGTTCTCTG 1740
 AAGCTCTGGG CTGACCTGG CATGACACTT GCTTTGTATG CTCAGTGTGT TGTGAAAGTT 1800
 TGAAGGTCA GACCTTTTTC TCCAAGAAG ACAAGCCCTT GTGTAAGAAA CATGCTCATT 1860
 CTGTGAATTT TTGAAGTCA ACAGTTCAGG AGAAGAGAAG GAATTTGAAG AGAAAAAGGA 1920
 AAATTAATAA TACTAATTAA TTTTATGATT CAATATTTAT ATGGAGTTT GAAAAATAA 1980
 AGTGGCCCTG AAGGAATAAA TTCCAGCTTT AAAAACCAAG TCTGAGGAAA TATTTGGCTT 2040
 CATAAAGTAA AGAGACGGTT TGGCATTTAT TATTACTTTT TCTGTATTT TATGCCATA 2100
 AAATAAGCTT TATAAAACC AATTTCTCTG TGGACTATTA AATTCATCTT AGAATAAAT 2160
 AGTGAAGAT TTAATTTTAG AATAAATAAT CCAATCTGAA ATAATTATAC CTCTTTCTCT 2220
 TGTAGTAGT TTATAGTAA ATCTGCAAAA GGCAATGAAA ATGCCCTAAA TTTTATCAAT 2280
 AACGAATTA TTGTATTTAA AAAAAACTA ATACTTATCT TTAATAAGT AAATAGGATT 2340
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 GCGCGGTGGC TCAGCGCTGT AATCCAGCA CTTTGGGAGG CCAAGGTGGG TGGACCACAT 2460
 GAGGTCAAGG GTTTGAGATC AGCCTGGCCA ACATGGTGAA ACCCCATCTC TACTAAAAAT 2520
 ACAAAATAA GCCCGACGCA GTGGCACGCG CCGTGAATCC CAGCTACTCA AGAGGCTGAG 2580
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 CACTCCAGC TGGGTGACAG AGTGAGACTC CGTCTCCAAA AAAAACTTT GCTGTATAT 2700
 TATTTTGGCC TTACAGTGA TCAATCTAGT AGGAAAGGAC AATAAGATT TTTATCAAAA 2760
 TGTGTATGTC CAGTAAGAGA TGTATATATC TTTTCTTATT TCTTCCCCAC CCAAAATAA 2820
 GCTACCATAT AGCTTATAAG TCTCAAAATT TTGCCCTTTA CTAATAATGT ATTGTTTCTG 2880
 TTCAATGTGT ATGCTTCACT ACCTATATTA GGCAAATTCC ATTTTTCCTC TTGCGCTAAG 2940
 GTAAGATT TAAATAATA TTTTGGCTC TCATAGTTT CTCTCTCTT AAAGAGAATA 3000
 AATAGAGGGC CAGGTGTGGT GGCTCAGGCC TGTGATCCCA GCATTTTGGG AGGCCAAGAC 3060
 GGGCGGATCA TGAGGTCAAG AGATCAAGAT CATCTGGGCC AACATGGTGA AACCTGTCT 3120
 CTACTAAAAA TACAAAAATG AGCTGGGCAT GGTGGGCGT GCCTGTAGTC CCATGTACTT 3180
 GGGAGGCTGA GGCAGGAAA TTCTTGAACC CAGGAGACGG AAGTGCAGT GAGCTGAGAT 3240
 CACACCCTG CACTCCAGCC TGGTGACAGA GCAAGACTCC GGCTCTT

SEQ ID NO:52 PAB9 Protein sequence
 Protein Accession #: NP_006448

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65
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1 11 21 31 41 51
 1 MSNYSVSLVG PAPWGFRLQG GRDFNMPLTI SSLKDGGKAA QANVRIGDVV LSIDGINAQQ 60
 61 MTHLEAQNKI KGCTGSLNMT LQRASAPKP EPVFPQKGEF KEVVKPVPIIT SPAVSKVTST 120
 121 NNMAYNKAPR PFGSVSSPKV TSIPSPSSAF TPAHATTSST ASPSPVAAT PPLFAASGLH 180
 181 ANANLSADQS PSALSAGKTA VNVPRQPTVT SVCSETSOEL AEGQRRGSQG DSKQNGPPR 240
 241 KHIVERYTEP YHVPTSDAS KRRLIEDTED WRPRITGTS RSFRILAQIT GTEHLKESEA 300
 301 DNTKKANNSQ EPSQLASLV ASTRSMPESL DSPTSGRPGV TSLTTAAAFK PVGSTGVKS 360
 361 PSWQRFNQQV PSTGRISNSA TYSGSVAPAN SALGQTQPSD QDTLVQRAEH IPAGKRTFMC 420
 421 AHCNQVIRGP FLVALGKSWH PEEFNCAHCK NTMAYIGFVE EKGALYCELC YEKFFAPECG 480
 481 RCQRKILGEV INALKQTHV SCFVCVACGK PIRNNVHLE DGEPCETDY YALFGTICHG 540
 541 CEPPIEAGDM FLEALGYTHV DTCFVCSVCC ESLEGQTFSS KDKPLICKKH AHSVNF

SEQ ID NO:53 PBH7 DNA SEQUENCE

Nucleic Acid Accession #: AA431407

Coding sequence: 1-864 (underlined sequences correspond to start and stop codons)

75
80

1 11 21 31 41 51
 ATGGCCAAC GTAAAAATGAC CAAAAGCATC AGGTTCCCTG CCTGGAGCA CTGCTATACT 60
 GCGGGGAGG TCGTGTGTGCC CAAGGATCAG GAGGAGTGA AAAGACGGAC GGGCTTCTG 120
 CTCTACGAGA ACTATGGGCA GTCGAAACG GGAATAATTT GTGCCACCTA CTGGGGAATG 180

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    AAGATCAAGC CGGGTTTCAT GGGGAAGGCC ACTCCACCCT ATGACGTCCA GTTTCATATG 240
    GAGGCTCAG TTGAAACTG CATTATTGTG AGCATGAACA CCGCTGACCC TGGCAGCCAG 300
    GGCATCACAC ACAGCCTCTT GCTACAGGTC ATTGATGACA AGGGCAGCAT CCTGCCACCT 360
    AACACAGAG GAAACATTGG CATCAGAATC AAACCTGTCA GGCTGTGAG CCTCTTCATG 420
    TGCTATGAGG GTGACCAGA GAAGACAGCT AAAGTGAAT GTGGGACTT CTACAACACT 480
    GGGGACAGAG GAAAGATGGA TGAAGAGGGC TACATTGTGT TCCTGGGGAG GAGTGATGAC 540
    ATCATTATG CTCTCGGGTA TCGCATCGGG CCTGCAGAGG TTGAAAGCGC TTTGGTGGAG 600
    CACCCAGCGG TGGCGGAGTC AGCCGTGGTG GGCAGCCAG ACCCGATTCC AGGGGAGGTG 660
    GTGAAGGCTT TTATTGTCTT GACCCACAG TTCTGTCTCC ATGACAAGGA TCAGCTGACC 720
    AAGGAATCTC AGCAGCATGT CAAGTCAGTG ACAGCCCAT ACAAATACCC AAGGAAGGTG 780
    GAGTTGTCT CAGAGCTGCC AAAAACATC ACTGGCAAGA TTGAACGGAA GGAATCTCG 840
    AAAAAGGAGA CTGGTCAGAT GTAAATCGCA GTGAACCTCAG AACGCACTGC ACACCTGAGG 900
    CAAATCCCTG GCCACTTTAG TCTCCCACT ATGGTGAGGA CGAGGGTGGG GCATTGAGAG 960
    TGTGTATTG GGAAGATATC AGGAGTGCCA TGATTCCAAT GTTTCTCTTC TTTTAAATTA 1020
    AATTCAATG CTCTGCTTCC TCCAAGTCTT CTGTATCTTT AGAATTTCCC AGGTGAGCAC 1080
    TCATAACGCA AGTAATAAAA TACTGATATC AACA
  
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SEQ ID NO:54 PBH7 Protein sequence

Protein Accession #: FGENSEH predicted

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 25

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    1      11      21      31      41      51
    |      |      |      |      |      |
    MANCKMTKSI RFPALHCYTT GGEVVLFPKD EEWKRRRTGLL LVENYQOSET GLICATYWGM 60
    KIKFGPMGKA TFPYDVQFHM EASVENCIV SMNTADPGSQ GITHSLLLQV IDDKGSILPP 120
    NTEGNIGIRI KPVRFVSLFM CYEGDPEKTA KVECGDFYNT GDRGKMDEEG YICFLGRSDD 180
    IINASGYRIG PAEVESALVE HPAVAESAVV GSPDPIRGEV VKAPIVLTPQ FLSHDKDQLT 240
    KELQQHVKSV TAPYKYPRKV EHVSELEKTI TGKIERKELR KKETGQM
  
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SEQ ID NO:55 PBJ5 DNA SEQUENCE

Nucleic Acid Accession #: AF388200

Coding sequence: 33-137 (underlined sequences correspond to start and stop codons)

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    1      11      21      31      41      51
    |      |      |      |      |      |
    GAGAGAGGGA GGCAGAAGAG GAAGTCAGAG CGATGTGCTG TGAATCTTAC TACCGTTTGC 60
    TGGTTTTGAA AATGGAGAAA AAGAGTGAGG AACTGAGAAA CATGGATGGC CTGGGAAACG 120
    TGGAAAAGGG TCACTGAAAT GGGACGACAT GAACTCAAGG AGGCTATTTA TGACCATGTC 180
    ATTTGCACAA TGAAGAAAGC TTATCTGGAG TGAAGATAAA TGAGACCAAC AGAGATAAGA 240
    GACCCGGAGA AATCCTGGTT ACACCTGCTG AATCCTGTCA GTCCATATACT GGAGTCCGTG 300
    TAATACAAAA TAATAGTAAT AATCCCTCTG TTCTTTATGT TTATGCCAAC TTCAACAAAA 360
    AGAAACTTGA CTAAGAGACA ATATAAGAAC TTAATGTGTA ATTAAGAAAG AACTCTCCAC 420
    CACGGGGAAT GTGAAAGGTA TATGAGTCCC TTTTCACGAT GCGATGTCAT GTCTTTTAAA 480
    TAAGCCATAC TTTATGTTCA ATAAAAAGAG AATAAGCAGG A
  
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SEQ ID NO:56 PBJ5 Protein sequence

Protein Accession #: AAK83352

45
 50

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    1      11      21      31      41      51
    |      |      |      |      |      |
    MCCEIYYRLI VLKMEKKSEE LRNM DGLGNV EKGH
  
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SEQ ID NO:57 PBJ7 DNA SEQUENCE

Nucleic Acid Accession #: AA876910

Coding sequence: 1-2064 (underlined sequences correspond to start and stop codons)

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    1      11      21      31      41      51
    |      |      |      |      |      |
    ATGGACAGTT GCCTGCAACA TATGAGAGAC CTACTTTACC TCCTTCAGGA GCTCAGGTGT 60
    TTAAATCCAG CTACACTACT CCCTGATCCA GACTCCACTA CTCCTGTPTCA TGACTGTTCAG 120
    GATCTGTGAG AAACCTACCA AACTGGCCAA CCTGATCTTC AAGATGTGCC CCTAGAAAAG 180
    GCAGATGCCA CTGTGTTTAC AGATGGTAGC AGCTTCCTCG AGCAGGGAGA ACGAAAAGCT 240
    GTTTCTTTTC CACAGCCAGA TCTGCCAGAC AATCCACAT ACTCAACAGA AGAAGAAAAA 300
    CTGGCTTCAG ATGTTGGAGC AAATAAAAAAT CAGGAAGGAC GTGTATTTCG AAACACTACT 360
    TGGAGGGCCG GTACCTCCAA GGAAGTCTCC TTTGCAGTTG ATTTATGTGT ACTGTTCCCA 420
    GAGCCAGCTC GTACCCATGA AGAGCAACAT AATTGCGCG TCATAGGAGC AGGAAGTGTG 480
    GACCTTGCAG CAGGATTTGG ACACCTCGGG AGCCAAACTG GATGTGGAAG CTCCAAGGT 540
    GCAGAAAAAG GGCTCCAAAA TGTGTACTTT TACCTCTGTC CTGGAATCA CCTGACGCT 600
    AGCTGTAGAG ATACTTACCA GTTTTCTGCT CCTGATTGGA CATGTGTAAC TTTAGCCACC 660
    TACTCTGGGG GATCAACTAG ATCTTCAACT CTTTCCATAA GTCTGTGTCC TCATCTTAAA 720
    TTAATGTAATA GAAAAAATTG TAATCTCTTT ACTATAACTG TCCATGACCC TAATGCAGCT 780
    CAATGGTATT ATGGCAATGC ATGGGGATTA AGACTTTATA TCCAGGATT TGATGTTGGG 840
    ACTATGTTCA CCATCAAAA GAAAACTTGT GTCTCATGGA GCTCCCCCAA GCCAATGGG 900
    CCTTTAACTG ATCTAGGTGA CCCTATATTC CAGAAACACC CTGACAAAGT TGATTAACT 960
    GTTCTCTTGC CATCTTAGT TCCTAGACCC CAGCTACAAC AACACACTCT TCAACCCAGC 1020
    CTAATGTCTA TACTAGGTGG AGTACCCAT CTCCCTTAAC TCACCCAGCC TAAACTAGCC 1080
    CAAGATTGTT GGCTATGTTT AAAAGCAAAA CCCCTTATT ATGTAGGATT AGGAGTAGAA 1140
    GCCACACTTA AACGTGGCCC TCTATCTTGT CATACACGAC CCCGTGCTCT CACAATAGGA 1200
    GATGTGTCTG GAAATGCTTC CTGTCTGATT AGTACCGGTT ATAACCTATC TGCTTCTCCT 1260
    TTTGAGGCTA CTGTGAATCA GTCCCTGCTT ACTTCCATAA GCACCTCAGT CTCTTACCAA 1320
    GCACCCAACA ATACCTGGTT GGCTGACACC TCAGGTCTCA CTCGCTGCAT TAATGGAAC 1380
  
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GAACCAGGAC CTCTCCTGTG CGTGTAGTTC CATGTACTTC CCCAGGTATA TGTGTACAGT 1440
 GGACGAGAAG GACGACAACCT CATCGCTCCC CCTGAGTTAC ATCCAGGTT GCACCAAGCT 1500
 GTCCCACTTC TGGTTCCTCC ATTTGGCTGGT CTTAGCATAG CTGGATCAGC AGCCATTGGT 1560
 ACGGCTGCC TGGTTCACAG AGAAACTGGA CTAATATCCC TGTCTCAACA GGTGGATGCT 1620
 GATTTTAGTA ACCTCCAGTC TGCCATAGAT ATACTACATT CCCAGGTAGA GTCTCTGGCT 1680
 GAAGTAGTTC TTCAAAACTG CCGATGCTTA GATCTGCTAT TCCTCTCTCA AGGAGGTTTA 1740
 TGTGACGCTC TAGGAGAAAG TTGTGCTTC TATGCCAATC AATCTGGAGT CATAAAAGGT 1800
 ACAGTAAAAA AAGTTCGAGA AAATCTAGAT AGGCACCAAC AAGAACGAGA AATAACATC 1860
 CCTGTGTATC AAAGCATGTT TAACTGGAAC CCAATGGCTAA CTACTTTAAT CACTGGGTTA 1920
 GCTGGACCTC TCCTCATCTT ACTATTAACT TTAATTTTTC GGCCTTGTAT ATTAATTCG 1980
 TTTCTTAAT TATATAAACA ACGCATAGCT TCTGTCAAAC TTACGTATCT TAAGACTCAA 2040
 TATGACACCC TTGTTAATAA CTGA

SEQ ID NO:58 PB7 Protein sequence

Protein Accession #: FGENSEH predicted

1 11 21 31 41 51

MDSCIQHRMD LLYLLQELRC LNPATLLPDP DSTTPVHDCQ DLLETTKTGQ PDLQDVPLEK 60
 ADATVFTDGS SFLEQGERKA VSPQPDLPD NPTTYSTEEER LASDVGANKN QEGRVFANTT 120
 WRAGTSKEVS FAVDLCLVLP EPARTHEEQH NLPVIGAGSV DLAAGFGHSG SQTGCGSSSKG 180
 AEKGLQNVDF YLCFQNHADA SCRDTYQFFC PDWTCVTLAT YSGGSTRSST LSISRVPHPK 240
 LCTRKCNPL TITVHDEMAA QWYVGMWGL RLYIPGFDVG TMPTIQKKIL VSWSSPKPIG 300
 FLTDLGDPPI QKHPDKVDLT VPLPFLVPRP QLQOQLQPS LMSILGGVHH LLNLTPQKLA 360
 QDCMLCLKAK PPYYVGLGVE ATLKRGLPSC HTRPRALTIG DVSGNASCLI STGYNLSASP 420
 FQATCNQSLT TSISTSVSYQ APNNTWLACT SGLTRCINGT EPGLLCVLV HVLPOVYVVS 480
 GPEGRQLIAP PELHPRLHQA VPLLVP LLG LSIAGSAAIG TAALVOGETH LISLSQGVDA 540
 DFSNLQSAID ILHSQVESLA EVVLQNCRL DLLFLSQGL CAALGESCCF YANQSGVIK 600
 TVKKVRENLD RHQDERENNI PWYQSMFNW PWTTLITGL AGPLLILLIS LIFGPCILNS 660
 FLNPIQRITA SVKLTYLKTQ YDTLVNN

SEQ ID NO:59 PCO1 DNA SEQUENCE

Nucleic Acid Accession #: NM_019005

Coding sequence: 182-1885 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51

TGATGGTGGG AATTTCTTGA AACCGCTCTC GTAATTGGCC ACGTGCTGTT GCAAAATATTC 60
 TGGTGAATGA ACACAGAATC AGCATGGCTT TCCTTTGCTG AGAAATCACT GATGGGAAGT 120
 GAGACTTGTT AAACCTTGAAA GTGAATGGAC CTGAGTGGAC CCTTTGATCA CATCAGTAAA 180
 CATGACGGCT ACCAAACCTG ATATTTTATG GGCACCAAC CATGTGATA GATTGTGTGT 240
 GTTGACTCA GAACCTAAGT TTTATCATGT GGAATCTACT GTGAATTCAG AACTCAAAGC 300
 TGGATCTTTA CGTTTATCTG AAGACTCTGC AGCTACATTA CTGTCAATAA ATTCAGATAC 360
 ACCCTATATG AAATGTGTGT CCTGGTATCT TAATTATGAT CCTGAATGTC TGCTGGCAGT 420
 TGGACAAGCA AATGGTCGAG TTGTACTTAC AAGCCPTGTT CAAGATCATA ACTCAAAGTT 480
 CAAAGATTTC ATAGGAAAAG AGTTTGTTC AAAACATGCA CGCAATATGA ATACCCCTTGC 540
 CTGGAATCA CTGGAATGTA ACTGGCTAGC TGCTGGTTTA GATAAGCACA GAGCTGACTT 600
 TTCACTGCTA ATATGGGATA TCTGCAGCAA ATATACTCCT GATATAGTTC CCATGGAAAA 660
 AGTGAACACT TCAGCAGGTT AAACCTGAAA AACATTATTA GTAAACAAAC CACTTTATGA 720
 GTTAGTACTT GCCACTTGTG GTCTGTCTCT TTGTGGCTTT CCACGAGACC AGAAACTTCT 780
 CCTGTCTGTT ATGCATCGTA ACCTAGCTAT ATTTGATCTT CGGAATACAA GCCCAAAGAT 840
 GTTCGTAAT ACRAAAGCTG TTCAGGGTGT GACGGTAGAC CCATATTTCC ACGATCGTGT 900
 TGCTTCCTTC TATGAAGGTC AGGTTGCAAT ATGGGATCTT AGAAAAATTC AGAAGCCAGT 960
 TTTGACATTC ACTGAGCAAC CAAAACCTTT AACAAAAGTA GCATGGTGTG CCACTAGGAC 1020
 TGGTCTACTT GCGACTTTAA CAAGGGATAG TAATATTATT AGATTGTATG ATATGCAGCA 1080
 TACACCCACT CCCATTGGGG ATGAAACTGA ACCCAACAATA ATTTGAAGAA GTGTGCAACC 1140
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 GGATCAGAAA TCTCCAGGCA ACAAAGGATC ATTTGTTTAT CGAGGAATTA AATCAATTGT 1560
 AAAGTCATCG TTGGGAATGG TGGAAAGCAG CAGACATAAT TGGAGTGGGT TGGATAAGCA 1620
 AAGTGATATT CAAAACCTTA ATGAAGAGAG AATCTTAGCT TTACAGCTTT GTGGGTGGAT 1680
 AAAGAAAGGA ACGGATGTAG ACGTGGGGCC ATTTTGAAC TCCCTGTGAC AAGAAGGGGA 1740
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 CCTGAATGAA GGGGCATCTT CTGAAAAGG CAGGAGATCT GAATCTCAAT GTGGTAGCAA 1860
 TGGCTTTATC GGGTTATACG GATGAGAAGA ACTCCCTTTG GAGAGAAATG TGTAAGCACAC 1920
 TGGGATTTAC GATTAATAAC CCGTATTTGT GTGTCAATGT TGCAATTTCT ACAAGTGAAA 1980
 CAGGATCTTA CGATGGAGTT TTGTATGAAA ACAAGTTGCG AGTACGTGAC AGAGTGGCAT 2040
 TTGCTGTGAA ATCTCTTAGT GATACTCAGA TACATCGAAA AGTTGACCAA TGAAATGAAA 2100
 GAGGCTGGAA ATTTGGAAGG AATTTTGCTT ACAGGCTTTA CTAAGATATG AGTGGACTTA 2160
 ATGGAGAGTT ATGTGTGATG AACTGGAGAT GTTCAACACG CAACTTACTG TATGTTACAG 2220
 GGTTCACCTT TAGATGTTCT TAAAGATGAA AGGGTTCACT ACTGGATTGA GAATTTATGA 2280
 AATTTATTAG ATGCTGGGAG GTTTTGGCAT AAACGAGCTG AATTTGATAT TCACAGGAGT 2340
 AAGTTGGATC CCGCTTCCAA GCCTTTAGCA CAAGTTTTCG TGAGTTGCAA TTTCTGTGCG 2400
 AAGTCAATCT CCTACAGCTG TTCAGCTGTG CCTCATCAGG GCAGAGGTTT TAGTCAGTAT 2460
 GGTGTGAGTG GCTCACCACG GAAATCTAAA GTCCACAAGT GTCTCGGCTG TCGAAAACCA 2520
 CTTCCTCGAT GTGCGCTTTC TCTCATTAAT ATGGGAACAC CAGTTTCTAG CTGTCTGGA 2580

5 GGAACCAAT CAGATGAAAA AGTGGACTTG AGCAAGGACA AAAAAATTAGC CCAATTTAAC 2640
 AACTGGTTTA CATGGGTGCA TAATTGCAGG CACGGTGGAC ATGCTGGACA TATGCTTAGT 2700
 TGCTTCAGG ACCATGCAGA GTGCCCTGTG TCTGCATGCA CGTGTAAATG TATGCAGTTG 2760
 GATACAACGG GGAATCTGGT ACCTGCAGAG ACTGTCCAGC CATAAAATGT TACCACTTA 2820
 AGAGAACCCT TCAAGTGTGG AGCTTTCTAG TAGGTGTCC TCAATAGTCA GAAACATACC 2880
 TCAGAACCAAG CCATTCATGA CTTACCTGTA ATGGGAAAAA AAATCATCTC ATCAGAAAAA 2940
 AAAAAAAAAA AAAAAAAAAA

10 SEQ ID NO:60 PCQ1 Protein sequence
 Protein Accession #: NP_061878

1 11 21 31 41 51
 15 MSGTKPDILW APHIVDRFPV CDELSLVYHV ESTVNSLKA GSLRLSEDSA ATLLSINSDT 60
 PYMKCAVWYL NYDPECLLAV GQANGRVVLT SLGQDHNSKP KDILIGKEFVP KHARQCNTLA 120
 WNPLDSNWL AGLDKHRAFP SVLIWDICSK YTPDIVPMEK VKLSAGETET TLLVTKPLYE 180
 LGQNDACLSS CWLPRDQKLL LAGMHRNLAI FDLRNTSQKM FVNTKAVQGV TVDPYFHDRV 240
 ASFYEQQVAI WDLRFKEFV LTLTEQPKPL TKVAMCPTRT GLLATLTRDS NIIRLYDMQH 300
 20 TPTPIGDETE PTIERSVQF CDNYIASFAW HPTSQNRMIV VTPNRTMSDF TVFERISLAW 360
 SPITSLMWAC GRHLYECTEE ENDSLEKDI ATKMLRLALS RYGLDTEQVW RNHILAGNED 420
 POLKSLWYTL HFMKQYTEEM DQKSPGNKGS LVYAGIKSIV KSSLGHVLESS RHNWSGLDKQ 480
 SDIQNLNEER ILALQLCGWI KRGTDVDVGP PLNSLVQEGE WERAAAVALF NLDIRRAIQI 540
 LNEGASSEKG RRSESCQGSN GFIGLYG

25 SEQ ID NO:61 PDG3 DNA SEQUENCE

Nucleic Acid Accession #: U42359

Coding sequence: 563-775 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 TTGTACATCT TAACAACCTT AAGCTGTACA AATAGANCAA TAATATCTAA ATGGTGTGAT 60
 GATCAGCCCA CAGTACACAT CATTGATGAG AATTTCACGT GTCTCAACCT TTCTCATGCT 120
 GAGTCTCTGC TTGTAAAAA GACTTATAAA GGTCCAAGGA TTTAGAGATG ATTAAGAGAT 180
 35 AAGCTGGCAT TCCTGTAAAG CACCATCGTC TATCCCTGT CTTATCTAGA TAAAGAATGT 240
 AGTGCTAAAT CTTGTAAATA TATTGTACAA ATGGAATTC AATCTTAAGG ATTATTTTTT 300
 CCATATTGTT GTATTTCATT GTGGTGTATT GGAAAGTGAT CTGGACTTTG AGTGAGAAGA 360
 TGTGATTTGG ACCATGGCAC TTAAAACTC TATAACCTCA GGCAAGCTCT TTAATCTTCT 420
 CTGAGCCCTCA GTTTTCTTCA TTTTCAAAT ATAGAGAGTA TAACATTTAT CTCATAAGAC 480
 40 AAGTTGTAGT AAATTACTGT TTTACAAATG TAAGATAACT TTTAATCTGT AGATTCCATA 540
 TTCCAGTCTT ACATTATTAT GTTTATCTGC CACAGGGAGA AGTCCCTAGA TAAAAATGTC 600
 TACCAAAAGA CTGACACGTG GAGTTAATCA TTTGACAGAT GCAAAATGCTT CCACCCCAAA 660
 CAAATATTTT TCTTTAAT TCTGTGTGGG TATCACTTAG GGAAGAAAAA GCAGGCAACA 720
 AAATATTTTT TAATCTATC TTAGGAAAAA TTGTAGNCAA ATCTTTTNTT CCCATTAAACA 780
 45 AATAATGTAA GCCTTAATAT TCAAGGGGTA ATAAAAATAC AAAGTCTTCC AACACAGTAA 840
 CTTACTTGAA AACTTT

SEQ ID NO:62 PDG3 Protein sequence

Protein Accession #: AAB18375

50 1 11 21 31 41 51
 MGARGAPSRR RQAGRRRLRYL PTGSFPFLLL LLLLCIQLGG GQKKKENLLA EKVEQLMEWS 60
 SRRSIFRMNG DKFRKFIKAP PRNYSMIVMF TALQPQRQCS VCRQANEEOY ILANSWRYSS 120
 55 AFCKNLFFSM VDYDEGTVDF QQLMNSAPT FXHPPKGRF KRADTFDLQR IGFAAEQLAK 180
 WIADRTDVHI RVFRPPNYSG TIALALLVSL VGGLLYKRRN NLEFIYKNTG WAMVSLCTVF 240
 AMTSQGMWNH IRGPPYAHKN PHNGQVSYIH GSSQAQFVAE SHIILVLNAA ITHGHWLLNE 300
 AATSKGDVKG RRIICLVGLG LVVFPFSPLL SIFRSKYHGY PYSOLDPE

60 SEQ ID NO:63 PDG8 DNA SEQUENCE

Nucleic Acid Accession #: AL080235

Coding sequence: 245-453 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 GGTGCGCGCA CCGGCGCGCT CCGGCGCGCC GCGGCGCGCA GCGGCGCGCC CGCCACCGCC 60
 GGGGCGCGCA CCGGCGCTGC AGCTACCCG GCGGCGGAGC CGCCCGGGCC GCTGTGGCTG 120
 CAGGCGCGAGC CGCTGCATTT CTGCTGCCTA GACTTCAGCC TGGAGGAGCT GCAGGCGGAG 180
 CCGGCGCTGC GGCCTGAACC TAAGCCCATT GAGTCCAGGC TGGTGGCTGT CTTCTAGACC 240
 70 CTGGTCATCG TGGTGTGGAG CGTGCGCGCC CTCATCTGGC CGGTGCCCAT CATCGCGCGC 300
 TTCTTGCCCA ACGGCATGGA ACAGCGCGCG ACCACCGCCA GCACCAACCG AGCCACCCCC 360
 GCGCGAGTGC CCGCAGGAGC CACCGCAGCC GCGGCGCGCG CCGCGCGTGC CGCGCGCGCC 420
 GCGGCGGCTA CTTGCGGGGT GCGGACCAAG TGACCGGCTC CGCTCGTCCC TGTGTCCGTC 480
 CTGTGTCGCG GCGGCGGGGT GCCTTCCCG CCGGGGACTC GCGCGGTGTG CTTGCTGCTG 540
 TAGTTATCGT TAGTTCTCT TCCCGAGATG GGGCGCGCGA GAGACCCAG CGCCTTTGAA 600
 75 AAGCAAGGTT TGTGCTGCGC TTCCAGTTCC GAAAGCAGA TGTTTAAGCC CTTGGACTGA 660
 GGTGCGGATC GCAGCTCCGA AGACGAGAG GAGGGAATG GGGCCCTTTC CCTCTATTG 720
 CATCCCCCTG CCGGACTCCT TCCCGCACC CACGTGCCCT AGATTCTAGG CAGAAAAATGA 780
 CCAATCTCTG TGTATTGTTT TTATATATT AATAACTGTT TTAATGAAA GTTTTAGTAA 840
 80 AAAAAATACA AAACAAAAAG ATTAATATGC TATTGCTGTA GTAAGAGAAG CTCTTTGTAT 900
 CTGAACATAG TTGTATTGA AATTGTGGT TTTTAAATT ATTTAAATT GGGGGGAGG 960

CATGGGAAGG ATTAAACACC GATATATTGT TACCGCTGAA AATGAACTTT ATGAACCTTT 1020
 TCCAAGTTGA TCTATCCAGT GACGTGGCCT GGTGGCGTT TCTTCTTGT CTTATGTGGT 1080
 TTTTGGCTT TTAATACAGA CATTTTCTC CAAAAAAAAA AAAAAAAGG

5 SEQ ID NO:64 PDG8 Protein sequence
 Protein Accession #: CAB45781

1 11 21 31 41 51
 10 GRRTGRLRPA AAPSAAAATA GAPTALPAYP AAEPPGPLWL QSEPLHFCCL DFSLEELQGE 60
 FGWRLNRKPI ESTLVACFMT LVIVVWSVAA LIWFVPIIAG FLPNGMEQRR TTASTTAATP 120
 AAVPAGTTAA AAAAAAAAAA AAVTSGVATK

SEQ ID NO:65 PDM1 DNA SEQUENCE

15 Nucleic Acid Accession #: NM_006765
 Coding sequence: 149-1195 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
 CGGCCGCGGC CCGGGTCCCT CGCAAAGCCG CTGCCATCCC GGAGGGCCCA GCCAGCGGGC 60
 TCCCGGAGGC TGGCCGGGCA GCGGTGGTGC GCGGTAGGAG CTGGGCGCGC ACGGCTACCG 120
 CCGGTGGAGG AGACACTGCC CTGCCGCGAT GGGGGCCCGG GCGGCTCCTT CACGCCGTAG 180
 25 GCAAGCGGGG CCGCGGCTGC GGTACCTGCC CACCGGGAGC TTTCCCTTCC TTCTCCTGCT 240
 CTGCTGCTC TGCACTCCAGC TCGGGGGAGG ACAGAAGAAA AAGGAGAATC TTTTAGCTGA 300
 AAAAGTAGAG CAGCTGATGG AATGGAGTTC CAGACGCTCA ATCTTCCGAA TGAATGGTGA 360
 TAAATTCCGA AAATTTATAA AGGCACCACC TCGAAACTAT TCCATGATG TTATGTTTAC 420
 TGCTCTTCAG CCTCAGCGGC AGTGTCTGT GTGCAGGCAA GCTAATGAAG AATATCAAAT 480
 30 ACTGGCGAAC TCCTGGCGCT ATTCACTGCG TTTTGTAAAC AAGCTCTTCT TCAGTATGGT 540
 GGACTATGAT GAGGGGACAG ACGTFTTTCA GCAGCTCAAC ATGAACCTCG CTCTACATT 600
 CAYGCATTW CCTCCAAAG GCAGACCTAA GAGAGCTGAT ACTTTTGACC TCCAAAGAAT 660
 TGGATTTGCA GCTGAGCAAC TAGCAAAGTG GATTGCTGAC AGAACGGATG TTCAATATCG 720
 GGTFTTCAGA CCACCCAAC ACTCTGGTAC CATTGCTTTG GCCCTGTTAG TGTGCTTGT 780
 35 TGGAGGTTTG CTTTATTNGA GAAGGAACAA CTTGGAGTTC ATCTATAACA AGACTGGTTG 840
 GGCCATGGTG TCCTCTGTGA TAGTCTTTGC TATGACTTCT GGCCAGATGT GGAACCATAT 900
 CCGTGGACCT CCATATGCTC ATAAGAACCC ACACAATGGA CAAGTGAGCT ACATTCATGG 960
 GAGCAGCCAG GCTCAGTTTG TGGCAGAAAT ACACATTATT CTGGTACTGA ATGCCGCTAT 1020
 CACCATGGGG ATGGTCTTC TAAATGAAG AGCAACTTCG AAGGCGGATG TTGGAAGAA 1080
 40 ACGGATAATT TGCCATAGTG GATTGGCCCT GGTGGTCTTC TTCTTCAGTT TTCTACTTTC 1140
 AATATTTCGT TCCAAGTACC ACGGCTATCC TTATAGTAT CTGGACTTTG AGTGAGAAGA 1200
 TGTGATTGG ACCATGGCAC TTAAGAACTC TATAACCTCA GCTTTTAAAT TAAATGAAGC 1260
 CAAATGGGAT TTGCAATAAG TGAATGTTTA CCATGAAGAT AAAGTGTTC TGACTTTATA 1320
 CTATTTTGA TTAATCATAT TCAATGTGAT CAGCTAGCTT ATCTTGTGT ACTTTTATA 1380
 45 AACTGTGGGT TTTCTTAGTA AATTTAATTT ACAGAAATCA ATGGTAGCAT TTAGTAATCT 1440
 ACAAAGGAAA TATCAAGTG TTTTCAAGC CTGTTATATY CAGTGTGTRC CACAGGATTG 1500
 CAATAAATGA CAATGTAATT A

50 SEQ ID NO:66 PDM1 Protein sequence
 Protein Accession #: NP_006756

1 11 21 31 41 51
 55 MGARGAPSRR RQAGRLRLYL PTGSFPFLLL LLLLCIQLGG GQKKKENLLA EKVEQLMEWS 60
 RRSIFRNG DKFRKFIKAP PRNYSMIVMP TALQPQRCS VCRQANEYQ ILANSWRYSS 120
 APCNKLFFSM VDYDEGTDVF QQLNMNSAPT FXHXPCKGRP KRADTFDLQR IGFAEQLAK 180
 WIADRTDVHI RVFRPPNYSY TIALALLVSL VGGLLYXRRN NLEFIYKNTG WAMVSLCIVP 240
 AMTSGQMWNH IRGPPYAHON PHNGQVSYIH GSSQAQFVAB SHIILVLNAA ITMGVLLNNE 300
 60 AATSKGDVKG RRIICLVGLG LVVFFSFLL SIFRSKYHGY PYSDLDFE

SEQ ID NO:67 PDM2 DNA SEQUENCE

65 Nucleic Acid Accession #: NM_000947
 Coding sequence: 88-1617 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 70 GGTTCATAT GAACCTCTCC GCCACCGGG AACAGCTGGC TGCCACCGTT TGTGTTTTC 60
 GAGTTTGAT TCTTGAGGT GACCAAGATG GAGTTTCTG GAAGAAGCG GAGGAAGCTG 120
 AGGTGGCAG GTGACCAGAG GAATGCTTCC TACCTCATTT GCCTTCAGTT TACTTGCAG 180
 CCACCTTCTG AATACATATC TTTAACAGAA TTTGAAACT TGGCTATTGA TAGAGTTAAA 240
 TTGTTAAAT CAGTTGAAA TCTTGGAGTG AGCTATGTA AAGGAAGTGA ACAATACCAG 300
 75 AGTAAGTTGG AGAGTGAGCT TCGGAAGCTC AAGTTTCTCT ACAGAGAGAA GCTAGAAGAT 360
 GAATATGAAC CACGAAGAAG AGATCATATT TCTCATTTTA TTTTGGGGCT TGCTTATTGC 420
 CAGCTGAAG AACTTAGACG CTGGTTTCATT CAACAAGAAA TGGATCTCCT TCGATTAGA 480
 TTTAGTATTT TACCCAAGGA TAAATTCAG GATTCTTAA AGGATAGCCA ATTGCAGTTT 540
 GAGGCTATAA GTGATGAAGA GAAGACTCTT CGAGAACAGG AGATTGTTGC CTCATACCA 600
 80 AGTTAAGTG GACTTAAGTT GGGGTTGAG TCCATTATA AGATCCCTTT TGCTGATGCT 660
 CTGGATTGT TTCGAGGAAG GAAAGTCTAT TTGGAAGATG GCTTTGCTTA CGTACCACCT 720

5 AAGGACATTTG TGGCAATCAT CCTGAATGAA TTTAGAGCCA AACTGTCCAA GGCTTTGGCA 780
 TTAACAGCCA GGTCTCTGCC TGCTGTGCAG TCTGATGAAA GACTTCAGCC TCTGCTCAAT 840
 CACCTTCAGTC ATTCTCTACAC TGGCCAAAGAT TACAGTACCC AGGGAATGT TGGGAAGATT 900
 TCTTTAGATC AGATTGATTT GCTTTCTACC AAATCCTTCC CACCTTGCAT GCGTCAGTTA 960
 10 CATAAAGCCT TGGGGGAAAA TCACCATCTT CGTCATGGAG GCCGAATGCA GTATGGCCTA 1020
 TTTCTGAAGG GCATTGGTTT AACTTTGGAA CAGGCATTGC AGTTCTGGAA GCAAGAATTT 1080
 ATCAAAGGAA AGATGGATCC AGACAAGTTT GATAAAGGTT ACTCTTACAA CATCCGTCAC 1140
 AGCTTTGGAA AGGAAGGCAA GAGGACAGAC TATACACCTT TCAGTTGCCT GAAGATTATT 1200
 CTGTCCAATC CACCAAGCCA AGGGGATTAT CATGGGTGCC CATTCGTGCA CAGTGATCCA 1260
 15 GAGCTGTGTA AGCAAAAGTT GCAGTCATAC AAGATCTCTC CTGGAGGGAT AAGCCAGATT 1320
 TTGGATTAG TAAAGGGAC ACATTACCAG GTAGCCTGTC AAAAATACTT TGAGATGATA 1380
 CACAATGTGG ATGATGTGG CTTTCTTTTG AATCATCTTA ATCAGTTCTT TTGTGAGAGC 1440
 CAACGTATTC TAAATGGTGG TAAAGACATA AAGAAGGAAC CTATCCAACC AGAAACTCCT 1500
 CAACCCAAC CAAGTGTCCA GAAAACCAAG GATGCATCAT CTGCTCTGGC CTCTTTAAAT 1560
 20 TCCTCTCTGG AAATGGATAT GGAAGGACTA GAAGATTACT TTAGTGAAGA TTCTTAGGCA 1620
 GTTTTATAAC CCTTTTCTCT CAATAGCCTG TTTCTGTGTT TTAAGATTTT GCCTTTGTTG 1680
 TTGAAAAGG GTTTCACTGT CACCAAGGCT TAGTGCACTG ACACAATTAC AGCTGATTGC 1740
 AGCCTTGACC TTCCAGCTC AAGTGATCCT CCTACCTCAG CCTCCAAGT AGTTAGGACA 1800
 CACAGGTGTG CACCTCATAT CCAGATAATT TTTTTCATTT TTTTGTGTA GAGGTGGGGG 1860
 25 GTCTCCCTAT GTTGCCAGG CAGATCTCAG ACTCCTGGGC TCAGCGATC CTCACACCTC 1920
 AGCGTCCCAG AGTGTCTGGA TTACAGTTGT GAGCCACTGT GCCTGGCCTT TTTTGTGTTT 1980
 TAACCTTTTC GTTTAACTTC TCTTTTCACT GCATCCCAAT CCATCTACAG GCATGCACAC 2040
 TTATTAGGAA AGGAGGTTTG AGGTAACAAC AGAGACTTTC ACTATATTTT GCTTTGACAG 2100
 AAGGAAAGAG GAGGAGTTTC TATTAAAAATC TGTCACTTGA GTGATGTCAT TTAAGTCCTA 2160
 30 TTTTAGGAGA TAAAAACAGC TTTGGGGACT GGTAAAGTC CCCCAGAAAC TACAATAAAG 2220
 AACAACTTTT GTTTTAACTC TTAATCACTT TGTAATTTTG ACTCAATCCT TTTCTGGACC 2280
 ATTTTGTGTA ATAAATATCA AAGTGT

30 SEQ ID NO:68 PDM2 Protein sequence:
 Protein Accession #: NP_000938

35 1 11 21 31 41 51
 MEFSGRKRRK LRLAGDQRNA SYPHCLQFYL OPPSENI SLT EFENLAIDRV KLLKSVENLG 60
 VSYVKGTEQY QSKLESELRK LKFSYREKLE DEYEPRRRDH ISHFILRLAY CQSEELRRWF 120
 IQQEMDLLRF RFSILPKDKI QDFLKDSQLQ FEALISDEEKT LREQEIVASS PSLSGKLKLF 180
 ESIYKIPFAD ALDLFRGRKV YLEDGFAYVP LKDIVAILN EFRKLSKAL ALTARSLPAV 240
 40 QSDERLQPLL NHLSHSYTGG DYSTQGNVCK ISLDQIDLLS TKSFPPCMRQ LHKALRENHH 300
 LRHGGRMQYQ LFLKIGLTL EQALQFWKQE FIKGKMDPK FDKGYSYNIR HSPFGKGRKT 360
 DYTPTFSLKI ILSNPPSQGD YHGCPRHSD PELLKQKLQS YKISPGGISQ ILDLVKGTHY 420
 QVACQKYPFM IHNVDCCGFS LNHPNQFFCE SQRILNGGKD IKKEPIQPET PQPKPSVQKT 480
 KDASSALASL NSSLEMDMEG LEDYFSEDS

45 SEQ ID NO:69 PDM3 DNA SEQUENCE
 Nucleic Acid Accession #: NM_024840
 Coding sequence: 108-491 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 AATTCATACA GGAGAGAAGT CATATATATG CAGTGATTGT GGAAGAGGCT TCATCAAGAA 60
 GTCTCGGCTC ATTAATCATC AGAGAGTTCA TACAGGAGAG AAACACATG GATGCAGCCT 120
 GTGTGGGAAG GCCTTCTCCA AAAGGTCAGG GCTCACTGAA CACCAGAGAA CTCATACAGG 180
 55 AGAGAGGCCC TATGAATGCA CTGAATGTGA CAAAGCATTC CGCTGGAAAT CACAGCTCAA 240
 TGCACATCAG AAAGCTCACA CAGGAGAGAA GTCATATATA TGCCGTGATT GTGGAAAAGG 300
 CTTCAATTCAG AAGGGAATC TCATTGTACA TCAGCGAATT CACTGTGGAG AAAACCCCTA 360
 TATATGCAAT GAATGTGGAA AAGGCTTCAT CCAAGAGGGC AACCTCCTTA TTATCGACG 420
 TACTCAGACT GGAGAGAAAC CCTATGAATG CAATGAATGT GGGAAAGGCT TCAGCCAGAA 480
 60 GACATGTTTA ATATCCCATC AGAGATTTCA CACAGGAAAG ACACCCTTTG TATGTACTGA 540
 GTGTGGAAAA TCCTGCTCAC ACAAGTCAGG TCTCATTAAC CACCAGAGAA TTCACACAGG 600
 AGAGAAACCC TATACATGCA GTGACTGTGG GAAAGCTTTC AGAGATAAAT CATGTCTGAA 660
 CAGACATCGG AGAACTCATA CAGGGGAGAG ACCGTATGGA TGCTCTGATT GTGGGAAAGC 720
 TTTCTCCAC TTGTCAATGCC TTGTTTATCA TAAGGGAATG CTGCATGCAA GAGAGAAATG 780
 65 TGTAGGTTCA GTCAAATGG AAAATCCTTG CTCAGAGAGT CATAGCTTAT CACATACACG 840
 TGATCTCATA CAGGATAAAG ACTCTGTAA CATGTGACT CTGCAGATGC CTCTGTGGC 900
 AGCTCAGACC TCATTAAC TAACAGTGCCTT CCAAGCAGAG AGCAAGTAG CCATTGTGAG 960
 CCAGCCTGTT GCCAGAAGTT CAGTCTCAGC AGATAGTAGA ATTTGCACAG AATAAAACC 1020
 ATATGAATCG AGTGAATCTG GTAGTGCTTT CAGTGATCAA TTACATCAT TAATCAAAA 1080
 70 AACACAGAGG AACAACTGA TATATTCAAG GTGGAAAGCC CTTGAATAAA ACCTTATGGC 1140
 TAATAAGCAT ATACTCAGAG AAAAATAGTA TGAAGTGGAG ACTGGGAAAT TCTTTATGAG 1200
 GAAGATAGAT CTCTCATCA GTGACCATAG ATCACAATCTT CAGTGAGCTT ATAGTTGGTA 1260
 GAAATATAAT GATCATGGAA AAGTCTTGT TCAGAAACAG TACGCCAGTA GGTATCAGGG 1320
 GGTTCACACA GGAGAGAAAC TTTTGGAAGA CCTTTGAAGG CTATGAATGT GGCAGGGTTG 1380
 75 CTAGTGGTAC ATCTGTGCTT ATCCTCAGAG GGAATCATAT AGAAATAAAA CTATGAAAT 1440
 GTAACTAGAA CATCTTCATC AAAATATGAA AGAACACACG AAGCAAATAA GCCCTGTGAA 1500
 AAGGAGTATT TTAGAGATTT CGATCAGAAA TCTAACATCA TTATATGCGA GATAATATAC 1560
 AGGATGTGTA TTTTAGGACA ATATACCTTG AATCACTAGT TGATATGTCA ATGACTAATT 1620
 AAAAGGGGTT GTACAGTGTA CACATCATTT GTTAAATTTA TAGCACAATG TACCTCTTCC 1680
 80 CCGTTTTTTG ATAAGAGTCT TCTATTCCCA ACCAAGATCA TTATATGATT AGCTCTGTG 1740
 TTTCTTTGAT TCCAAATTTT TTCACTTGTT ATTTCAAGCT ACTGAAGCTC TTCAAAAGGA 1800

AAAATGTATT TAATTTAATA ATGTAACACA ACAAGTTTGG ATGTGTTTAA CTTTATAAAT 1860
AATCACCCCA GAGGAATGAA GTTCAAACT TGTGAATAAC C

5 SEQ ID NO:70 PDM3 Protein sequence:
Protein Accession #: NP_079116

1 11 21 31 41 51
10 MDAACVGRPS PKGPGSLNTR ELIQERSPMN ALNVTKHSAG NHSSMHIRKL TOERSHIYAV 60
IVEKASFRRE ISLYISEFIL EKNPIYAMNV EKASSKRATS LFDVLTLER NPMNAMNVGK 120
ASARRHV

15 Nucleic Acid Accession #: NM_018455 SEQ ID NO:71 PDM8 DNA SEQUENCE
Coding sequence: 341-955 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
20 AATTTCGGCA CGGGGGGGAG GCACAGTGA GACTCTGGG CACGGCAGCG TCTAAGCCAC 60
AAGCCGACTG ACATAAGCCA GGTCTTAACG GAGCCTATGT GTAAGTCCAC TACTGGTGCA 120
AGGTTGCACA CTCTTAAGAA GAGCGGCGTG GGGGGCTCGG CGACCTTCGC TTCAGTCGCT 180
CCCCCGTGCA GTCCCTGTGT CCCAAGACAC AGCCTGATGC TTGTGCTCCG GTGGGCGGAC 240
TTGGAGGCGG CGGGAAGTGC AATTGGTGCG TTTGAAGGGG GCGGAGCGGG AACAGCTCTT 300
25 GAGGAGTGAG ACTGCAGGAG ATGTGGGCGG TGCCAAAGAG ATGGATGAGA CTGTTGCTGA 360
GTTTCATCAAG AGGACCATCT TGAATAATCCC CATGAATGAA CTGACAACAA TCCTGAAGGC 420
CTGGGATTTT TTGCTGAAA ATCAACTGCA GACTGTAAAT TTCCGACAGA GAAAGGAATC 480
TGATGTTTCA CACTGTATCC ATCTGTGTGA GGAAGAGCGT GCAAGTATCA GTGATGCTGC 540
30 CCTGTTAGAC ATCATTTATA TGCAATTICA TCAGCACCAG AAAGTTTGGG ATGTTTITCA 600
GATGAGTAAA GGACCAGGTG AAGATGTTGA CCTTTTGTAT ATGAAACAAT TTAATAATTC 660
GTTCAAGAAA ATCTCTCAGA GAGCATTAAA AAATGTGACA GTGAGCTTCA GAGAACTGA 720
GGAGAATGCA GTCTGGATTG GAATTGCGTG GGGACACAG TACACAAAGC CAAACCAAGT 780
CAAACTTACC TACGTGGTGT ACTACTCCCA GACTCCGTAC GCCTTCACGT CCTCTCCAT 840
35 GCTGAGGCGC AATACACCGC TTCGGGTCA GGAGTTAGAA GCTACTGGGA AAATCTACCT 900
CCGACAAGAG GAGATCATTT TAGATATTAC CGAAATGAAG AAAGCTTGCA ATTAGTGAAC 960
ATGAAAGGAA AATAAAATTT CCTCACAGTC AAAAAAAAAA AAAAA

40 SEQ ID NO:72 PDM8 Protein sequence:
Protein Accession #: NP_060925

1 11 21 31 41 51
40 MDETVAEFIK RTILKIPMNE LTTILKAWDF LSENQLOTVN FRQKESVVO HLIHLCEEKR 60
ASISDAALLD IYMQFHHQK KVVWDFQMSK GPGEVDLFD HKQFKNSFKK ILQRLKNVT 120
45 VSPRETEENA VWIRIANGTQ YTKPNQYKPT YVVYYSQTPY APTSSSMLRR NTPLLGQELE 180
ATGKIYLRQE EIIIDITEMK KACN

50 Nucleic Acid Accession #: NM_016192 SEQ ID NO:73 PDM9 DNA SEQUENCE
Coding sequence: 1-1125 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
55 ATGGTGCTGT GGGAGTCCCC GCGGCAGTGC AGCAGCTGGA CACTTTGCGA GGGCTTTTGC 60
TGGCTGCTGC TGGTGGCCGT CATGCTACTC ATCGTAGCCC GCCCGGTGAA GCTCGCTGCT 120
TTCCCTACCT CCTTAAGTGA CTGCCAAACG CCCACCGGCT GGAATTGCTC TGGTTATGAT 180
GACAGAGAAA ATGATCTCTT CCTCTGTGAC ACCAACACCT GTAAATTGTA TGGGGAATGT 240
TTAAGAAATTG GAGACACTGT GACTTGCGTC TGTCAATTCA ACTGCAACAA TGAATATGTG 300
60 CCTGTGTGTG GCTCCAATGG GGAGAGCTAC CAGAAATGAGT GTTACCTGCG ACAGGCTGCA 360
TGCAAAACAGC AGAGTGAGAT ACTTGTGGTG TCAGAAGGAT CATGTGCCAC AGATGCAGGA 420
TCAGGATCTG GAGATGGAGT CCATGAAGGC TCTGGAGAAA CTAGTCAAAA GGAGACATCC 480
ACCTGTGATA TTGCCCAGTT TGGTGCAGAA TGTGACGAAG ATGCCGAGGA TGTCTGGTGT 540
GTGTGTAATA TTGACTGTTT TCAAAACCAAC TTCAATCCCC TCTGCGCTTC TGATGGGAAA 600
65 TCTTATGATA ATGCATGCCA AATCAAAGAA GCATCGTGTG AGAAACAGGA GAAATTTGAA 660
GTCATGTCTT TGGGTCTGATG TCAAGATAAC ACAACTACAA CTACTAAGTC TGAAGATGGG 720
CATTTATGCA GAACAGATTA TGCAGAGAAAT GCTAACAAAT TAGAAGAAAG TGCCAGAGAA 780
CACCACATAC CTGTGTCGGA ACATTACAAT GGCTTCTGCA TGCATGGGAA GTGTGAGCAT 840
70 TCTATCAATA TGCAGGAGCC ATCTTGCAAG TGTGATGCTG GTTATACTGG ACAACACTGT 900
GAAAAAAGG ACTACAGTGT TCTATACGTT GTTCCCGGTC CTGTACGATT TCAGTATGTC 960
TTAATCCGAG CTGTGATTGG AACAAATTCAG ATTGCTGTCA TCTGTGTGGT GGTCTCTGTC 1020
ATCAAGAGGA AATGCCCCAG AAGCAACAGA ATTCACAGAC AGAAGCAAAA TACAGGCAC 1080
TACAGTTTCA ACAATACAAC AAGAGCGTCC ACGAGGTTAA TCTGA

SEQ ID NO:74 PDM9 Protein sequence:
Protein Accession #: NP_057276

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5      1      11      21      31      41      51
      1 MVLWESPRQC SSWTLCEGFC WLLLLPVMLL IVARPVKLAA FPTSLSDCQT PTGWNCSGYD 60
      61 DRENDLPLCD TWTCKFDGEC LRIGDTVTCV CQFKCNNDYV PVCSGNGESY QNECYLRQAA 120
      121 CKQOSEILVV SEGSCATDAG SSGSDGVHEG SGETSQKETS TCDICQFGAE CDEDAEDVMC 180
      181 VCNIDCSQTN FNPLCASDGK SYDNACQIKE ASCQKQEKIE VMSLGRQDN TTTTTRSEDG 240
10    241 HYARTDYAEN ANKLEBSARE HHIPCPHYN GFCHGKCEH SINMQEPCSR CDAGYTGQHC 300
      301 EKKDYSVLVY VGPVPRQYV LIAAVIGTIQ IAVICVVLC ITRKCPRSNR IHRQKQNTGH 360
      361 YSSDNTTRAS TRLI

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SEQ ID NO:75 PDO1 DNA SEQUENCE

Nucleic Acid Accession #: NM_014324
Coding sequence: 89-1237 (underlined sequences correspond to start and stop codons)

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      3 GTCCGGCCTG GCCCGGGGCC GTNCTGTGTC TATGGTCCTG GCTGACTTCG GGGCGCGTGT 180
      4 GGTACGCGTG GACCGGGCCG GCTCCCGCTA CGAGCTGAGC CGCTTGGGCC GGGGCAAGCG 240
      5 CTGCTAGTGT CTGACCTGA AGCAGCCGCG GGAGCCGCGT GCTGCGGCGT CTGTGCAAGC 300
25    6 GTCCGATGT GCTGCTGGAG CCTTCCGCC GCGGTGTCAT GGAGAAACTC CAGCTGGGCC 360
      7 CAGAGATTCT GCAGCGGGAA AATCCAAGGC TTATTTATGC CAGGCTGAGT GGATTGGGCC 420
      8 AGTTTCAAGAA AGCTTCTGCC GGTAGCTGG CCACGATATC AACTATTTCG CTTTGTGAGG 480
      9 TGTCTCTCA AAAATTGGCA GAAGTGGTGA GAATCCGTAT GCCCGCTGA ATCTCGTGGC 540
      10 TGACTTTGCT GGTGGTGGCC TTATGTGTGC ACTGGGCATT ATAATGGCTC TTTTGTACCG 600
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      13 CATGTTGGAT GGTGGAGCAC CTTTCTATAC GACTTACAGG ACAGCAGATG GGAATTTCAT 780
      14 GGCTGTTGGA GCAATAGAAC CCCAGTCTTA CGAGCTGCTG ATCAAGGAC TTGGACTAAA 840
      15 GTCTGATGAA CTTCCTCAAT AGATGAGCAC GGATGATTGG CCAGAAATGA AGAAGAAGTT 900
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      17 TGCTGTGTGT ACTCCGGTTC TGACTTTTGA GGAGGTGTGT CATCATGATC ACAACAAGGA 1020
      18 ACGGGGCTCG TTTATCACCA GTGAGGAGCA GGAGCTGAGC CCGCGCCTTG CACTCTGTCT 1080
      19 GTTAAACACC CCAGCCATCC CTTCTTCCAA AGGGGATCCT TCTATAGGAG AACCACTGA 1140
      20 GGAGATACCT GAAGAATTTG GATTACGCCG AGAAGAGATT TATCAGCTTA ACTCAGATAA 1200
40    21 AATCATTGAA AGTAATAAGG TAAAAGCTAG TCTCTAAGT CCAGGCCACG GGCTCAAGTG 1260
      22 AATTTGAATA CTGCATTTAC AGTGTAGAGT AACACATAAC ATTGTATGCA TGGAAACATG 1320
      23 GAGGAACAGT ATTACAGTCT CTTACCACTC TAATCAAGAA AAGAATTACA GACTCTGATT 1380
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      25 TGGGTACTTA TACTAAATTA TGGTAGTTAT TCTGCCTTCC AGTTTGCTTG ATATATTTGT 1500
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      27 TCTTGAAGAC ATCGATATAC ATTATTTTAC ACTCTTGATT CTACAAATGA GAAAATGAGG 1620
      28 AATGACACA AATTGTATGG TGATAAAGT CACGTGAAAC AGAGTGATTG GTTGCAATCA 1680
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      32 GGGACAGTCA GTTTTAGGGT TGCGTGTATC CAGTAACCTG GGGCCTGTTT CCCCGTGGGT 1920
      33 CTCTGGGCTG TCAGCTTTTC TTCTCCATG TGTTTGATT CTCTCAGGC TGGTAGCAAG 1980
      34 TTCTGGATCT TATACCAAC ACACAGCAAC ATCCAGAAAT AAGATCTCA GGACCCCCCA 2040
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SEQ ID NO:76 PDO1 Protein sequence:
Protein Accession #: NP_055139

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      61 REPRAASVQ AVGCAAGALP PRCHGETPAG PRDSAAGKSK AYLCQAEWIW PVQESFCRLA 120
      121 GHDINYLALS GVLSKIGRSG ENPYAPLNLV ADPAGGGLMC ALGIIMALFD RTRTRDKQVI 180
      181 DANMVEGTAY LSSFLWKTQK SSLWEAPRQK NMLDGGAPFY TTYRTADGEF HAVGAIEPQF 240
      241 YELLIKGLGL KSDLPNQMS TDDWPEMKKK FADVFAKTK AEWQIFDGT DACVTPVLTP 300
      301 EEVVRHDHNR ERGSFITSEE QDVSPRLAPL LLNTPAIPSS KGDFFIGEHT EEILEEFGFS 360
      361 REEIVQLNSD KIESNKKVA SL

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SEQ ID NO:77 PDO3 DNA SEQUENCE

Nucleic Acid Accession #: AB028951
Coding sequence: 97-1128 (underlined sequences correspond to start and stop codons)

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      2 CTTCACAGAG ACTTGAAACC AGCAAAATATC CTAGTAATGG GAGAAGGTCC TGAGAGGGGG 120
      3 AGAGTCAAAA TAGCTGACAT GGGTTTGGCC AGATTATTCA ATTCTCTCTT AAAGCCACTA 180
      4 GCAGATTGGG ATCCAGTAGT TGTGACATTT TGGTATCGGG CTCCAGAACT TTTGCTTGGT 240
      5 GCAAGGCATT ATACAAAGGC CATTGATATA TGGGCAATAG GTTGATATAT TGCTGAATTG 300
80    6 TTGACTTCGG AACCTATTTT TCACTGTCGT CAGGAAGATA TAAAAACAAG CAATCCCTTT 360

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	CATCATGATC	AACCTGGATCG	GATATTTAGT	GTCATGGGGT	TTCTGTCAGA	TAAAGACTGG	420
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5	GTGTCTCT	TGCTTCAGAA	ACTCTGACC	ATGGATCCAA	CCAAGAGAAT	TACCTCGGAG	600
	CAAGCTCTGC	AGGATCCCTA	TTTTTCAGGAG	GACCTTTTGC	CAACATTAGA	TGTATTGTCC	660
	GGCTGCCAGA	TTCCATACCC	CAAAACGAGAA	TTCTTTAATG	AAGATGATCC	TGAAGAAAAA	720
	GGTGACAAGA	ATCAGCAACA	GCAGCAGAAC	CAGCATCAGC	AGCCACACG	CCCTCCACAG	780
	CAGGCAGCAG	CCCTCCACA	GGCGCCCCCA	CCACAGCAGA	ACAGCACCAC	GACCAACGGG	840
10	ACCGCAGGTG	GGGTGGGGC	CGGGTCTGGG	GGCACCGGAG	CAGGGTTGCA	GCACAGCCAG	900
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	AACCTCAGGT	GACCTGTGAT	GCCTCTGGAT	TATCAGCACT	CCAGTTCTCG	CCTGAATTAC	1020
	CAAAAGCAGC	TTCAGGGATC	CTCTCAGTCC	CAGAGCACAC	TTGGCTACTC	TTCTCTGCTC	1080
	CAGCAGAGCT	CACAGTACCA	CCCATCTCAC	CAGGCCACAC	GGTACTGACC	AGCTCCCGTT	1140
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15	CAAAAAAATG	CAAACTATGA	TGCCATTAA	AATCATAACA	CATGGGAGGA	AAACCTTATA	1260
	TACTGAGCAT	TGTGACGAGC	TGATAGCTCT	TCTTTATTGA	CTTAAAGAAG	ATTCTTTGTA	1320
	AGTTTCCCCA	GCACCCCTTC	CCTGCATGTG	TTCCATTGTG	ACTTCTCTGA	TAAAGCGTCT	1380
	GATCTAATCC	CAGCACTTCT	GTAACCTTCA	GCATTTCTTT	GAAGGATTTT	CTGGTGACCC	1440
20	TTTCTCATGG	TGTAGCAATC	ACTATGGTTT	ATCTTTTCAA	AGCTTTTATA	ATAGGATTTT	1500
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	AACACAGGTA	AAAATGCACC	TTTTTAAAGCA	CTACGTTTTT	ACAGACAATA	ACTGTTCTGC	1620
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	TTCTTCACAT	CTGGGTCTGC	GTGAGTAACT	TTCTTGCATA	ATCAAGGTTA	CTCAAGTAGA	2160
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	TATGTATTAT	GTATGCATAA	TTTTGCTGTT	GTACTGAAA	CTTAATTTCTA	TCAAGAACTC	2340
35	TTTTTCATGC	ACTGAATGAT	TTCTTTTGCC	CCTAGGAGAA	AACCTAATAA	TTTGTGCTAA	2400
	AAACTATGGG	CGGATAGTAT	AAGACTATAC	TAGACAAAGT	GAATATTGTC	ATTTCCATTA	2460
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40	AAATAGCTGA	TTATTGTATA	TGCAAAATTAC	ATGCATTTT	AAAACTATT	CTTCTGAAC	2700
	TTATCTACCT	GGTTATGATA	CTGTGGGTCC	ATACACAAGT	AAAAAAGAT	TAGACAGAAG	2760
	CCAGTATACA	TTTTGCACATA	TTGATGTGAT	ACTGTAGCCA	GCCAGGACCT	TACTGATCTC	2820
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	GTTACCTTTA	ATAAAGAAAG	ACAAACCCAG	ATAGATATGT	AAACCAAAAT	ACTATGCCCC	3540
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	GATCATGACG	TGACATACAA	AGACCAAGGA	TTATGTATAT	TTTTATATCT	CTGTGGTTTT	4620
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	TGGACTCTTA	AGAATGGAAA	GGGATGACAT	TTACCTARGT	GTGCTGCCCT	ATTCCTGGTG	4740
75	AAGCAACTGC	TACTTGTGTT	CTATGCCCTC	AAAATGATGC	TGTTTCTCT	GCTAAAGGTA	4800
	AAAGAAAAGA	AAAAAATAGT	TGGAAAATAA	GACATGCAAC	TTGATGTGCT	TTTGAGTAAA	4860
	TTTATGACGC	AGAACTATA	CAATGAAGGA	AGAATTTCTAT	GGAAATTACA	AATCCAAAAC	4920
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80	CATAATCTCT	AAAAATAGTC	ACAAATATAA	CAAAGTTTCT	TGTTTTAGGG	TTTTTAAAAA	5100
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10
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SEQ ID NO:78 PD03 Protein sequence:

Protein Accession #: BAA82980

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HHDQLDRIFS VMGFPAADKDW EDIRKMEPYE TLQKDFRRTT YANSSLIKYM EKHKVKPDSK 180
VFLLLQKLLT MDPTKRTISE QALQDPYFQE DPLPTLDVFA GCQIPYPKRE FLNEDDPPEEK 240
GDKNQQQQN QHQQTAPFP QAAAPPQAPP PQQNSTQTNG TAGGAGAGVG GTGAGLQHSQ 300
DSSLNQVPEFN KKPRLGPSGA NSGGPVMPSD YQHSRSSLAY QSSVQSSQS QSTLGYSSSS 360
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SEQ ID NO:79 PD05 DNA SEQUENCE

Nucleic Acid Accession #: XM_002922

Coding sequence: 1-2190 (underlined sequences correspond to start and stop codons)

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ATTCCAGCCA ACAAAATGTC CATTCGCTGG CAGTACCAC AATATGCCCT GGTTCACGCT 1860
GGGGAGGTCA TGTCTCTGT CACAGGCTCT GAGTTTCTT ATTCTCAGGC TCCCTCTAGC 1920
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SEQ ID NO:80 PD05 Protein sequence:

Protein Accession #: XP_002922

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YVLGHVIKSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAPGGD QFEKHAER 180
TRYFVYFYS INAGSLISTP ITFHLRGDVQ CPGEDCYALA FGVPGLLMVI ALVVPAMGSK 240
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RVLFYLIPLP MFWALLDQGG SRWTLQALRM NRNLGFFVLQ PDQMQLVLPF LVLIPIPLFD 360
FVIYRLVSKC GINFSLLRKM AVGHILACLA FAVAAAEVIE INEMAPAQSG POEVPLQVLN 420
LADDEVKVTV VGNENNSLLI ESIKSFQKTP HYSKLHLKTK SQDFHPLKY HNLSLYTEHS 480

5 VQEKWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSINVG 540
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SEQ ID NO:81 PDO6 DNA SEQUENCE

Nucleic Acid Accession #: NM_020448

Coding sequence: 1-1221 (underlined sequences correspond to start and stop codons)

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SEQ ID NO:82 PDO6 Protein sequence

Protein Accession #: NP_065181

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 | | | | |
 HDGSHSAALK LQQLPPTSS SAVSEASFSY KENLIGALLA IFGHLVVSIA LNLQKYCHIR 60
 LAGSKDPRAY FKTKTWLWGL FLMLLGELGV FASYAPAPLS LIVPLSAVSV IASAIIGIIF 120
 IREKWKPKDF LRRYVLSFVG CGLAVVGTYL LVTFAPNSHE KMTGENVTRH LVSWPFLLYM 180
 LVEIILFCLL LYFYKEKNAN NIVVILLVA LLSMTVVTV KAVAGMLVLS IQGNLQLDYP 240
 45 IFYVMEVCMV ATAVQMAFL SQASQMYDSS LIASVGYILS TTIATAGAI FYLDFIGEDV 300
 LHICHPALGC LAIFGLVPLI TRNRKKPIPF EPVISMAMP GMQNMHDKGM TVQPELKASF 360
 SYGALENNDN ISEIYAPATL PVMQEEHGRS SASGVPYRVL EHTYKKE

SEQ ID NO:83 PDO8 DNA SEQUENCE

Nucleic Acid Accession #: NM_032712

Coding sequence: 555-908 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | |
 CACTCATTAA GAACAGAGGA GGCTGCCTGT TACTCCTGGT GTTGATCCCT TCCAGACACT 60
 55 CTGCTGTTTC CTGCCTAGGC GTGGCTGCAG CCATGGCTAG GAAAGCGCTG CCACCCACCC 120
 ACCTGGGCCA GAGCTGGTTC TGCTCCTGCT GCAGGGACAC TGAGCTGGCT ATCTUGGCGC 180
 TTGGGGCAAG AACTGCAACA GGCTCTCCTG GGTCTGTCAG GTGTACAGCC GGGCCCTGTC 240
 CTGTGCTCCT AGCTCTCGAG AGCTGCTGCT GCCGGGTGAC CTGATCCAAC CTGATAAGGT 300
 60 GCCATCTTCA GCTACCACTG CAAGGCCCTG AGGGCAACAG CAGCACGGCA CTGCCACACC 360
 GGCTGCTGAT GGCTGGTGC CAGCTGGGAG TCCTCCCGGC ACTTCGAGGC CACTGAGCCA 420
 CCTTCCAGC CCCAGCCACG CATGGACAGG GGTATCCAGC TTCTCTCTCA ACCTGCTCCT 480
 CTGCCCTGA GCCAGTGAGC CCAAGGACA TGCTCTGTAC CCAGGTCTCT TACCAGCACT 540
 AGCTGGTCAA GGGCATGACA GTGCTGGAGG CCGTCTTGGA GATCCAGGCC ATCACTGGCA 600
 65 GCAGGCTGCT CTCCATGGTG CCAGGGCCCG CCAGGCCACC AGGCTCATGC TGGGACCCAA 660
 CCCAGTGAC AAGGACTTGG CTGCTGAGCC ACACACCCAG GAGAAGTGG ATAAGTGGC 720
 TACCAAGGCG TTCTGCAAGG CTAGGGGAGG AGCCACCCCC GCTTCCCTAT TGTGACCAGG 780
 CCTATGGGGA GGAGCTGTCC ATACGCCACC GTGAGACCTG GGCTTGGCTC TCAAGGACAG 840
 ACACCGCTCG CCTCGTGTCT CCAGGGGTGA AGCAGGCCAG AATCCTGGGG GAGCTGTCTC 900
 70 TGGTTTGAGC TGCAATTCAGG AAGTGCGGGA CATGGTAGGG GAGGCAAAAA GCCTTGGGGA 960
 CTACCTCTCC TGTGGAGCTG TTCGGTGTCC GTGAGCTAG CCACACCTG ACACCATGTT 1020
 CAAGGTACG GGAAGAGAGG GGTGTCTGCC CCCAACCTCC CCGTGGGGTG TCACTGGCCA 1080
 GATGTCATGA GGAAGACAGG CCTTGTGAGT GGACACTGAC CATGAGTCCC TGGGGGGAGT 1140
 GATCCCCCAG GCATCGTGTG CCATGTTGCA CTCTCTGCCA GGCAGCAGGG TGGGTGGGTA 1200
 75 CCATGGGTGC CCACCCCTCC ACCACATGGG GCCCCAAAGC ACTGCAGGCC AAGCAGGGCA 1260
 ACCCCACACC CTTGACATAA AAGCATCTTG AAGCTTTTAA AAAAAAAAAA AAAAAA

SEQ ID NO:84 PDO8 Protein sequence

Protein Accession #: NP_116101

80 1 11 21 31 41 51

MTVLEAVLEI QAITGSRLLS MHPGPARPPG SCWDPQTQCTR TWLLSHTPRR RWISGLPRAS 60
CRLGEEPPPL PYCDQAYGEE LSIRHRETWA WLSRTDTAMP GAPGVKQARI LGLELLLV

5

SEQ ID NO:85 PDT1 DNA SEQUENCE

Nucleic Acid Accession #: NM_000693

Coding sequence: 53-1591 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
AGCCGGTGGC CCGCAGACTA GGGCGCCTCG GGCCAGGGAG CGCGGAGGAG CCATGGCCAC 60
CGCTAACGGG GCCGTGGAAA ACGGGCAGCC GGACGGGAAG CCGCCGGCCC TGCCGCGCCC 120
CATCCGCAAC CTGGAGGTCA AGTTACACAA GATATTATC AACAAATGAAT GGCACGAATC 180
CAAGAGTGGG AAAAAGTTTG CTACATGTAA CCCTTCAACT CGGGAGCAAA TATGTGAAGT 240
15 GGAAGAAGGA GATAAGCCCG ACGTGGACAA GGCTGTGGAG GCTGCACAGG TTGCCTTCCA 300
GAGGGGCTCG CCAATGGCCG GGCTGGATGC CCTGAGTCGT GGGCGGCTGC TGCACCAAGT 360
GGCTGACCTG GTGGAGAGGG ACCGCGCCAC CTGGCGGCCG CTGGAGACGA TGGATACAGG 420
GAAGCCATTG CTTCATGCTT TTTTCATCGA CCTGGAGGGC TGTATTAGAA CCCTCAGATA 480
CTTTGCGAGG TGGCGAGACA AAATCCAGGG CAAGACCATC CCCACAGATG ACAACGTCGT 540
20 ATGCTTCACC AGGCATGAGC CCATTTGGTG CTGTGGGGCC ATCACTCCAT GGAACCTCCC 600
CTGCTGTAGT CTGTTGTGGA AGCTGGCACC CGCCCTCTGC TGTGGGAACA CCATGGTCCT 660
GAAGCTGGG GAGCAGACAC CTCTACCCG CCTTTATCTC GGCTCTCTGA TCAAAGAGGC 720
CGGGTCCCTC CCAGGAGTGG TGAACATTGT GCCAGGATTC GGGCCACAG TGGGAGCAGC 780
AAATTTCTCT CACCCTCAGA TCAACAAGAT CGCCTTCACC GGCTCCACAG AGGTTGGAAA 840
25 ACTGGTTAAA GAAGCTGCGT CCGGAGACAA TCTGAAGCGG GTGACGCTGG AGCTGGGGGG 900
GAAGAACCCC TGCAATCGTG GTGCGGACGC TGACTTGGAC TTGGCAGTGG AGTGTGCCCA 960
TCAGGCTGGG TTCTTCAACC AAGGCCAGTG TTGCACGGCA GCCTCCAGGG TGTTCGTGGA 1020
GGAGCAGGTC TACTCTGAGT TTGTACGGCG GAGCGTGAG TATGCCAAGA AACGGCCCGT 1080
GGGAGACCCC TTGATGTCA AAACAGAACA GGGGCTCAG ATTGATCAAA AGCAGTTCCA 1140
30 CAAAATCTTA GAGCTGATCG AGAGTGGGAA GAAGGAAGGG GCCAAGCTGG AATGCGGGGG 1200
CTCAGCCATG GAAGACAAGG GGCTCTTCAT CAAACCCACT GTCTTCTCAG AAGTCACAGA 1260
CAACATGCGG ATTGCCAAG AGGAGATTTT CGGGCCAGTG CAACCAATAC TGAAGTTCAA 1320
AAGTATCGAA GAAGTGATAA AAGAGCGGAA TAGCACCAGC TATGGACTCA CAGCAGCCGT 1380
GTTCACAAAA AATCTCGACA AAGCCCTGAA GTTGGCTTCT GCCTTAGAGT CTGGAACGGT 1440
35 CTGGATCAAC TGCTACAACG CCTCTATGC ACAGGCTCCA TTTGGTGGCT TTAATAATGTC 1500
AGGAAATGCG AGAGAACTAG GTGAATACGC TTTGGCCGAA TACACAGAAG TGAATACTGT 1560
CACCATCAAA CTTCGGCAGA AGAACCCCTG AAGGAAGGCG GGGGCTCCTT CCTCAACAT 1620
CGGACGGCGG AATGTGGCAG ATGAATGTG CTGGAGGAAA AAAATGACAT TTCTGACCTT 1680
40 CCGGGGACAC ATTCTTCTGG AGGCTTTACA TCTACTGGAG TTGAATGATT GCTGTTTTTC 1740
TCTCACTTAC CTGTATTATC ACCAGACTGG GGATGCCTAT AGGTGTGCTG TGAATTCGCA 1800
GTCTCGCCTG GGAAGGAGCG TGTGTGCCAT TTCTGTGTTT CCCTTTAAAC CAGATCTCTG 1860
AGACAGTGAG ATACTCAGGG CGTTGTTAAC AGGGAGTGGT ATTTGAAGTG TCCAGCAGTT 1920
GCTTGAATAG CTTCGCCGAA TCTGACTCCA GTAAGAATGT GGGAAAAACC CTGTGTGTT 1980
45 CTGCAAGCAG GGCTCTTGCA CCAGCGGTCT CCTCAGGGTG GACCTGCTTA CAGAGCAAGC 2040
CAGCGCTCTT TCCGAGGTGA AGGTGGGACC ATTCTTTGGG AAAGGATTCA CAGTAAGGTT 2100
TTTTGTTTTT TGTTTTTTGT TTTCTTGTIT TTAATAAAGG GATTTCACAG TGAGAAAGTT 2160
TTGGTTAGTG CATACCGTGG AAGGGCGCCA GGGTCTTTGT GGATTGCTG TTGACATTGA 2220
CCGTGAGATT CGGCTTCAAA CCAATACTGC CTTTGGAATA TGACAGAATC AATAGCCAG 2280
50 AGAGCTTAGT CAAAGACGAT ATCAGCGTCT ACCTTAACCA AGGCACCTTC TTAAGCAGAA 2340
AATATTGTTG AGGTATACCTT TGCTGCTAAA GATCCAATCT TCTAACGCCA CAACAGCATA 2400
GCAAAATCCTA GGAATAATCA CCTCCTCAT TGCACAAATC GAGCTGTAAT TCACCTTAAC 2460
AAATTACGCA TTCTATACAC GTTCACTAAC AGCTTATGAT AAGTCTGTGT AGTCTTCCTT 2520
TTCTCCAGTT CTGTTACCCA ATTTAGATTA GTAAGCGTA CACAACCTGA AAGACTGCTG 2580
55 TAATAACACA GCCTTGTAT TTTTAAGTCC TATTTTGATA TTAATTCTG ATTAGTTAGT 2640
AAATAACACC TGGATTCTAT GGAGGACCTC GGTCTTCATC CAAGTGGCCT GAGTATTICA 2700
CTGGCAGGTT GTGAATTTTT CTTTTCTCT TTGGGAATCC AAATGATGAT GTGCAATTTT 2760
ATGTTTTAAC TTGGGAAACT GAAAGTGTTC CCATATAGCT TCAAAAACAA AAACAAATGT 2820
GTTATCCGAC GGATACTTTT ATGGTTACTA ACTAGTACTT TCCTAATTGG GAAAGTAGTG 2880
60 CTTAAGTTTG CAAATTAAGT TGGGGAGGCG AATAATAAAA TGAGGGCCCC TAACAGAACC 2940
AGTGTGTGTA TAACGAAAAC CATGTATAAA ATGGGCTAT CACCTTGTG AGAGATATAA 3000
ATTACACAT TTGGCTTCCC TTATCAGCT AACACTTATC ACTTATACTA CCAATAACTT 3060
GTTAAATCAG GATTGGCTT CATACACTGA ATTTTCAGTA TTTTATCTCA AGTAGATATA 3120
GACACTAACC TTGATAGTGA TACGTTAGAG GGTTCCTATT CTTCCTATGT ACGATAATGT 3180
65 CTTTAATATG AAATGTACA TTATTTATAA TTGGTAGAGT TATGTATCT TTTTATAGTT 3240
GTAAGTACAC AGAGGTGGTA TATTTAAACT TCTGTAATAT ACTGTATTTA GAAATGGAAA 3300
TATATATAGT GTTAGGTTTC ACTTCTTTTA AGGTTTACCC CTGTGGTGTG GTTTAAAAAT 3360
CTATAGGCTT GGAATTCG ATCCTAGCTG CAGATCGCAT CCCACAATGC GAGAATGATA 3420
AATAAAATT GGATATTTGA GA

70 SEQ ID NO:86 PDT1 PROTEIN SEQUENCE

Protein Accession #: NP_000684

75 1 11 21 31 41 51
MATANGAVEN GQPDGKPPAL PRPIRNLEVK FTKIPINNEW HESKSGKKPA TCNPSTREQI 60
CEVEEGDRPD VDKAVEAAQV AFQRGSPWRR LDALSRGRL HQLADLVERD RATLAALETH 120
DTGKFFLHAF FIDLEGGIRT LRYFAGWADK IQGKTIPTDD NVVCPTRHEP IGVCGAITPW 180
NFPLLMLVLF LAPALCCGNT MVLKPAEQTP LTALYGLSLI KEAGFPFGVV NIVPFGPGTV 240
GAAISSHPQI NKIAFTGSTG VGKLVKEAAS RSNLKRVTLE LGGKNPCIVC ADADLDLAVE 300

CAHQGVFFNQ GQCCTAASRV FVEEQVYSEF VRRSVEYAKK RPVGDPDFVK TEQGPQIDQK 360
QFDKILELIE SGKKKEGAKLE CGGSAMEDKG LFIKPTVPSE VTDNHRIAKE EIFGPVQPIIL 420
KFKSIEIEVIK RANSTDYGLT AAVFTKNLDK ALRLASALEK GTVWINCYNA LYAQAPFGGF 480
KMSGNGRELK EYALAEYTEV KTVTIKLGDK NP

5

SEQ ID NO:87 PDV3 DNA SEQUENCE

Nucleic Acid Accession #: NM_032642

Coding sequence: 184-1263 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
| | | | | |
GACCATAGC AGGCACCCAG GCCTGTCTTT GGCTCGGAAA CGGTGGCCCC CAATGTAGCC 60
TAGTTTGAAC CTAGGAACCTG CAGGACCAGA GAGATTCCAC TGGAGCCTGA TGGACGGGTG 120
ACAGAGGGAA CCCTACTCTG GAAACTGTCA GTCCCAGGCC ACTGGGGAGG GCTGAGGCCG 180
15 ACCATGCCCA GCCTGTCTGT GCTGTTCACG GCTGCTCTGC TGTCAGCTG GCCTCAGCTT 240
CTGACAGACG CCAACTCCTG GTGGTCATTA GCTTTGAACC CGGTGCAGAG ACCCGAGATG 300
TTTATCATCG GTGCCAGGCC CGTGTGCAGT CAGCTTCCCG GGCTCTCCCG TGGCCAGAGG 360
AAGCTGTGCC AATTGTACCA GGAGCACATG GCCTACATAG GGGAGGGAGC CAAGACTGGC 420
ATCAAGGAAT GCCAGCACCA GTTCCGGCAG CGGCGGTGGA ATTGCAGCAC AGCGGACAAAC 480
20 GCATCTGTCT TTGGGAGAGT CATGCAGATA GGCAGCCGAG AGACCGCCTT CACCCACCGG 540
GTGAGCGCCG CGGGCGTGGT CAACGCCATC AGCCGGGCCT GCCCGGAGGG CGAGCTCTCC 600
ACCTGCGGCT CGAGCCGAGC GCGCGGGCCC AAGGACCTGC CCGGGGACTG GCTGTGGGGC 660
GGCTGTGGGG ACAACGTGGA GTACGGCTAC CGCTTCGCCA AGGAGTTTGT GGATGCCCGG 720
GAGCGAGATA AGAACTTTCG CAAAGGATCA GAGGAGCAGG CCGGGTGTCT CATGAACCTG 780
25 CAAACAAACG AGCCCGGTCT CAGGGCTGTG TATAAGATGG CAGACGTAGC CTGCAAAATGC 840
CACGGCGCTT CGGGGTCTCT CAGCCTCAAG ACCTGCTGGC TGCAGCTGGC CGAGTTCCGC 900
AAGGTTCGGG ACCGCTGGA GAGAGAAGTAC GACAGCGCGG CCGCATGCG CGTCACCCGC 960
AAGGGCGGGC TGGAGCTGGT CAACAGCCGC TTCAACCCAGC CCACCCCGGA GGACCTGGTC 1020
TATGTGGACC CCAGCCCCGA CTACTGCCCTG CGCAACGAGA GCACGGGCTC CTTGGGCAG 1080
30 CAGGGCGGCC TCTGCAACAA GACCTCGGAG GGCATCGATG GCTGTGAGCT CATGTGCTGC 1140
GGGCGTGGCT ACAACCAAGT CAAGAGCGTG CAGGTGGAGC GCTGCCACTG CAAGTTCCAC 1200
TGGTCTGCTT TCGTCAAGTG TAAGAAGTGC ACGGAGATCG TGGACCACTA CATCTGTAA 1260
TAGCCCGGAG GGCTGTCTCC CGGCCCCCCC TGCACTCTGC CTCACAAAGG TCTATATTAT 1320
ATAAATCTAT ATAAATCTAT TTTATATTG TATAAGTAA TGGGTGGGTG CTATACAATG 1380
35 GAAAGATCAA AATGGAAGG AAGAGCTTAT TTAAGAGACG CTGAGATCT CTGAGGAGTG 1440
GACTTGTCTG GTTCTCTCTT CTGTGTGGGT GGGAGACAGG GCTTTTCTCT TCCCTCTGGC 1500
GAGGACTCTC AGGATGTAGG GACTTGGAAA TATTTACTGT CTGTCCACCA CGGCTTGAG 1560
GAGGGAGGTT GTGGTTGGAT GGAGGAGATG ATCTGTCTG GAACTCTAGA GTCTTGTGTT 1620
GTTAGGAGAC TGCTGTGATG CTTGCCACT AGGCCAAGAG GCCCTATGAA GGTGGCGGGA 1680
40 ACTCAGCTTC AACCTCGATG TCTTCAGGCT CTTGTCCAGA ATGTAGATGG GTTCCGTAAG 1740
AGGCTGGTGT CTCTCTTACT CTTTCATCCA CGTGCACCTG TCGGCATCT CGAGTTTACA 1800
GGAACGGCTC CTTCCTTAAA ATGAGAAATC CAAGGTCTAT CTGTGCCAGG TGACCACAGA 1860
GAGATCTGCA CCTCCCCGAC TTCCAGGCTG CTTTCCAGC GAGAAATCTT CATCTCCAC 1920
GGTTCATGAT CTCTTACTG AAGAGGAAAG GGGGCCATTT GACTGACAT GTACGAAAG 1980
45 CCCTAAACTG AATGTTTGGC CTTGGGCTGC AGAAGCCAGG GTGATGACC AGGCTGCGTG 2040
GACGTTATAC TGCTTCTCCC CACCCCGGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100
CTCCACCGAG GGAGGCTTCA CAAACACAG GACGCTGCAA CGGTCAGGC TGGCGGGCCC 2160
GGCGTGTCTA TCATCTCTGC CCCAGGTGTA CGGTTCCTCT CTGACATTAA ATGCCCTTCA 2220
50 TGGAAAAAAA AAAAAAGAAA AAAAAAATAA AA

SEQ ID NO:88 PDV3 Protein sequence

Protein Accession #: NP_116031

55 1 11 21 31 41 51
| | | | | |
MPSLLLLFTA ALLSSWAQLL TDANSWWSLA LNFVQRPENF IIGAQPVCSSQ LPGLSPGQRK 60
LCQLYQEHMA YIGEGAKTGI KECQHQRQR RMNCSTADNA SVFGRVMQIG SRETAFTHAV 120
SAAGVVAIS RACREGLST CGCSRTARPK DLPRDWLMWG CGDNVEYGYR FAKEFVDARE 180
REKNFAKGE EQGRVLHNLQ NNEAGRRVY KMADVACKCH GVSQSCSLKT CWLQLAERFK 240
60 VGDRLEKYD SAAAMRVTRK GRLELVNSRF TQPTPEDLVY VDFSPDYCLR NESTGSLGTQ 300
GRLCNKTSRG MDGCELMCCG RGYNQFKSVQ VERCHCKFW CCFVRCKKCT EIVDQYICK

SEQ ID NO:89 PDT9 DNA SEQUENCE

Nucleic Acid Accession #: NM_033280

Coding sequence: 58-636 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
| | | | | |
GGCAGCCGTC TGTGCCACCC AGAGCCGGCG GGCCGCTAGG TCCCGGAGA CCTGCTATG 60
70 GTGCGTGGG GCGCGTGGG GGCTCATCTC CCGCGTCCG GCTTGGATAT CTTGCGGGAC 120
CTGAAGAGA TGAACAAGCG CCAGCTCTAT TACCAGGTTT TAAACTCTCG CATGATCGTG 180
TCTTCTGCAC TCATGATATG GAAAGGCTTG ATCGTGCTCA CAGGCAGTGA GAGCCCCATC 240
GTGTGTGTG TGAGTGGCAG TATGGAGCCG GCCTTTCACA GAGGAGACCT CCGTGTCTC 300
75 ACAAAATTC CCGGAAGACC AATCAGAGCT GGTGAATAG TTGTTTTTAA AGTTGAAGGA 360
CGAGACATTC CAATAGTTCA CAGAGTAATC AAGTTTCATG AAAAAATAA TGGAGACATC 420
AAATTTCTGA TGAAGAGAGA TAATAATGAA GTTGATGATA GAGGCTTGTA CAAAGAAAGC 480
CAGAACTGGC TGGAAAAGAA GGACGTGGTG GGAAGAGCAA GAGGGTTTTT ACCATATGTT 540
GGTATGTGCA CCATATAAT GAATGACTAT CCAAAATCA AGTATGCTCT TTTGGCTGTA 600
80 ATGGGTGCAT ATGTGTTACT AAAACGTGAA TCCTAAATG AGAAGCAGTT CTTGGGACCA 660
GATTGAATG AATTCTCTTG AAAAAGAGAA AACTAATAT ATTTGAGATG TTCCATTTTC 720

TGTATAAAAG GGAACAGTGT GGAGATGTTT TTGTCTTGTC CAAATAAAAG ATTACCAGT 780
 AAAAAAAAAA AAAA

SEQ ID NO:90 PDV9 Protein sequence

Protein Accession #: NP_150596

1 11 21 31 41 51
 | | | | |
 10 MVRAGAVGAH LPASGLDIFG DLKIMNKRQL YYQVLNFAMI VSSALMIWKG LIVLTGSESP 60
 IVVVLSSGME PAFHRGDLIF LTNFREDPIR AGEIVVFKE GRDIPVHRV IKVHEKDNGD 120
 IKFLTGDNN EVDDRGLYKE GQNWLEKRDV VGRARGFLPY VGMVTIIMND YPKFYALLA 180
 VMGAYVLLKR ES

SEQ ID NO:91 PDV5 DNA SEQUENCE

Nucleic Acid Accession #: NM_016590

Coding sequence: 691-975 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 20 GATTACTCAC ACAGTCTTGA AGATGCAATG TCAGCTATTT AGGACAGAAA CATCCAAGGC 60
 CGTGTGAGAA CTCAATTAGC ACTACATATG CATTAAAGGCA GGAACCTGGCA GGCCTCAGGG 120
 TACGCCAAGT ATAGGACTCG TGCTTCTCGT ACGCTGGGCT ATAATCTATG AAAGCTGAGCT 180
 CCAGAGCCAG CCAATCACTT AGCTCCTCAT AACAGTCTA ACTGGCTCTG GAAAGCTGAA 240
 AGGGCTGCAC TGGAAACAACA CAGATGAGAT ATTCTACACA TTAATCTACT TATCTGGAAT 300
 25 CACTTTGCCCT CTAAGGCCA GAGAAAAATC ACAGCTTCCT TGTCCGAGGG GAAAAGGACA 360
 GGTGATCTGG GGAAGACGCA GCTACACCTG GAGCAAGGTC TCTTCCCGGC TTGGCAATCT 420
 CAGCTGTGCC GGCCTTACGG GACCCGAGCC GTCCCAAGAA CCAAGGGGCA GGCACGGCAG 480
 CAAACGCCCT AGTCTGCTG CCTTCGGTGA CTATATGAGA ATGGAAACTT CTAAGGAAGC 540
 CAGGTGTGTA GAATTGTTAC CCCCTTACT CAGAGATAAC ATAGATTATC CAGGCTGAGA 600
 30 TGGAAAAACA GCCCTTTATT GAATTTTCAA CACAGACTCC CTGCTTCTCA TCTCCTTAAT 660
 AAAATTTTCA TAAATCCCC TTGAATCTCC ATGTCTCAAT CTCCATTGTG TGACAGACAA 720
 AGCCAACAAT ACTTAAACT GAGGCTGCA AGTCATTTC A TTGTATTTT TGTCCAGAAA 780
 TTTCCCATAG GAAGACTTCA CCTCTTACAA CTCCGAAGAA AACCTTACT GTCCAAGACC 840
 35 GTCAACAGCA ACCATCCGCA GTCATTCAAG TCGAAGCTTT CACAGCTTTT GTACATTCTC 900
 TGTGTCAATA TACAAGTGA TTAACAGACTG TCCCTGGCT CCTGACCTT TACAAACACT 960
 AAAAGTTTGG TTTGACTCAA CTTCAGCTG CTATCTGTT AGTAAGTGAT GTTCACTCCA 1020
 GAACACATTC ATGATGAGAA CTCTTCAAAA GACCAGCACT GCTCTTCCCC TCCTATAATC 1080
 ATAATAATCA TGATAACCTG AAACATGTTA CTGGGACTCG ACATTTTCTT GGGGATTGAA 1140
 40 ATCTTAGTTC CTTGGAGCTG TCACATAGCA GGGGCAACCT CACACTGAAA CAAAGGAAGT 1200
 GATGTCCCAT TATTATCCAC CCTGAGCCAC CATAATATGC TGTTTACATT TATTTTCTTC 1260
 AGCCTGTGCA AAACAAAGCA ATGGAAGAGG AAACATAAAA ATATACATAC TAGTACCATT 1320
 ATCTTCTTTT GCTTAAATTT ACTAATGCAC CACGTCACTG TGCTTCTCTC AGGCATCATT 1380
 CTCATATCAT CAGGACTTGT ATTAGCAGGT TCTGGCTAGA GAGACTATCT CCTGTCATCA 1440
 45 CGATCAATTA ATGTTTCTCT GTGATCACAT CAGGCCCTAT CTAAGAAGCT CATGGTATAC 1500
 AAGGTCACAC CAAATAGCTG AGTGCAGTCC TTGCTCATAT TCTCTTCATC TTAACCCCGC 1560
 AAACAAGAAT TAAGATGATC CCAATAAAAG AAAAATTGCT CAGGAACCTG AACCTTTTTC 1620
 TGAACCAAGC ACTGTGAGCA AATCTCAGGT ATTAGAGCAA CTATGGTTGA TTGAAAAGTG 1680
 TCTCAAAATC TGGGCCAAGA ATGATGCTA GGTCCATAAG CTAATTTGTC TGGCCTTGCC 1740
 50 ATTATGATAA GCCAAGAAA GTCACATG AGTAAACTAT AGAAAACGTT CAGACCCATC 1800
 CTGTTAGTAT GTCAATCAA CTAAGACTGG CAGGGTATTA ACTCCATTCC AGGTGACATG 1860
 GATAAAGAGC CCCATTATTT TCACAGTGCC AGCCTCTACC TAAGGAAACC CTAGACCTTG 1920
 GAACCAATTT CCTGGTAGGG AACTGCTGAC AGTTTCAATG CTGACAGTTG GAGCCAATGC 1980
 CTCATAGTTT AAACGAAAG AAAAATAGTT GCTTTTAAAA ATGTCAGCAA GAAGGCCCTG 2040
 55 CTCATCTTAA CAAAGCAAAA AAAATGCTT TAATTCAAAT TAAAAATCAT GATACTAAAA 2100
 AAAAAAA

SEQ ID NO:92 PDV5 Protein sequence

Protein Accession #: NP_057674

1 11 21 31 41 51
 | | | | |
 60 MQCQLFRTET SKAVSELNYD YICIKAGTGR PQGTPTIGLV LLVRWAIHYE TELQSQPTT

SEQ ID NO:93 PEE6 DNA SEQUENCE

Nucleic Acid Accession #: NM_002606

Coding sequence: 61-1842 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 70 CGCGCGCGCT GCGTCGGGA AAGTACAGTA AAAAGTCCGA GTGCAGCCGC CGGGCGCAGG 60
 ATGGGATCCG GCTCCTCCAG CTACCGGCCC AAGGCCATCT ACCTGGACAT CGATGGACGC 120
 ATTCAAGAAG TAACTCTCAG CAAGTACTGC AACTCCAGCG ACATCATGGA CCGTCTCTGC 180
 ATCGCCACCG GCTTGCTCG GAACACGACC ATCTCCCTGC TGACACCGA CGACGCCATG 240
 75 GTCTCCATCG ACCCCACCAT GCCCGCGAAT TCAGAACGCA CTCCGTACAA AGTGAGACCT 300
 GTGGCCATCA AGCAACTCTC CGCTGGTGTG GAGGACAAGA GAACCAACA CCGTGGCCAG 360
 TCTGCTGAGA GACCACTGAG GGACAGACGG GTTGTGGGCC TGGAGCAGCC CCGGAGGGAA 420
 GGAGCATTTG AAAGTGGACA GGTAGAGCCC AGGCCAGAG AGCCCAAGG CTGCTACCG 480
 GAAGGCCAGC GCATCCCTCC AGAGAGAGAA GAATTAATCC AGAGCGTGCT GCGCAGGTT 540
 80 CGACAGCAGT TCTCAAGAGC ATTCAAAATC AATGAAGTGA AAGCTGAAGT TGCAATCAC 600
 TTGGCTGTCC TAGAGAAACG CGTGGAAATG GAAGGACTAA AAGTGGTGA GATTGAGAAA 660

5
10
15
20
25

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TGCAAGAGTG ACATTAAGAA GATGAGGGAG GAGCTGGCGG CCAGAAGCAG CAGGACCAAC 720
TGCCCTGTGA AGTACAGTTT TTTGGATAAC CACAAGAAAT TGACTCTTCG ACGCGATGTT 780
CCCACTTACC CCAAGTACCT GCTCTCTCCA GAGACCATCG AGGCCCTCGG GAAGCCGACC 840
TTTGACGTCT GGCTTTGGGA GCCCAATGAG ATGCTGAGCT GCCTGGAGCA CATGTACCAC 900
GACCTCGGGC TGTTCAGGGA CTTACAGCAT AACCTGTCA CCCTCAGGAG GTGGCTGTTC 960
TGTGTCCACG ACAACTACAG AAACAACCCC TTCCACAACT TCCGGCAGTG CTCTGCGGTG 1020
GCCACAGTGA TGTACAGCAT GGTCTGGCTC TGCAGTCTCC AGGAGAAGTT CTCACAAACG 1080
GATATCTTGA TCCTAATGAC AGCGGCCATC TGCCACGATC TGGACCATCC CGGCTACAAC 1140
AACACGTACC AGATCAATGC CCGCACAGAG CTGGCGGTCC GCTACAATGA CATCTCACCG 1200
CTGGAGAACC ACCACTGCGC CGTGGCCTTC CAGATCCTCG CCGAGCCTGA GTGCAACATC 1260
TTCTCCAACA TCCACCTGTA TGGGTTCAGG CAGATCCGAG AGGGAATGAT CACATTAATC 1320
TTGGCCACTG ACATGGCAAG ACATGCAGAA ATTATGGATT CTTTCAAAGA GAAAAATGAG 1380
AATTTTGACT ACAGCAACGA GGAGCACATG ACCCTGCTGA AGATGATTTT GATAAAATGC 1440
TGTGATATCT CTAACGAGGT CCGTCCAATG GAAGTCGCAG AGCCTTGGGT GGACTGTTTA 1500
TTAGAGGAAT ATTTTATGCA GAGCGACCGT GAGAAGTCAG AAGGCCTTCC TGTGGCAGCG 1560
TTCTATGGACC GAGACAAAGT GACCAAGGCC ACAGCCAGAG TTGGGTTCAT CAAGTTTGTG 1620
CTGATCCCAA TGTTTGAAC AGTGACCAAG CTCTTCCCA TGGTTGAGGA GATCATGCTG 1680
CAGCCACTTT GGAATCCCG AGATCGCTAC GAGGAGCTGA AGCGGATAGA TGACGCCATG 1740
AAGAGTTTAC AGAAGAAGAC TGACAGCTTG ACGTCTGGGG CCACCGAGAA GTCCAGAGAG 1800
AGAAGCAGAG ATCTGAAGAA CAGTGAAGGA GACTGTGCGT GAGGAAAGCG GGGGGCTGG 1860
CTGACGTTCT GGACGGGCTG GCCGAGCTGC CCGGGATCCT TGTGCAGGGA AGAGCTGCC 1920
TGGGCACCTG GCACCAAG ACCATGTTTT CTAAGAACCA TTTTGTTCAC TGATACAAAA 1980
AAAAA A

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SEQ ID NO:94 PEE6 Protein sequence
Protein Accession #: NP_002597

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35
40

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1 11 21 31 41 51
| | | | |
MSGSSSYRP KAIYLDIDGR IQKVIFSKYC NSSDIMDLFC IATGLPRNTT ISLLTTDDAM 60
VSDIPTMPAN SERTPYKVRP VAIKQLSAGV EDKRTTSRQ SAERPLRRR VVGLEQPRRE 120
GAFESGQVEP RPREPQGCYQ EGQRIPPERE ELIQSVLAQV AEQFSRAFKI NELKAEVANH 180
LAVLEKRVLE EGLKVVEIEK CKSDIKMRE ELAARSSRTN CPCKYSFLDN HKKLTFRDV 240
PTYPKYLLSP ETTEALRKPT FDVWLWEPNE MSLCLEMYH DLGLVRDFS I NPVTLRRWLF 300
CVHDNYRNP FHNFRHCFV AQMYSMVWL CSLQEKFSQT DILILMTAAI CHDLDRPGYN 360
NTYQINARTE LAVRYNDISP LENHHCVAFA QILABPECNI FSNIPDPGFK QIRQGMITLI 420
LATDMARHAE IMDSFKEME NFDYSNEEHM TLLKMLIKC CDISNEVRFM EVAEPWVDCL 480
LEEYPMQSDR EKSEGLPVAP FMDRDKVTKA TAQIGFIKVF LIPMFETVK LFPVHEEIML 540
QPLWESDRY EELKRIDDAM KELQKKTDSL TSGATEKSRE RSRDVKNSEG DCA

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SEQ ID NO:95 PEG4 DNA SEQUENCE

Nucleic Acid Accession #: none
Coding sequence: 41-559 (underlined sequences correspond to start and stop codons)

45
50
55
60

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1 11 21 31 41 51
| | | | |
CAGTCACAGG CGAGAGCCYT GGGATGCACC GGCAGAGGC ATGCTGCTGC TGCTCACGCT 60
TGCCCTCTCTG GGGGGCCCCA CCTGGGCAGG GAAGATGTAT GGCCCTGGAG GAGGCAAGTA 120
TTTCAGCACC ACTGAAGACT ACGACCATGA AATCACAGGG CTGCGGGTGT CTGTAGGTCT 180
TCTCTGTGTG AAAAGTGTCC AGGTGAACT TGGAGACTCC TGGGACGTGA AACTGGGAGC 240
CTTAGGTGGG AATACCCAGG AAGTCACCTC GCAGCCAGGC GAATACATCA CAAAGTCTT 300
TGTCGCTTC CAAGCTTTC TCCGGGGTAT GGTCACTAC ACCAGCAAGG ACCGCTATT 360
CTATTTTGGG AAGCTTGATG GCCAGATCTC CTCTGCCTAC CCCAGCCAAG AGGGGCAGGT 420
GCTGTGGGG ATCTATGGCC AGTATCAACT CCTTGGCATC AAGAGCATTG GCTTTGAATG 480
GAATTATCCA CTAGAGGAGC GCACCACTGA GCCACCACTT AATCTCACAT ACTCAGCAAA 540
CTCACCCGTG GGTGCTAGG GTGGGGTATG GGGGCATCCG AGCTGAGGCC ATCTGTGTGG 600
TGGTGGCTGA TGGTACTGGA GTAACCTGAGT CGGGACGCTG AATCTGAATC CACCAATAAA 660
TAAAGCTTCT GCAGAAATCAG TGA A

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SEQ ID NO:96 PEG4 Protein sequence
Protein Accession #: FGENESH predicted

65
70

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1 11 21 31 41 51
| | | | |
MLLLLTLALL GGPTWAGKMY GPGGGKYFST TEDYDHEITG LRVSVGLLLV KSVQVKLGDS 60
WDVKLGALGG NTQEVTLQPG EYITKVFVAP QAFLRGMVMY TSKDRYFYFG KLDGQISSAY 120
PSQEGQVLVG IYQYQLLGI KSIQFEWYYP LEEPTTEPFV NLTYANSFPV GR

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SEQ ID NO:97 PEL5 DNA SEQUENCE

Nucleic Acid Accession #: NM_006953
Coding sequence: 33-896 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
CCGTTCCCGG CTCTGGCGGC TCCTCCCGGG CGATGCCTCC GCTCTGGGCC CTGCTGGCCC 60
TCGGCTGCCT GCGGTTCCGC TCGGCTGTGA ACTTGCAGCC CCAACTGGCC AGTGTGACTT 120
TCGCCACCAA CAACCCACA CTTACCACTG TGGCCTTGGA AAGGCTCTC TGATGTTTG 180
ACAGCAAAGA GGCCTCACT GGCACCCACG AGGTCTACT GTATGCTCTG GTCGACTCAG 240
CCATTTCAG GAATGCCTCA GTGCAAGACA GCACCAACAC CCCACTGGGC TCAACGTTC 300

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TACAAACAGA GGGTGGGAGG ACAGGTCCCT ACAAAGCTGT GGCCTTTGAC CTGATCCCTT 360
 GCAGTGACCT GCCCAGCCTG GATGCCATTG GGGATGTGTC CAAGGCCTCA CAGATCCTGA 420
 ATGCTTACCT GGTGAGGGTG GGTGCCAAGC GGACCTGCCT GTGGGATCCC AACTTCCAGG 480
 GCCTCTGTAA CGCACCCCTG TCGGCAGCCA CGGAGTACAG GTTCAAGTAT GTCTTGGTCA 540
 ATATGTCCAC GGGCTTGGTA GAGGACCAGA CCCTGTGGTC GGACCCATC CGCACCAACC 600
 AGCTCACCCC ATACTCGACG ATCGACACGT GGCAGGCGCG GCGGAGCCGA GGCATGATCG 660
 TCATCATCTC CATCTTGGG TCCCTGCCCT TCTTCTACT TGTGGGTPTT GCTGGCGCCA 720
 TTGCCCTCAG CCTCTGTGAC ATGGGGAGTT CTGATGGGGA AACGACTCAC GACTCCCAAA 780
 TCACTCAGGA GGCTGTTCCG AAGTCGCTGG GGGCCTCGGA GTCTTCTTAC ACGTCCGTGA 840
 ACCGGGGGCC GCCACTGGAC AGGGCTGAGG TGTATTCCAG CAAGCTCCAA GACTGAGCCC 900
 AGCACCACCC CTGGGCAGCA GCATCCTCCT CTCTGGCCCT GCCCAGGCC CTGCAGCGGT 960
 GGTGTGCACA CCTGACTTC AGGGAAGGTG AAACAGGGCT TGTCCCTCCA ACTGCAGGAA 1020
 AACCCCTAAT AAAATCTTCT GATGAGTTCT AAAAAAAA

SEQ ID NO:98 PEL9 Protein sequence
 Protein Accession #: NP_008884

1 11 21 31 41 51
 MPPLMALLAL GCLRFGSAVN LQPQLASVTF ATNNPTLTTV ALEKPLCMFD SKEALTGTHE 60
 VVLYVLVDSA IGRNASVDQS TNTPLGSTFL QTEGGRTGPFY KAVAFDLIPC SDLPFLDAIG 120
 DVSKASQILLN AYLVVRVANG TCLWDENFQG LCNAPLSAAT EYRFKYVLVN MSTGLVEDQT 180
 LWSDPIRTNQ LTPYSTIDTW PGRRSQGMIV ITSILGSLPF FLVVPAGAI ALSLVDHMGSS 240
 DGETTHDSQI TQEAVPKSLG AESSYTSVN RGPPLDRAEV YSSKLQD

SEQ ID NO:99 PEN1 DNA SEQUENCE

Nucleic Acid Accession #: NM_012391
 Coding sequence: 416-1423 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GTCTGACTTC CTCCAGCAC ATTCTGCAC TCTGCCGTGT CCACACTGCC CCACAGACCC 60
 AGTCTTCCAA GCTCTGTGCC AGCTCCCTGC AAGCCCTCA GGTGGGCCTT TGCCACGGTG 120
 CCAGCAGGCA GCCCTGGGCT GGGGGTAGGG GACTCCCTAC AGGCACGCAG CCTGAGACC 180
 TCAGAGGGCC ACCCTTGAG GGTGGCCAGG CCCCAGTGG CCAACTGAG TGTGCTCTCT 240
 GCCACCAGCC CTGCTGGCCC CTGGTTCCGC TGGCCCCCA GATGCCCTGG TGAGACAGCG 300
 CAGTGGCCTC AGCTGCCAC ACCTCTTCCC GGCCCCGTAA GTTGGCAGTG CAGCAGACAG 360
 TCCCTTGGCG ACCAGTCAGC TAACAGACAC AGCCGCCAGC CCAACAGCA GCGGCATGGG 420
 CAGCGCCAGC CCGGGCTGGA GCAGCGTATC CCCCAGCCAC CTCTGCTGC CCCCAGCAC 480
 GGTGTCCGGG ACAGGCTTGG AGAAGGCGGC AGCGGGGGCA GTGGGTCTCG AGAGACGGGA 540
 CTGGAGTCCC AGTCCACCCG CCACGCCCGA GCAGGGCCTG TCCGCTTCT ACCTCTCCTA 600
 CTTTGACATG CTGTACCCCTG AGGACAGCAG CTGGGCAGCC AAGGCCCTTG GGGCCAGCAG 660
 TCGGGAGGAG CCACCTGAGG AGCCTGAGCA GTGCCGGTCT ATTGACAGCC AAGCCCGAGC 720
 GGGCAGCCTG GACTTGGTGC CCGGCGGGCT GACCTTGGAG GAGCACTCGC TGGAGCAGGT 780
 CAGATCCATG TGTGTGGGCG AAGTGTCTAA GGACATCGAG ACGGCTGCA TACTGCTCAA 840
 CATCACCCGA GATCCCATGG ACTGGAGCCC CAGCAATGTG CAGAAGTGGC TCTGTGGAC 900
 AGAGCACCAA TACCGGCTGC CCCCAGTGGG CAAGGCCTTC CAGGAGCTGG CCGGCAAGGA 960
 GCTGTGCGCC GACTGCGAGG AGCAGTTCGG CCAGCGCTCG CCCCTGGGTG GGGATGTGCT 1020
 GCACGCCAC CTGGCATCTT GGAAGTCAGC GGCCTGGATG AAAGAGCCGA CTTCACCTGG 1080
 GCGGATTCAC TGTGTGCTCT CGACCACTGA GAGAGCTGG ACCGACAGCG AGGTGGACTC 1140
 ATCATGCTTC GGGCAGCCCA TCCACCTGTG GCAGTTCCTC AAGGAGTTGC TACTCAAGCC 1200
 CCACAGCTAT GGCCGCTTCA TTAGTGGCTT CAACAAGGAG AAGGGCATCT TCAAAATTGA 1260
 GGACTCAGCC CAGGTGGGCC GGCTGTGGGG CATCCGCAAG AACCGTCCCG CCATGAACCTA 1320
 CGACAAGCTG AGCCGCTCCA TCCGCCAGTA TTACAAGAAG GGCACTATCC GGAAGCCAGA 1380
 CATCTCCAGC CGCTCTGCTT ACCAGTTCGT GCACCCATC TGAGTGCCTG GCCCAGGGCC 1440
 TGAACCCCGC CCTCAGGGGC CTCTCTCCTG CCTGCCCTGC CTCAGCCAGG CCTGAGATG 1500
 GGGGAAAACG GGCAGTCTGC TCTGTGCTC TGACCTTCCA GAGCCCAAG TCAGGGAGGG 1560
 GCAACCAACT GCCCAGGGG GATATGGGTC CTCTGGGGCC TTCGGGACCA TGGGGCAGGG 1620
 GTGCTTCTC CTCAGGCCCA GCTGCTCCCT TGGAGGACAG AGGGAGACAG GGTGCTCCC 1680
 CAACACCTGC CTCTGACCCC AGCATTTCCA GAGCAGAGCC TACAGAAGGG CAGTGACTCG 1740
 ACAAAGGCCA CAGGCACTCC AGGCTCTCT CTGCTCCATC CCCCTGCCTC CCATTCTGCA 1800
 CCACACCTGG CATGGTGCAG GGAGACATCT GCACCCCTGA GTTGGGCAGC CAGGAGTGCC 1860
 CCGGGAATG GATAATAAAG ATACTAGAGA ACTG

SEQ ID NO:100 PEN1 Protein sequence
 Protein Accession #: NP_036523

1 11 21 31 41 51
 MGSASPLGSS VSPSHLLLPF DTVSRTGLEK AAAGAVGLER RDWSPSPPAT PEQGLSAFYI 60
 SYFDMLYPED SSWAAKAPGA SSREEPPEEP EQCFVIDSQA PAGSLDLVPG GLTLEHSLE 120
 QVQSMVVGVEV LKDIETACKL LNITADPMDW SPSNVQKWLW WTEHQYRLPP MGKAPQELAG 180
 KELCAMSEEQ FRQRSPLGGD VLHAHLDIWK SAAMWKERTS PGAIHYCAST SEESWTDSEV 240
 DSSCSGQPIH LWQFLKELLK KPHSYGRFIR WLNKEKGIFK IEDSAQVARL WGIRKNRPAM 300
 NYDKLSRSIR QYTKGIIIRK FDISQRLVYQ FVHPI

SEQ ID NO:101 PEN3 DNA SEQUENCE

Nucleic Acid Accession #: NM_000742
 Coding sequence: 555-2144 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GAGAGAACAG CGTGAGCCTG TGTGCTTGTG TGTGAGCCCT TCATCCCTCTC CTGGGGCCAG 60
GCTTGGGTTT CACCTGCAGA ATCGCTTGTG CTGGGCTGCC TGGGCTGTCC TCAGTGGCAC 120
5 CTGCATGAAG CCGTTCTGGC TGCCAGAGCT GGACAGCCCT AGGAAAACCC ACCTCTCTGC 180
AGAGCTTGCC CAGCTGTCCC CGGGAAGCCA AATGCCTCTC ATGTAACTCT TCTGCTCGAC 240
GGGGTGCTCT CTAAACCCCT ACTCTTCAGC CTCTGTTTGA CCATGAAATG AAGTGACTGA 300
GCTCTATTCT GTACCTGCCA CTCTATTCTT GGGGTGACTT TTGTACAGTG CCCAGAATCT 360
10 CCAAGCCAGG CTGGTTCTCT GCATCTTTTC AATGACCTGT TTTCTTCTGT AACCACAGGT 420
TCGGTGGTGA GAGGAAGCCT CGCAGAATCC AGCAGAATCC TCACAGAATC CAGCAGCAGC 480
TCTGCTGGGG ACATGTGCTCA TGGTGCAACC CACAGCAAAG CCCTGACCTG ACCTCTGTAT 540
GCTCAGGAGA AGCCATGGGC CCCTCCTGTC CTGTGTTCTC GTCTTCACA AAGCTCAGCC 600
TGTGGTGGCT CCTTCTGACC CCACAGGTG GAGAGGAAGC TAAGCCGCCA CCTCCAGGG 660
15 CCTCTGGAGA CCCACTCTCC TCTCCAGTC CCACGGCATT GCCGAGGGA GGCTCGCATA 720
CCGAGACTGA GAGACGGCTC TTCAAACACC TCTTCCGGGG CTACAACCCG TGGGCGCGCC 780
CGGTGCCCAA CACTTCAGAC GTGGTGATTG TGCCTTTGG ACTGTCCATC GCTCAGCTCA 840
TGCATGAGGA TGAGAAGAAC CAAATGATGA CCACCAACGT CTGGCTAAAA CAGGAGTGA 900
GCGACTACAA ACTGCGCTGG AACCCTCGTG ATTTTGGCAA CATCACATCT CTCAGGGTCC 960
20 CTCTCTGAGT GATCTGGATC CCGGACATTG TCTCTACAA CAATGCAGAT GGGGAGTTTG 1020
CAGTGACCCA CATGACCAAG GCCCACTCTC TCTCCACGGG CACTGTGCAC TGGGTGCCCC 1080
CGGCCATCTA CAAGAGCTCC TGCAGCATCG ACGTCACTCT CTCTCCCTTC GACCAGCAGA 1140
ACTGCAAGAT GAAGTTTGGC TCTTGACTT ATGACAAGG CAAGATCGAC CTGGAGCAGA 1200
TGGAGCAGAC TGTGGACCTG AAGGACTACT GGGAGAGCGG CAGATGGGCC ATCGTCAATG 1260
25 CCACGGGCAC CTACAACAGC AAGAAGTACG ACTGCTGCGC CGAGATCTAC CCCGACGTCA 1320
CCTACGGCTT CGTCTATCCG CGGCTGCCCG TCTTCTACAC CATCAACCTC ATCATCCCTC 1380
GCCTGCTCAT CTCTGCTCTG ACTGTGCTGG TCTTCTACCT GCCCTCCGAC TGGGCGCAGA 1440
AGATCAAGCT GTGCAATTCG GTGCTGCTGT CACTCACCGT CTCTCTGCTG TCTATCATG 1500
AGATCATCCC GTCCACCTCG CTGCTCATCC CGCTCATCGG CAGATACCTG CTGTTCAACA 1560
30 TGATCTTCTG CACCTGTCTC ATGCTCATCA CCGTCTCTGT GCTCAATGTG CACCACCGCT 1620
CCCCAGCAC CCACACCATG CCCCCTGGG TGGGGGGGGC CCTTCTGGGC TGTGTGCCCC 1680
GGTGCTCTCT GATGAACCGG CCCCACCCAC CCGTGGAGCT CTGCCACCCC CTACGCGCTG 1740
AGCTCAGCC CTCTTATCAC TGGCTGGAGA GCAACGTGGA TGGCAGGAG AGGGAGGTGG 1800
TGTGAGGAGA GGAGGACAGA TGGGCATGTG CAGGTCATGT GGGCCCTCTT GTGGGCACCC 1860
35 TCTGCAGCCA CGGCCACCTG CACTCTGGGG CCTCAGGTCC CAAGGCTGAG GCTCTGCTGC 1920
AGGAGGGTGA GCTGCTGCTA TCACCCACCA TGCAGAAGGC ACTGGAAGGT GTGCACTACA 1980
TTGCCGACCA CCTGCGGCTG GAGGATGCTG ACTCTTCGGT GAAGGAGGAC TGGAGTATG 2040
TTGCCATGGT CATGACAGG ATCTTCTCTC GGCTGTTTAT CATCTGCTGC TTCTTGGGGA 2100
CCATCGGCTT CTCTCTGCTT CCGTTCCTAG CTGGAATGAT CTGACTGCAC CTCCCTCGAG 2160
40 CTGGCTCCCA GGGCAAAGGG GAGGGTCTCT GATGTGGAA GGGCTTTGAA CAATGTTTAG 2220
ATTGAGGAT GAGCCCAAG TGCCAGGGAG AACAGCCAGG TGAGGTGGGA GGTGGAGAG 2280
CAGGTGAGG TCTCTTAAG TCAGGCTGGG GTTGAAGTTT GAGTCTGTG CGAGTTTGA 2340
GGGTGCTGAG CTGTATGCTC CAGCAGGGGA GTAATAAGG CTCTTCCGGA AGGGAGGAA 2400
GGGGAGGCA GGCTGACCC TGATGTGGAG GTACAGGCAG ATCTTCCCTA CCGGGAGGG 2460
45 ATGGATGGTT GGATACAGGT GGCTGGGCTA TTCCATCCAT CTGGAAGCAC ATTTGAGGCT 2520
CCAGCTTCT CTCTGACGTC ATTCTCTCTC TTCTTCTGCT CAAAATGGCT CTCGACCCAG 2580
CGGCCCCAG GAGGCTTGGC AGAGCTGAGA GCCATGGCT GCAGGGGCTC CATATGTCCC 2640
TACGCGTCA GCAGGCAAC AAGA

SEQ ID NO:102 PEN3 Protein sequence

Protein Accession #: NP_000733

1 11 21 31 41 51
MGPSCPVFLS FTKLSLWML LTPAGGEEAK RPPPRAPGDP LSSPSPTALP QGGSHTETED 60
55 RLPKHLFRGY NRWARVPENT SDVVIVRFLG SIAQLIDVDE KNQMTTNNW LKQEWSDYKL 120
RWNPAIDFNI TSLRVPSEMI WIPDIVLYNN ADGEFAVTHM TKAHLFSTGT VHWVPPAIYK 180
SSCSIDVTFF PPDQONCKMK FGSWTYDKAK IDLEQMEQTV DLKALWESGE WAINVATOTY 240
NSKKYDCAE IYPDVTYAFV IRRPLFYTI NLIIPCLLIS CLTVLVFYLP SDGGEKITLC 300
ISVLLSLTVF LLLITEIIPS TSLVPLIGE YLLFTMIFVT LSIVITVFVL NVHHRSPSTH 360
60 TMPHVVRGAL LGCVRPRLM NRPPPFVELC HPLRLKLSPS YHWLESNVDA EEREVVVEEE 420
DRWACAGHVA PSVGTLCSHG HLHSGASGPK AEALLQEGEL LLSPHMQKAL EGVHYIADHL 480
RSEDADSSVK EDWKYVAMVI DRIFLWLFII VCFLOTIGLF LPFLAGMI

SEQ ID NO:103 PEU4 DNA SEQUENCE

Nucleic Acid Accession #: NM_018670

Coding sequence: 87-893 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CACGAGGCTG GAAGGGGCCA CTTACACCTT CGGGCTCGGC ATAAAGCGGC CGCCGGCCGC 60
70 CGGCCCCAGC ACGCCCGGCC GCTGCCATGG CCCAGCCCTT GTGCCCGCGC CTCTCCGAGT 120
CCTGGATGCT CTCTGCGGCC TGGGGCCCAA CTCGGCGGCC CGCCGCCCTC GACAAGGACT 180
CGCGCCGCTC CCTGCTCTCG TCCCAGACTC CATGGGGCAG CACCCAGACC GACAGCCCGC 240
75 TGGCAGAGCC CGCGCGGCCA GGCACTCTCC GGGACCCCGC CGCCCTCTCC GTAGGTAGGC 300
CGCGCGCGGC CAGCAGCCGC CTGGGACGCG GGCAGAGGCA GAGCGCAAGT GAGCGGAGA 360
AACTGCGCAT GCGCAGCTG GCGCGCGGCC TGACAGAGCT GCGCGCTTT CTACCGCGCT 420
CCGTGGCGCC CGCGGGCCAG AGCCTGACCA AGATCGAGAC GCTGCGCTG GCTATCCGCT 480
ATATCGGCCA CCTGTGCGCC GTGCTAGGCC TCAGCGAGGA GAGTCTCCAG CGCCGGTGCC 540
80 GGCAGCGCGG TGACGCGGGG TCCCTCGGG GCTGCGGCT GTGCCCGAC GACTGCGGCC 600
CGCAGATGCA GACACGGAGC CAGGCTGAGG GGCAGGGGCA GGGGCGCGGC CTGGCCCTGG 660

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TATCCGCCGT CCGCGCCGGG GCGTCTGGG GATCCCCGCC TGCCTGCCCC GGAGCCCGAG 720
 CTGCGATCGA GCCGCGCGAC CCGCCTGCGC TGTTCCGCCA GCGCGCGTGC CCGGAAGGGC 780
 AGGCGATGGA GCCAAGCCCA CCGTCCCGCC TCCTTCCGGG CGACGTGCTG GCTCTGTTGG 840
 AGACCTGGAT GCCCTCTCG CCGTCTGGAGT GGCTGCCTGA GGAGCCCAAG TGACAAGGGA 900
 CAACTGACGC CGTCTCTGTG AGCACCAGAG CTCTTTTGGC TCAGCACCTT CGAAGTGGTT 960
 CCTTGGCAGA CTGCTTTTCC TGGAAAGAGG CACGGGCGAT CCCGACGGGG GCATTCTCTG 1020
 GGGTAGAGGC CGTCCCAACC GCGGCGGCCC TTCTCAGCCC CTCCTTCCAT GGAGGGACCC 1080
 ATAGGGCTAG ACACTTTGAG GCAAGCAGGA GGCTCTGCCT AATGTGAATT TATTTATTTG 1140
 TGAATAAAT GTACTGGTGT CAAAAA AAAA AAAAAA A

SEQ ID NO:104 PEU4 Protein sequence

Protein Accession #: NP_061140

1 11 21 31 41 51
 15 MAQPLCPPLS ESWMLSAAMG PTRRPPPSDK DCGRLVSSP DSWGSTPADS PVASPARPGT 60
 LRDPRAPSVG RRGARSSRLG SGQRQSASER EKLRMRTLAR ALHELRRFLP PSVAPAGQSL 120
 TKIETLRLAI RYIGHLSAVL GLSEESLQRR CRQRGDAGSP RGCPLCPDDC PAQMOTRTOA 180
 EGQGGGRGLG LVSAVRAGAS WGSPPACFGA RAAPEPRDPP ALFAEAACPE GQAMEPSPPS 240
 20 PLLPGDVLAL LETWMLSP EWLPEEPK

SEQ ID NO:105 PEU5 DNA SEQUENCE

Nucleic Acid Accession #: NM_017636

Coding sequence: 324-3374 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
 CCACGGAGAA GCCCACCAGT GCCTACGGAG AGCTGGACTT CACGGGGGCC GGCCGCAAGC 60
 ACAGCAATTT CCTCCGGCTC TCTGACCGAA CGGATCCAGC TGCAATTTAT AGTCTGGTCA 120
 CAGCGACATG GGGCTTCCGT GCCCCGAACC TGCTGGTGTG AGTGTCTGGG GGATCGGGGG 180
 GCCCGCTCCT CCAGACTTGG CTGCAGGACC TGCTGCGTCG TGGGCTGGTG CGGGCTGCCC 240
 AGAGCACAGG AGCCTGGATT GTCACTGGGG GTCTGCACAC GGGCATCGGC CGGCATGTTG 300
 GTGTGGCTGT ACGGGACCAT CAGATGGCCA GCACTGGGGG CACCAAGGTG GTGGCCATGG 360
 TGTGCGCCCC CTGGGGTGTG GTCCGGAATA GAGACACCCCT CATCAACCCC AAGGGCTCTG 420
 TCCCTGCGAG GTACCGGTGG CGCGGTGACC CGGAGGACGG GGTCCAGTTT CCCCTGGACT 480
 ACAACTACTC GGCCTTCTTC CTGTGGGACG ACGGCACACA CGGCTGCCCT GGGGGCGAGA 540
 ACGGCTTCCG CTTCGGCTCG GAGTCTTACA TCTCACAGCA GAAGACGGGC GTGGGAGGGA 600
 CTGGAATTGA CATCCCTGTC CTGCTCCTCC TGATGTATGG TGATGAGAAG ATGTTGACGC 660
 GAATAGAGAA CGCCACCCAG GCTCAGCTCC CATGTCTCCT CGTGGCTGGC TCAGGGGGAG 720
 CTGCGGACTG CTTGGCGGAG ACCCTGGAAG ACACCTTGGC CCCAGGGAGT GGGGGAGCCA 780
 GGCAAGGCCA AGCCCGAGAT CGAATCAGGC GTTCTTTTCC CAAAGGGGAC CTTCAGGTTCC 840
 TGCAAGGCCA GTTGGAGAGG ATTATGACCC GGAAGGAGCT CCGTACAGTC TATCTCTCTG 900
 AGGATGGGTC TGAGGAATTC GAGACCATAG TTTTGAAGGC CCTGTGAAG GCCTGTGGGA 960
 GCTCGGAGGC CTCAGCTTAC CTGGATGAGC TGCGTTTGGC TGTGGCTTGG AACCCGCTGG 1020
 ACATTGCCCC GATGTAACTC TTTCCGGGGG ACATCCAAAT GCGGTCCTTC CATCTCGAAG 1080
 CTTCCTCTAT GGACGCCCTG CTGAATGACC GGCCTGAGTT CGTGCCTTGG CTCAATTTCCC 1140
 ACGGCTCAGT CTTGGGCTCG TTCTTGACCC CGATGCGCCT GGCCCAACTC TACAGCGCGG 1200
 CGCCCTCCAA CTCGCTCATC CGCAACCTTT TGGACCAGGC GTCCCAAGC GCAGGCACCA 1260
 AAGCCCCAGC CCTAAAAGGG GGAGCTGCGG AGCTCCGGCC CCCTGACGTG GGGCATGTGC 1320
 TGAGGATGCT GCTGGGGAAG ATGTGCGCGC CGAGGTACCC CTCGCGGGGG GCGTGGGACC 1380
 CTCACCCAGG CCAGGGCTTC GGGGAGAGCA TGTATCTGCT CTCGGCAAG GCCACCTCGC 1440
 CGCTCTGCTG GATGCTGGC CTCGGGAGG CCCCCTGGAG CGACTGCTT CTTTGGGCAC 1500
 TGTGTCTGAA CAGGGCACAG ATGGCCATGT ACTTCTGGGA GATGGTTCCT AATGCAGTTT 1560
 CCTCAGCTCT TGGGGCTGTG TTGCTGCTCC GGGTGATGGC ACGCTGGAG CCTGACGCTG 1620
 AGGAGGCAGC ACGGAGGAAA GACCTGGCGT TCAAGTTTGA GGGGATGGGG GTTGACCTCT 1680
 TTGGCGAGTG CTATCGCAGC AGTGAGGTGA GGGCTGCCCG CCTCTCTCTC CGTGGCTGCC 1740
 CGCTCTGGGG GGATGCCACT TGCCCTCAGC TGGCCATGCA AGCTGACGCC CGTGCTTCTT 1800
 TTGCCACAGA TGGGGTACAG TCTCTGCTGA CACAGAAGTG GTGGGAGAT ATGGCCAGCA 1860
 CTACACCCAT CTGGGCCCTG GTTCTCGCTT TCTTTTGGCC TCCACTCATC TACACCCGCC 1920
 TCATCACCTT CAGGAAATCA GAAGAGGAGC CCACACGGGA GGAGCTAGAG TTTGACATGG 1980
 ATAGTGTCAAT TAATGGGGA GGGCCTGTGC GGACGGCGGA CCCAGCCGAG AAGACCCGCC 2040
 TGGGGGTCCC GCGCCAGTGC GGCCTGTCGG GTTGTGTCGG GGGCGCTGCG GGGGGCGGCC 2100
 GGTGCTTACG CCGCTGCTTC CACTTCTGGG GCGCGCCGGT GACCATCTTC ATGGGCAACG 2160
 TTGTCAGCTA CCTGCTGTTT TTGCTGCTTT TCTCGCGGGT GCTGCTCGTG GATTTCCAGC 2220
 CGGCGCCGCC CGGCTCCCTG GAGCTGTGTC TCTATTTCTG GGTCTTCAAG CTGCTGTGCG 2280
 AGGAACCTGC CCAGGGCCTG AGCGGAGGCG GGGGCGAGCT CGCCAGCGGG GGGCCCGGGC 2340
 CTGGCCATGC CTCACTGAGC CAGCGCCTGC GCCTCTACCT CGCCGACAGC TGGAAACAGT 2400
 GCGACCTAGT GGCTCTCACC TGCTTCTTCC TGGGCGTGGG CTGCGCGCTG ACCCCGGGTT 2460
 TGTACCACCT GGGCCGCACT GTCTCTGCA TCGACTTCAT GGTCTTTCAG GTGCGGCTGC 2520
 TTACATCTTT CACGATCAAC AAACAGCTGG GGCCCAAGAT CGTCACTGTC AGCAAGATGA 2580
 TGAAGGACCT GTTCTTCTTC CTCTTCTTCC TCGGCGTGTG GCTGTGATGC TATGGCGTGG 2640
 CCACGAAAGG GCTCCTGAGG CCACGGGACA GTGACTTCCC AAGTATCTCT GCGCGGCTCT 2700
 TCTACCTGTC CTACCTGAGC ATCTTCTGGG AGATTCGCCA GGAGGACATG GACGTGGCCC 2760
 TCATGGAGCA CAGCAACTGC TCGTCCGAGC CCGGCTTCTG GGCACACCTT CTTGGGGCCC 2820
 AGGCGGGCAC CTGGCTCTCC CAGTATGCCA ACTGGCTGGT GGTGCTGCTC CTCGTCATCT 2880
 TCCTGTCTGT GGGCAACATC CTGCTGGTCA ACTTGCTCAT TGCCATGTTT AGTTCACAT 2940
 TCGGCAAGAT ACAGGGCAAC AGCGATCTCT ACTGGAAGGC CGACGCTTAC CGCCTCATCC 3000
 GGGAAATCCA CTCTCGGCCC GCGCTGGCCC CGCCCTTTAT CGTCTATCTC CACTTGGGCC 3060
 TCCTGTCTAG GCAATTTGTC AGGCGACCCC GGAGCCCCCA GCGCTCTCTC CCGGCGCTCG 3120
 AGCATTTTCC GGTTTACCTT TCTAAGGAAG CCGAGCGGAA GCTGCTAACG TGGGAATCGG 3180

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TGCATAAGGA GAACTTTCCTG CTGGCAGCG CTAGGACAA GCGGGAGAGC GACTCCGAGC 3240
GTCTGGAGCG CACGTCCAG AAGGTGGACT TGGCACTGAA ACAGCTGGA CACATCCCGC 3300
AGTACGAACA GCGCTGAAA GTGCTGGAGC GGGAGGTCCA GCAGTGTAGC CGCGTCCCTG 3360
GGTGGGTGAC GTAGGCCGTT AGCAGCTCTG CCATGTTGCC CTCAGGTGGG CCGCCACCCC 3420
TTGACCTGCA TGGGTCCAAA GAGTGAGCCA TGCTGGCGGA TTTTAAGGAG AAGCCCCCAC 3480
AGGGGATTTT GCTCTTAGAG TAAGGCTCAT GTGGGCTCG GCGCCCGCAC CTGGTGGCCT 3540
TGTCCTTAGG GTGAGCCCCA TGTCCATCTG GGCCACTGTC AGGACCACCT TTGGGAGTGT 3600
CATCCTTACA AACCACAGCA TGCCCGGCTC CTCCAGAAC CAGTCCAGC CTGGGAGGAT 3660
CAAGGCTGG ATCCCGGGCC GTTATCCATC TGGAGGCTGC AGGGTCTCTG GGGTAAACAG 3720
GACCACAGAC CCTCACCAC TCACAGATTC CTCACACTGG GGAATAAAG CCATTTCAGA 3780
GAAAAA AAAAAA AAAAAA
```

SEQ ID NO:106 PEU5 Protein sequence

Protein Accession #: NP_060106

15
20
25
30
35

```
1 11 21 31 41 51
| | | | |
MASTGGTKVV AMGVAFWGVV RNRDTLINPK GSFPARYRWR GDPEDGVQFP LDYNYSAFFL 60
VDDGTHQCLG GENFRRLRLE SYISQOKTGV GGTGIDIPVL LLLIDGDEKM LTRINATQA 120
QLPCLLVAGS GGAADCLAEI LEDTLAPGSG GARQGEARDR IRRFFPKGDL EVLQAQVERI 180
MTRKELLTVY SSEDGSEEF E TIVLKALVKA CGSSEASAYL DELRLAVAWN RVDIAQSELP 240
RGDIQWRSFH LEASLMDALL NDRPEFVRLI ISHGLSLGHF LTFMRLAQLY SAAPSNSLIR 300
NLLDQASHSA GTKAPALKGG AAE LRPPDVG HVLRLMLGKH CAPRYPSGGA WDPHPGGQFG 360
ESMYLLSDKA TSPSLSDAGL GQAPWSDLLI WALLLNRAQM AMYFWEMGSN AVSSALGACL 420
LLRVMARLEP DAEAEARRKD LAFKFEQMGV DLFGEYRVS EVRAARLLLR RCPLMGDATC 480
LQLAMQADAR AFFAQDGVQS LLTQKWWGDM ASTTPIWALV LAFFCPPLIY TRLITFRKSE 540
EETPRELEF DMDSVINGEG PVGTADPAEK TPLGVPRQSG RPPCCGGRCG GRRCLRRWFH 600
FWGAFVTIFM GNVVSYLLFL LLFSRVLLVD FQAPPPGSLE LLLYFWAFTL LCEELRQGLS 660
GGGGSLSAGG PGPGHASLSQ RLRLYLADSW NQCDLVALTC FLLGVGCRIT PGLYHLGRITV 720
LCIDFMVFTV RLLHIFTVNM QLGPKIVIVS KMKKDVFFPL FFLGVWLVA VATEGLLRP 780
RDSDFPSILR RVFYRPLYQI FGQIPQEDMD VALMEHSNCS SEPFPWAHPP GAQAGTCVSQ 840
YANWLVVLLL VIFLLVANIL LVNLLIAMFS YTFGKVQNS DLYWKAQRYR LIREPHSRPA 900
LAPFFIVISH LRLLLRLQCR RPRSPQSSP ALEHFRVYLS KEAERKLLTW ESVHKNFLL 960
ARARDKRESL SERLERTSQK VDLALKQLGH IREVEQLKV LEREVOQCSR VLGMVT
```

SEQ ID NO:107 PEW3 DNA SEQUENCE

Nucleic Acid Accession #: NM_005982

Coding sequence: 276-1130 (underlined sequences correspond to start and stop codons)

40
45
50
55
60
65

```
1 11 21 31 41 51
| | | | |
GGTAGCAGCA TCACCGGGC GGGAGGTCGG AGGCAGCAAG GCCTTAAAG CTACTGAGTG 60
CGCCGGCCGT TCCGTGTCCA GAACCTCCCC TACTCTCTCC CCTTCTCTTC CTGGCCCGCC 120
CACCGCCACG TCCGACTGCG GGTTTTCGCC TTTGCAAGC CTAAGGAGGA GGTAGGAAC 180
AGCCGCGCCC CCCTCCCTGC GGC CGCGCC CCCTGCCTCT CGGCTCTGCT CCCTGCGCGC 240
TGCGCCTGGG CCGTGCGCC CGGCAGGCGC CAGCCATGTC GATGCTCGCC TCGTTTGGCT 300
TTACGCAAGG CCAAGTGGCG TGCGTGTGCG AGGTTCTGCA GCAAGGCGGA AACCTGGAGC 360
GCCTGGGCAG GTTCTGTGG TCACTGCCCG CCTGCGACCA CTGTCACAAG AACGAGAGCG 420
TACTCAAGG CAAGCGCGTG GTCCCTTCC ACCCGGCA CTTCCGTGAG CTCTACAAGA 480
TCCTGGAGAG CCACCACTTC TCGCCTCACA ACCACCCCA ACTGCAGCAA CTGTGGCTGA 540
AGCGCGATTA CGTGGAGGCC GAGAAGCTGC GCGGCGGACC CCTGGCGGCC GTGGGCAAA 600
ATCGGGTGGC CCGAAATTT CCACTGCCCG GCACCATCTG GGACGGCGAG GAGACCACT 660
ACTGCTTCAA GGAGAAGTCG AGGGGTGTCC TGCGGGAGTG GTACGCGCAC AATCCCTACC 720
CATCGCCGCG TGAGAAGCGG GAGCTGGCCG AGGCCACCGG CCTCACCACC ACCCAGGTCA 780
GCAACTGTTT TAAGAACCGG AGGCAAGAG ACCGGGCGCG GGAGGCCAAG GAAAGGGAGA 840
ACACCGAAAA CAATAACTCC TCCTCCAACA AGCAGAACCA ACTCTCTCTT CTGGAAGGGG 900
GCAAGCCGCT CATGTCCAGC TCAGAAGAGG AATTCTCACC TCCCAAAAGT CCAGACCAGA 960
ACTCGGCTCT TCTGCTGCAG GGCATATGG GCCACGCCAG GAGCTCAAA TATCTCTTCC 1020
CGGGCTTAAC AGCTCCGAG CCCAGTCAG CCCTGCAGAC CCACCAAGAT CAGCTCCAAG 1080
ACTCTCTGCT CGGCCCCCTC ACCTCCAGTC TGGTGGACTT GGGGTCTTAA GTGGGGAGGG 1140
ACTGGGCGCT CGAAGGGATT CCTGAGCAG CAACCACTGC AGCGACTAGG GACACTTCTA 1200
AATAGAAATC AGGAACATTT TTGCAGCTTG TTCTGGAGT TGTTTGCGCA TAAAGGAATG 1260
GTGGACTTTC ACAATATCT TTTTAAAAAT CAAAACCAAC AGCGATCTCA AGCTTAATCT 1320
CCTCTTCTCT CCAACTCTTT CCACCTTTGC ATTTTCTTTC CCAATGCAGA GATCAGGG
```

SEQ ID NO:108 PEW3 Protein sequence

Protein Accession #: NP_005973

70
75

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1 11 21 31 41 51
| | | | |
MSMLPSFGFT QEQVACVCEV LQGGNLERL GRFLWSLPAC DHLKKNESVL KAKAVVAFHR 60
GNFRELYKIL ESHQFSPHNH PKLQQLWLKA HYVEAEKLRG RPLGAVGKYR VRRKFPPLRT 120
IWDGEETSYC FKEKSRGVLR EHYAHNPYP PREKRELAEA TGLTTTQVSN WFKNRQRDR 180
AAEAKERENT EDDNSSSNKQ NQLSPLEGCK PLMSSSEEF SPFQSPDQNS VLLLQGNMGH 240
ARSSNYSLPG LTASQPSHGL QTHQHQLQDS LLGPLTSSLV DLGS
```

SEQ ID NO:109 PFJ8 DNA SEQUENCE

Nucleic Acid Accession #: NM_005069

Coding sequence: 57-2060 (underlined sequences correspond to start and stop codons)

80

1 11 21 31 41 51
GGGGCTCCGC GGGCCTGGAG CACGGCCGGG TCTAATATGC CCGGAGCCGA GGGCGGATGA 60
AGGAGAAGTC CAAGAATGCG GCCAAGACCA GGAGGGAGAA GGAAAATGGC GAGTTTACG 120
5 AGCTTGCCAA GCTGCTCCCG CTGCCGTCGG CCATCACTTC GCAGCTGGAG AAAGCGTCCA 180
TCATCCGGCT CACCACGAGC TACCTGAAGA TGCGCGCGT CTCCCCGAA GGTTTAGGAG 240
ACGCGTGGGG ACAGCCGAGC CGCGCCGGG CCCTGGACGG CGTCGCCAAG GAGCTGGGAT 300
CGCACTTGCT GCAGACTTTG GATGGATTGG TTTTGTGGT AGCATCTGAT GGCAAAATCA 360
TGTATATAT CGAGACCGCT TCTGTCCATT TAGGCTTATC CCAGGTGGAG CTCACGGGCA 420
10 ACAGTATTTA TGAATACATC CATCCTTCTG ACCACGATGA GATGACCGCT GTCCTCACGG 480
CCCACGACC GCTGCACCAC CACCTGTCC AAGAGTATGA GATAGAGAGG TCGTTCTTTC 540
TTGGAATGAA ATGTGTCTTG GCGAAAAGGA ACGCGGGCCT GACCTGCAGC GGATACAAGG 600
TCATCCACTG CAGTGCTTAC TTGAAGATCA GGCAGTATAT GCTGGACATG TCCCTGTACG 660
ACTCCTGCTA CCAGATTGTG GGGCTGGTGG CCGTGGGCCA GTCGCTGCCA CCCAGTGCCA 720
15 TCACCGGAT CAAGCTGTAC AGTAACATGT TCATGTTTCA GGCCAGCCTT GACCTGAAGC 780
TGATATTCTT GGATTCCAGG GTGACCGAGG TGACGGGTGA CGAGCCGAG GACCTGATCG 840
AGAAGACCTC AGAAAGCAGT GACCTTCTGT ACACGCCATC CTACAGCCTG CCCTTCTCCT 900
ACCTCCTGTT GGTGAAGGGC CAGGTACCA CCAAGTACTA CCGGCTGCTG TCCAAGCGGG 960
GCGGCTGGGT GTGGGTGCG AGTACGCCA CCGTGGTGCA CAACAGCCGC TCGTCCCGGC 1020
20 CCCACTGAT CCGTAGTGTG AATTATGTAC TCACGGAGAT TGAATACAAG GAACCTCAGC 1080
TGTCCCTGGA GCAGGTGTCC ACTGCCAAGT CCCAGGACTC CTGGAGGACC GCCTTGTCTA 1140
CCTACAAGA AACTAGGAAA TTAGTAAAC CCAAAAATAC CAAGATGAAG ACAAAGCTGA 1200
GAACAAACCC TTACCCCCA CAGCAATACA GCTCGTTCCA AATGGACAAA CTGGAATGCG 1260
GCCACTCGG AAACCTGGAGA GCCAGTCCCC CTGCAAGCGC TGCTGTCTCT CCAGAACTGC 1320
25 AGCCCACTC AGAAAGCAGT GACCTTCTGT ACACGCCATC CTACAGCCTG CCCTTCTCCT 1380
ACCATTCAGG AACTTCCCT CTGGACTCTC ACGTCTTAC CAGCAAAAAG CCAATGTGTC 1440
CGGCCAAGT CGGGCAGGCC CAAGGATCCC CTGTGAGGT GGCACGCTT TTCTTGAGCA 1500
CACTGCCAGC CAGCGGTGAA TGCCAGTGGC ATTATGCCA CCCCCTAGTG CCTAGCAGCT 1560
30 CGTCTCAGC TAAAAATCT CCAGAGCCAC CGGCGAACAC TGCTAGGCAC AGCCTGGTGC 1620
CAAGCTACGA AGCGCCCGCC GCGCCGCTGC GCAGGTTCGG CGAGGACACC GCGCCCCGA 1680
GCTTCCCGAG CTGCGGCCAC TACGCGAGG AGCCGCGCT GGGCCCGGCC AAAGCCGCC 1740
GCCAGGCCG CCGGACGGG GCGCGGCTGG CGCTGGCCG CCGGCCACCC GAGTGTGCG 1800
CGCCCCGAC CCCCAGGCC CCGGGCGCGC CGGCGCAGCT GCCCTTCTGT CTGCTCAACT 1860
ACCAACCGCT GCTGGCCCG GCGCGACCGC TGGGGGGCGC CGCACCCGCC GCCTCCGGCC 1920
35 TGGCTGGCG TCCCGCGCG CCGAGGCGG CGACCGGCGC GCTGCGGCTC CGGCACCCGA 1980
GCCCGCGGC CACCTCCCC CCGGCGCGC CCCTGCCGA CTACCTGGGC GCCTCGGTCA 2040
TCATCACAA CCGGAGGTGA CCGCTGGCC GCCCGGCCA GGAGCCTGGA CCGGCCCTCC 2100
CGGGCTCGC GCGCCACCGA GCCCGGCAAA TGCGCAACGAC CTACATTAAT TTATCGAGAG 2160
40 ACAGCTGTTT GAATTGGAC CCGCGCCGA CTTCGGGATT TCCACCGCG AGGCCCGCG 2220
CGCGGTGCC GAGGGCCGAG GAGCGCCCG GTCCGGGCG GTGACCGCCC GCCTTGTGTC 2280
TGCGAGGGCC GGTGCGACCC AGTTGCTGGG GGCTTGGTT CCTCACCTT AAATCGGGCT 2340
TCACGCGTCT TGCTTGTCC CCAACGTTC ACAACAGTCC CGCTGGGGGA TTGAAGCGGT 2400
TTCACTCCG AATATCTCT CACTTTCAGG AGGGAACACC CACCCTACCA CAGTCCGCTC 2460
45 TTCCAAGTGG ACGGCAGACC TGGGAGGGGA CGCTGTGTC ACGAGCCCTT TTAGATGCTT 2520
AGGTGAAGGC AGAAGTGATG ATTGTAAGTC CCATGAATAC ACACTCCAC TGCTTTTAAA 2580
AGTCATTCAA GAGTCTCAT ATTITTTGTT TTATTTAAAC CTITCTTCAA TACAAAAAGC 2640
CAACAAACCA AGACTAAGGG GGTGACCATG CAATTCCATT TTGTGTCTGT GAACATAGGT 2700
GTGCTTCCA AATACATTAA CAAGCTCTTA CTTCGCCCTA ACCCTATGA ACTCTTGATA 2760
50 ACACCAAGAG TAGCACCTTC AGAATATATT GAATAGGCAT TAAATGCAAA AATATATATG 2820
TAGCCAGACA GTTATGAGA ATGACCCTGT CAAGCTTCAT TATTACGTGG CAAATCCCT 2880
CTGCCCCACA GCGCTCTGA ATCACTAGG CTCGTGTTG CTACAAATAG TGCTAATAAA 2940
GTTAAATGTC ACGTGAATA CGGAACACTG TCAATGGACT GCACCTTGTG AAGGAAAAAC 3000
ATGCTTAAGG GGGTGAATG AAAATGATGT AGACATTTTA AGCATTTTCT ACACAGCGAG 3060
55 AAACTTCTG AAGAATATG TACGTGTGCA ACAGGTAAC AGAATCCTT TCATAAAGCA 3120
CCAGCAGTGT TAAAAAATG AGCTTCCATT AATTTTACT TTTATGGGT TTTGCTTAAA 3180
GATCTCAACA TGGAAAAATC CTGTATGGC TGTGAACGAC ACAATGCATT GAACCGCGT 3240
CTTCAATTT TCTTCACT ATCAACACTG CAGCATTTTG CTGCTTATC AAAATGGTTT 3300
ATTTAGGAA ACTTTTCCA CTTTCTGAA TGGAAAGAGG TTTTCAAAA TGTTTTAAAC 3360
60 TCATCGTCT AAAATCAAGT GCACCTACAC CACTGCTCT CAAATGTGA ACTGACTTTT 3420
TTTTTTTTT TTTTGCAAC CCGTGTGAC TTAGTGAGGA CTGACACAA TCCCTACAGG 3480
GTGCTGTGCA GTGGGCTCA TGGTAAGAGT CACAATTGTC AAATTTAGGA CCGTGGGTCA 3540
TGCAGCGAAG GGGCTGGATG GTAGGAAGGG ATGTGCCCCG CTCTCCACGC ACTCAGCTAT 3600
ACCTCATCA CAGCTCCTTG TGAGTGTGTG CACAGGAAAT AAGCCGAGGG TATTATTTTT 3660
65 TTATGTTTAT GAGTCTTGA ATTAACCGT GATTCTTGA AGGTGTAGGT TTGATTACTA 3720
GGAGATACCA CCGACATTT TCAATAAAGT ACTGCAAAAT GCTTTTGTG CTACCTTGT 3780
ATTAACITTT GGGGCTGTAT TTAGTAAAA TAAATCAAGG CTATCGGAGC AGTTCATAA 3840
CAAAGTTAC TGTGAGAAA AAAGACCCTA TCATAGATTT ACAAG

SEQ ID NO:110 PFJ8 Protein sequence:
Protein Accession #: NP_005060.1

1 11 21 31 41 51
MKEKSKNAAK TRREKENGFE YELAKLLPLP SAITSQLDKA SIIRLTTSYL KMRVFFPEGL 60
75 GDAWGGQPSRA GPLDGVAKEL GSHLLQTLDG FVFVVASDGK IMYISETASY HLGLSQVELT 120
GNSIYEIHP SDHDEMTAVL TAHQPLHHHL LQYEIERSF FLRMKCVLAK RNAGLTCSGY 180
KVIHCSGYLK IRQYMLMSL YDSCYQIVGL VAVGQSLPPS AITEIKLYN MFMFRASLDL 240

KLIFLDSRVTV ETVGYEPQDL IEKTLVHHVH GCDVFHLRYA HILLVVKQV TTKYYRLLSK 300
RGGWVWVQSY ATVVHNSRSS RPHCIVSVNY VLTEIEYKEL QLSLEQVSTA KSQDSWRTAL 360
STSQETRLV KPNKTKMTK LRTNPPYPPQ YSSFQMDKLE CGQLGNWRAS PPASAAAPPE 420
LQPHSESSDL LYTPSYSLPF SYHYGHFPLD SHVFSSKKPM LPAKFGQPG SPCEVARFFL 480
STLPASGECQ WHYANPLVPS SSSPAKNPPE PPANTARHSL VPSYEAPAAA VRRFGEDTAP 540
PSFPCGHYR EEPALGPAA ARQAARDGAR LALARAAPCE CAPPTPEAFG APAQLPFVLL 600
NYHRVLARRR PLGGAAPAS GLACAPGGPE AATGALRLRH PSPAATSPPG APLPHYLGAS 660
VIITNGR

SEQ ID NO:111 PFJ7 DNA SEQUENCE

Nucleic Acid Accession #: NM_006549

Coding sequence: 1-1254 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGAACGGAC GCTGCATCTG CCGTCCCTG CCCTACTCAC CCGTCAGTC CCCGCACTCC 60
TCGCCTCGGC TGCCCCGGCG GCCGACAGTG GAGTCTCACC ACGTCTCCAT CACGGGTATG 120
CAGGACTGTG TGCAGCTGAA TCAGTATACC CTGAAGGATG AAATTGGAAA GGGCTCCTAT 180
GGTGTGCTGA AGTTGGCCTA CAATGAAAAT GACAATACCT ACTATGCAAT GAAGGTGCTG 240
TCCAAAAAGA AGCTGATCCG GCAGGCCGGC TTCCACGTC GCCCTCCACC CCGAGGCACC 300
CGGCCAGCTC CTGGAGGCTG CATCCAGCCC AGGGGCCCCA TTGAGCAGGT GTACCAGGAA 360
ATTGCCATCC TCAAGAACTG GGACCACCCC AATGTGGTGA AGCTGGTGA GGTCCCTGGAT 420
GACCCCAATG AGGACCATCT GTACATGGTG TTCGAACTGG TCAACCAAGG GCCCGTGATG 480
GAAGTGCCCA CCCTCAAACC ACTCTCTGAA GACCAGGCCG GTTCTACTT CCAGGATCTG 540
ATCAAAAGCA TCGAGTACTT ACACTACCAG AAGATCATCC ACCGTGACAT CAAACCTTCC 600
AACCTCTGG TCGGAGAAGA TGGGCACATC AAGATCGCTG ACTTGGTGT GAGCAATGAA 660
TTCAAGGGCA GTGACGCGCT CCTTCCAAC ACCGTGGGCA CGCCCGCCTT CATGGCACC 720
GAGTCGCTCT CTGAGACCCG CAAGATCTTC TCTGGGAAGG CTTGGATGT TTGGGCCATG 780
GGTGTGACAC TATACTGCTT TGTCTTGGC CAGTGCCCAT TCATGGACGA GCGGATCATG 840
TGTTTACACA GTAAGATCAA GAGTCAGGCC CTGGAATTTC CAGACCAGCC CGACATAGCT 900
GAGGACTTGA AGGACCTGAT CACCCGATG CTGGACAAGA ACCCGAGTC GAGGATCGTG 960
GTGCCGAAA TCAAGCTGCA CCCCTGGGTC ACGAGGCATG GGGCGGAGCC GTTCCGCTCG 1020
GAGGATGAGA ACTGCACGCT GGTGGAAGTG ACTGAAGAGG AGGTCGAGAA CTCAGTCAAA 1080
CACATTCCTA GCTTGGCAAC CGTGATCCTG GTGAAGACCA TGATACGTAA ACGCTCCTTT 1140
GGGAACCCAT TCGAGGGCAG CCGCGGGGAG GAACGCTCAC TGTACGCGCC TGGAAACTTG 1200
CTCACCAAAA AACCACCAAG GGAATGTGAG TCCCTGTCTG AGCTCAAGAC CTAGAAAATA 1260
AGTCCCCTTC CTGCCTGTG CAAAGTAACG TAAGAGTTCC CTCACCCGAG TGGATGCAGA 1320
CGTTCTTGCT GTCAGCCACC TTCTTCATA CACATAGCCA GCCCAGGGTG ACCAGAACGT 1380
CCCAGGACAG ATGAGGCTTT GTGTCCTTAT GAGAGTGGGA GAACCTGGTG GGCACCCCTG 1440
GTGACGGTGC TGTGGTGGGT GGGGACCCCA CTGCCTTTCC CACTGAGCAC ATCATGGCTA 1500
CCTGACTTGG TGGGAGTTC ATTACGTCAC TTCTGTTTCT TAAACATAGC TTTACTGAGG 1560
TACAATTCAC ATACCATGTA ATTACCCAC GGGAAAGTGA TGATTCACTG GTTTCTAATA 1620
CACACTCTG CAGCCATTAC CACCGTCAAC TTACGACAT TTTCATCAGC CCAAGAAGAC 1680
ACCCTACACT CCTAGCTGT CCCCATCAA CTCGCCACC CCAGTAACCA CTCAGAATAG 1740
GTATGGATTG GCCTATTCTG GACGTTTCGT AATAATGGCG TCATACACTA AAAAAAAAAA 1800
AAAA

SEQ ID NO:112 PFJ7 Protein sequence:

Protein Accession #: NP_006540.1

1 11 21 31 41 51
MNGRCICPSL PYPVSSPQS SPRLPRRPTV ESHVHSITGM QDCVQLNQYT LKDEIGKGSY 60
GVVKLAYNEN DNTYYAMKVL SKKKLIRQAG FPRRPPRGRT RPAPGGCIQF RPIEQVYQE 120
IAILKKLDHP NVVKLVEILD DPNEHLYMV FELVNQGPVM EVPTKLPLSE DQARFYFDL 180
IKGIEYLHYQ KIHREDIKPS NLLVGEDGHI KIADFGVSNE FKGS DALLSN TVGTPAFMAP 240
ESLSETRKIF SGKALDVWAM GVTLYCFVFG QCFPMDERIM CLHSKIKSQA LEFPDQPDIA 300
EDLKDILTRM LDKNPESRIV VPEIKLHPWV TRHGAELPLS EDENCTLVEV TEEEVENSVK 360
HIPSLATVIL YKTMIRKRSF GNPFGSRRE ERSLSAPGNL LTKKPTRECE SLSELKT

SEQ ID NO:113 PFJ6 DNA SEQUENCE

Nucleic Acid Accession #: NM_021810

Coding sequence: 1-429 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGAACCTC TGATATGGAC ATGGTCAGAT GTTGAAGGCC AGAGGCCGGC TCTGCTCATC 60
TGCACAGCTG CAGCAGGACC CACGCAGGGA GTTAAGGGTT ATGGCAAGCC CTTTGAGCCA 120
AGAAGTGTGA AAAACATACA CTCTACTCTT GCTTACCCAG ATGCCCAAT GCACAGACAA 180
CTCCTGGCTC CGGTGGAAGG AAGGATGGCA GAGACATTGA ATCAGAACT CCATGTTGCC 240
AATGTGCTGG AAGATGACCC CGGCTACCTA CCTCAGTCT ACAGCGAGGA AGGGGAGTGT 300
GGAGGGGCC CATCCCTCAG CTCTCTGGCC AGCTTGAAC AGGAGTTGCA ACCTGATTG 360

CTGGACTCTT TGGGTTCAAA AGCGACTCCG TTTGAGGAAA TATATTCAGA GTCAGGTGTT 420
CCTTCCTAA

5 SEQ ID NO:114 PFJ6 Protein sequence:
Protein Accession #: NP_068582.1

1 11 21 31 41 51
| | | | |
10 MKPLIWTWSD VEGQRPALLI CTAAGPTQG VKGYGKPFEP RSVKNIHSTP AYPDATMHRQ 60
LLAPVEGRMA ETLNQKLHVA NVLEDDPGYL PHVYSEEGEC GGAPSLSSLA SLEQELQPD 120
LDSLGSKATP FEIYSESGV PS

15 SEQ ID NO:115 PFJ5 DNA SEQUENCE
Nucleic Acid Accession #: NM_006361
Coding sequence: 131-985 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
| | | | |
CGAATGCAGG CGACTTGCGA GCTGGGAGCG ATTTAAACG CTTTGGATTG CCCC GGCGCTG 60
GGTGGGGAGA GCGAGCTGGG TGCCCCCTAG ATCCCCGCC CCGCACCTC ATGAGCCGAC 120
CCTCGGCTCC ATGGAGCCCG GCAATTATGC CACCTTGGAT GGAGCCAAGG ATATCGAAGG 180
25 CTTGCTGGGA GCGGGAGGGG GCGGGAATCT GGTGCGCCAC TCCCCTCTGA CCAGCCACCC 240
AGCGGCGCTC ACCTGTATGC CTGCTGTCAA CTATGCCCC TTGGATCTGC CAGGCTCGGC 300
GGAGCCGCCA AAGCAATGCC ACCCATGCCC TGGGTGCCC CAGGGGACGT CCCCAGCTCC 360
CGTGCTTAT GGTACTTTG GAGCGGGTA CTACTCTGC CGAGTGTCCC GGAGCTCGCT 420
GAAACCTGT GCCCAGGAG CCACCTTGGC CGGTACCCC GCGGAGACTC CCACGGCCGG 480
30 GGAAGAGTAC CCCAGTCGCC CCACTGAGTT TGCCTTCTAT CCGGATATC CGGGAACCTA 540
CCACGCTATG GCCAGTTACC TGGACGTGTC TGTGGTCAG ACTCTGGGTG CTCCTGGAGA 600
ACCGGACAT GACTCCCTGT TGCCTGTGGA CAGTTACCAG TCTTGGGCTC TCGCTGGTGG 660
CTGGAACAGC CAGATGTGTT GCCAGGAGA ACAGAACCCA CCAGTCCCT TTTGGAAGGC 720
AGCATTGCA GACTCCAGCG GGCAGCACCC TCCTGACGCC TCGCCTTTC GTCGCGCCG 780
35 CAAGAAACGC ATTCCGTACA GCAAGGGGCA GTTGGGGAG CTGGAGCGGG AGTATGCGGC 840
TAACAAGTTC ATCACAAGG ACAAGAGGCG CAAGATCTCG GCAGCCACA GCCTCTCGGA 900
GCGCCAGATT ACCATCTGGT TTCAGAACCG CCGGGTCAAA GAGAAGAAGG TTCTCGCCAA 960
GGTGAAGAAC AGCGCTACCC CTAAGAGAT CTCCTTGCCT GGGTGGGAG AGCGAAAGTG 1020
40 GGGGTGTCT GGGGAGACCA GAAACCTGCC AAGCCAGGC TGGGGCCAAG GACTCTGCTG 1080
AGAGGCCCTC AGAGACAAGA CCCTTCCAG GCCACTGGCT GCTGGACTGT TCCTCAGGAG 1140
CGGCTGGGT ACCCAGTATG TGCAGGGAGA CGGAACCCA TGTGACAGGC CCACTCCACC 1200
AGGTTCCCA AAGAACCTGG CCCAGTCATA ATCATTATC CTCACAGTGG CAATAATCAC 1260
GATAACCACT

45 SEQ ID NO:116 PFJ5 Protein sequence:
Protein Accession #: NP_006352.1

50 1 11 21 31 41 51
| | | | |
MEPGNYATLD GAKDIEGLG AGGGRNLVAH SPLTSHPAAP TLMPAVNYAP LDLPGSAEPP 60
KQCHPCGPV QGTSPAPVPY GYFGGGYSC RVSRSLLKPC AQAATLAAYP AETPTAGEEY 120
PSRPTFAFY PGYPGTYHAM ASYLDVSVVQ TLGAPGEPRH DSLLPVDYSQ SWALAGGWNS 180
55 QMCCQGEQNP PGFWKAAFA DSSGQHPDA CAFRRGRKKR IPYSGQLRE LEREYAANKF 240
ITKDKRRKIS AATSLSERQI TWFOQNRVK EKKVLAKVKN SATP

60 SEQ ID NO:117 PFJ4 DNA SEQUENCE
Nucleic Acid Accession #: NM_005628
Coding sequence: 591-2216 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
| | | | |
GTAACCGCTA CTCCCGGACA CCAGACCACC GCCTCCGTA CACAGGGGCC CGCATCCAC 60
CCTCCCGGAC CTAAGAGCCT GGGTCCCTG TTTCCGAGG TCCGCTTCCC GGCCCCCAGA 120
TTCTGGCATC CCAGCCCTCA GTTCCAAGA CCCAGGCAGC CCGGTCCCC GCCTCCCGGA 180
70 TCCAGGCGTC CGGATCTGC GCCACCAGAA CCTAGCCTCC TGCAGACCTC CGCATCTGG 240
GGGCACTCAA CCTCTGGAG CCAAGGGCCC CAGTCCCAAC CCAGAGAAAC TCTCGTATC 300
CCAGCTCCTA GGGCCAAGA ACCCGGGCGC TCCGAACCTC CAGCTTTCGG ACATCTGGCA 360
CACGGGGCAG AGCAGAGAAG CTCAGCGCCC AGCCTGGGGA ATTTAAACAC TCCAGCTTCC 420
AAGAGCCAAG GAACCTCAGT GCTGTGAAC CACAACCTA AGGAGCCCTC CAAAGTTCCA 480
75 GTCTCCAGGT GCTGTACTC AACTCAGTCC TAGGAACGTC GGGTCTGGG AAGGAGCCCA 540
AGCGCTCCCA GCCAGCTTCC AGGCGCTAAG AAACCCCGGT GCTTCCATC ATGTGGCCG 600
ATCTCTCTG AGACTCCAAG GGGCTCGCAG CGGCGGAGCC CACCGCCAAC GGGGGCTGG 660
CGCTGGCCTC CATCGAGGAC CAAGGCGCGG CAGCAGGCGG CTACTGCGGT TCCCGGGACC 720
AGGTGCGCCG CTCCTTCCA GCCAACCTGC TTGTGCTGCT GACAGTGGTG GCCGTGGTGG 780
CCGGCTGGC CTGCGGACTG GGGGTGTCG GGGCGGGGGG TGCCTGGCG TTGGGCCCGG 840

AGCGCTTGAG CGCCTTCGTC TTCCCGGGCG AGCTGCTGCT GCGTCTGCTG CGGATGATCA 900
 TCTTGGCGCT GGTGGTGTGC AGCTTGATCG GCGGCGCCGC CAGCTGGAC CCCGGCGCGC 960
 TCGGCGCTCT GGGCGCCTGG GCGCTGCTCT TTTTCTGGT CACCACGCTG CTGGCGTGG 1020
 CGCTCGGAGT GGGCTTGGCG CTGGCTCTGC AGCCGGGGCG CGCCTCCGCC GCCATCAACG 1080
 5 CCTCCGTTGG AGCCGCGGGC AGTGCCGAAA ATGCCCCAG CAAGGAGGTG CTCGATTCTG 1140
 TCCTGGATCT TGGAGAGAAAT ATCTTCCCTT CCAACCTGGT GTCAGCAGCC TTTCGCTCAT 1200
 ACTTACCAC CTATAGAGAG AGGAATATCA CCGGAACCAG GGTGAAGGTG CCCGTGGGGC 1260
 AGGAGGTGGA GGGGATGAAC ATCCTGGGCT TGGTAGTGTG TGCCATCGTC TTGGTGTGG 1320
 10 CGCTGCGGAA GCTGGGGCCT GAAGGGGAGC TGCATTATCCG CTCTTCAAC TCCTTCAATG 1380
 AGGCCACCAT GGTCTGGTC TCCTGGATCA TGTGGTACCG CCCTGTGGGC ATCATGTTCC 1440
 TGGTGGCTGG CAAGATCGTG GAGATGGAGG ATGTTGGTGT ACTTCTTGGC CGCCTTGGCA 1500
 AGTACATTCT GTGCTGCGTG CTGGGTACCG CCATCCATGG GCTCTGGTA CTGCCCTCA 1560
 TCTACTTCTT CTTCACCCGC AAAAACCCCT ACCGCTTCTT GTGGGGCATC GTGACGCGC 1620
 TGGCCAATGC CTTTGGGACC TCTTCCAGTT CCGCCACGCT GCCGCTGATG ATGAAGTGCG 1680
 15 TGGAGGAGAA TAATGGCGTG GCCAAGCACA TCAGCCGTTT CATCTGGCC ATCGGCGCCA 1740
 CCGTCAACAT GGACGGTGCC GCGCTTCTCC AGTGCGTGGC CGCAGTGTTC ATTGCACAGC 1800
 TCAGCCAGCA GTCCTTGGAC TTGTAAGA TCATCACTT CCTGGTACG GCCACAGCGT 1860
 CCAGCGTGGG GGCAGCGGGC ATCCCTGCTG GAGGTGTCTT CACTCTGGCC ATCATCTCG 1920
 AAGCAGTCAA CCTCCGGTC GACCATATCT CTTGTATCCT GGCTGTGGAC TGGTAGTTCG 1980
 20 ACCGTTCTCT TACCGTCTCT AATGTAGAAG GTGACGCTCT GGGGGCAGGA CTCCTCCAAA 2040
 ATTATGTGGA CGGTACGGAG TCGAGAAGCA CAGAGCCTGA GTTGATACAA GTGAAGAGTG 2100
 AGTGCCTCTT GGATCCGCTG CCAGTCCCA CTGAGGAAGG AAACCCCTCT CTAAACACT 2160
 ATCGGGGGCC CGCAGGGGAT GCCACGGTCG CCTCTGAGAA GGAATCAGTC ATGTAAACCC 2220
 CGGGAGGGAC CTTCCTGGCC CTGCTGGGGG TGCTCTTTGG ACATGGATT ATGAGGAATG 2280
 25 GATAAATGGA TGAGCTAGGG CTCTGGGGGT CTGCTGTCAC ACTCTGGGGA GCCAGGGGCC 2340
 CCAGCACCTT CCAGGACAGG AGATCTGGGA TGCCTGGCTG CTGGAGTACA TGTGTTCACA 2400
 AGGGTTACTC CTAAAACCC CCAGTTCTCA CTCATGTCCC CAACTCAAGG CTAGAAAAACA 2460
 GCAAGATGGA GAAATAATGT TCTGTGCGT CCCCACCGTG ACCTGCTGG CCTCCCTGT 2520
 30 CTAGGGAGC AGGTACAGG TCACCATGGG GAATCTAGC CCCCCTGGG GGGATGTAC 2580
 AACACCATGC TGGTTATTTT GCGGGCTGTA GTTGTGGGGG GATGTGTGTG TGCACGTGTG 2640
 TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TTCTGTGACC TCTGTCCCC ATGGTACGTC 2700
 CCACCTGTCT CCCAGATCCC CTATCCCTC CACAATAACA GAAACACTCC CAGGACTCT 2760
 GGGAGAGGC TGAGGACAAA TACCTGCTGT CACTCCAGAG GACATTTTTT TTAGCAATAA 2820
 AATTGAGTGT CAACTATTTA AAAAAAAAAA AAAAAA

SEQ ID NO:118 PFJ4 Protein sequence:
 Protein Accession #: NP_005619.1

40 1 11 21 31 41 51
 | | | | |
 MVADPPRDSK GLAAAEPTAN GGLALASIED QGAAAGGYCG SRDQVRRCLR ANLLVLLTVV 60
 AVVAGVALGL GVSGAGGALA LGPERLSAFV FPGELLRLRL RMILPLVVC SLIGGAASLD 120
 45 PGALGRLGAW ALLFLVTL LASALGVGLA LALQPGAASA AINASVGAAG SAENAPSKEV 180
 LDSFLDLARN IFFSNLVSAA FRSYSTTYEE RNITGTRVKV PVQGEVEGMN ILGLVVFATV 240
 FGVALRLGP EGELLIRFFN SFNEATMVLV SWIMWYAPVG IMFLVAGKIV EMEDVGLLFA 300
 RLKGYLCLL LGHAIHGLLV LPLIYFLFTR KNPYRFLWGI VTPLATAFGT SSSSATPLM 360
 MKCVEENGV AKHISRFLP IGATVNM DGA ALFQCVAAVF IAQLSQSLD FVKITLVT 420
 50 ATASSVGAAG IPAGGVLT LA ILEAVNLPV DHISLILA VD WLVDRSCTVL NYEGDALGAG 480
 LLQNYVDRTE SRSTEPELQ V KSELPLDPL PVPTEEGNPL LKHYRGPAGD ATVASEKESV 540
 M

55 SEQ ID NO:119 PFJ3 DNA SEQUENCE
 Nucleic Acid Accession #: NM_006708
 Coding sequence: 88-642 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 | | | | |
 CTAGTTAAGG CGGCACAGGG CCGAGGCGTA GTGTGGGTGA CTCCTCCGTT CCTTGGGTCC 60
 CGTCTGCTGT GATACTGCAG TTCAGCCATG GCAGAACC GCACCCCGTC CGGCGGCTC 120
 ACGGACGAGG CCGCCCTCAG TTGCTGCTCC GACGCGGACC CCAGTACCAA GGATTTTCTA 180
 65 TTGCAGCAGA CCATGCTACG AGTGAAGGAT CCTAAGAAAGT CACTGGATTG TTATACTAGA 240
 GTTCTTGGAA TGACGCTAAT CCAAAAATGT GATTTTCCCA TTATGAAGTT TCACTCTAC 300
 TTCTTGGCTT ATGAGGATAA AAATGACATC CCTAAGAAAA AAGATGAAAA AATAGCCTGG 360
 GCGCTCTCCA GAAAAGCTAC ACTTGAGCTG ACACACAATT GGGGCACCTA AGATGATGCG 420
 ACCGAGATT ACCACAATG CAATTACAGC CCTCGAGGAT TCGGTATAT TGGAAATGCT 480
 70 GTTCTGATG TATACAGTGC TTGTAAAAGG TTGAAGAAC TGGGAGTCAA ATTTGTGAAG 540
 AAACCTGATG ATGGTAAAT GAAAGGCTG GCATTTATTC AAGATCTGTA TGGCTACTGG 600
 ATTGAAATTT TGAATCTTAA CAAAATGGCA ACCTTAATGT AGTGCTGTGA GAATCTCCT 660
 TTGAGATTTC AGAAGAAAGG AAACAATGTG ATTCAAGATA TTACATACC AGAAGCATCT 720
 AGGACTGATG GATCACTGTC CCGATTCAAA TTATTCTTCA GTCCATTTC CCTTCCTATT 780
 75 TCAGCTGTTC CTTTACCTT AACTGTTCAG TCATTCTGGT TTCAAGCAG TGCTTTATCT 840
 CATGCTCTGT AATATAGTGT TGTAACCTTA TTTTATAGGT AATAATTAGA ACAGTTCCT 900
 TCAGAGGCTG CATTTGCCCT CTCTGCCAC CTAATATTA CTTCCTTCA AATCTGCCCT 960
 TGAATCATCA TTTTAAAAA AAAATTAACA TGTTTTGTG GTAGTTATCT TCTGGGGTTT 1020
 CAATTCTCTA GAAACAACCT TTTTCAAC GGAAGGAAAA GAACACTAGT GTTCTTCA 1080
 TAAAGTACAA AGTGTATTAT TTACAAAAGA GTAGGTACTC TTGAGAGCAA TTCAATCAT 1140

GCTGACAAGG ATACTGATAG AAAAAGTGAT TTCTTCTTAT TATAAAGTAC ATTTAAAGTT 1200
 CAAGGACTAA CCTTATTTAT TTGGGAAAGG GGAGGAGGAA GGAAATGATA TGGTACCCAG 1260
 AACTGGGCT AGGCTGCAAC TTTATCTCAT TTAATACTCC CAGCTGTCAT GTGAGAAAGA 1320
 AAGCAGGCTA GGCATGTGAA ATCACTTTCA TGGATTATTA ATGGATTTAA GAGGGCATCA 1380
 ATCAGCTCAA CTCAAGATTT CATAATCAT TTTAGTATTT AGATTGTGCC TCAAAGTTGT 1440
 AGTACCTCAC AATACCTCCA CTGGTTTCCT GTTGTAAGAA CCTTCAGTGA GTTTGACCAT 1500
 TGTGCTCTTG GCTCTGGGC TGGAGTACCG TGGTGAGGGA GTAAACACTA GAAGTCTTTA 1560
 GTACAAAAC TGTCTAGGGA CACCTGGTGA TTCTACACA AGTGATGTTT ATATTTCTCA 1620
 TAAAGAGTCT TCCTATCCCC AAGGTCTTCA TGATGCCAGT AGCCATATAT GATAAATTAT 1680
 GTTCAGTGAT AACTTAGTGA TCAGAAATCA GCTCAGTGGT CTCCCCGCC ATGATTCA 1740
 TTTGATGAGT TTTTAAAAAT CAAAGTGATT TTGAAAATCT CTAATGGCTC AGAAAAATAA 1800
 AACATCCAGT TGTGGATGA CTATATTAG ATTTCTCTAG ACTCTAGTGG AAGACCTTTG 1860
 GAAAGGCCAT GCCAACCGTG CTGTACTGC TAGAAGCACT TTATGTTTCC TTTTGGGTG 1920
 AAATGGATT ATGTAGTGC TTTAAACAAA TAGCAATACT TATAGACTGA AATAAAATGA 1980
 AACTCAAAT AAG

SEQ ID NO:120 PFJ3 Protein sequence:
 Protein Accession #: NP_006699.1

1 11 21 31 41 51
 | | | | |
 MAEPQPPSGG LTDEAALSCC SDADPSTKDF LLQQTMLRVK DPKKSLDFYT RVLGMTLIQK 60
 CDFPIMKFSL YFLAYEDKND IPKEKDEKIA WALSRKATLE LTHNWGTEDD ATQSYHNGNS 120
 DPRGRGHIGI AVPDVYSACK RFEELGVKFV KKPDDGKMKG LAFIQDPDGY WIEILNPNKM 180
 ATLM

SEQ ID NO:121 PFJ2 DNA SEQUENCE

Nucleic Acid Accession #: NM_002867
 Coding sequence: 70-729 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CCGACGCCAG GTCCTGCCGT CCCGCCGACC GTCCGGGAGC GAACCCGTCG TCCCGCACTG 60
 GAGTCCCGCA TGGCTTCAGT GACAGATGGT AAACATGGAG TCAAAGATGC CTCTGACCAG 120
 AATTTTGACT ACATGTTTAA ACTGCTTATC ATTGGCAACA GCAGTGTGG CAAGACCTCC 180
 TTCTCTTGC GCTATGCTGA TGACACGTTT ACCCAGCCT TCGTTAGCAC CGTGGGCATC 240
 GACTTCAAGG TGAAGACAGT CTACCGTCAC GAGAAGCGGG TGAACCTGCA GATCTGGGAC 300
 ACAGCTGGGC AGGAGCGGTA CCGGACCATC ACAACAGCCT ATTACCGTGG GGCCATGGGC 360
 TTCATTCTGA TGATGACAT CACCAATGAA GAGTCCTTCA ATGCTGTCCA AGACTGGGCT 420
 ACTCAGATCA AGACCTACT CTGGGACAAT GCACAAGTTA TTCTGGTGGG GAACAAGTGT 480
 GACATGGAGG AAGAGAGGGT TGTCCCACT GAGAAGGGCC AGCTCCTTGC AGAGCAGCTT 540
 GGGTTTGATT TCTTTGAAGC CAGTGCAAAAG GAGAATATCA GTGTAAGGCA GGCCTTTGAG 600
 CGCCTGTGG ATGCCATTTG TGACAAGATG TCTGATTCCG TGGACACAGA CCGTCTGATG 660
 CTGGGCTCCT CCAAGAACAC GCGTCTCTCG GACACCCAC CGCTGCTGCA GCAGAACTGC 720
 TCATGCTAGC AAGGCCACCC TTCTGACCT CCCCTCATTG TGGCCCCACA CCCAAGTCTG 780
 CTTCCTCCTG TTACACACTG TCCGCTCT

SEQ ID NO:122 PFJ2 Protein sequence:
 Protein Accession #: NP_002658.1

1 11 21 31 41 51
 | | | | |
 MASVTDGKHG VKDASDQNFQ YMFKLLIGN SSVGKTSFLL RYADDTFIPA FVSTVGIDFK 60
 VKTVYRHEKR VKLQIWDTAG QERYRTITTA YYRGAMGFIL MYDITNEESF NAVQDWATQI 120
 KTYSDNAQV ILVGNKCDME EERVVPTEKG QLLAEQLGFD FFEASAKENI SVRQAFERLV 180
 DAICDKMSDS LDTDPMSLGS SKNTRLSDTP PLLQNCSC

SEQ ID NO:123 PFJ1 DNA SEQUENCE

Nucleic Acid Accession #: NM_001844
 Coding sequence: 158-4621 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 ACGCAGAGCG CTGCTGGGCT GCCGGGTCTC CCGCTTCCTC CTCTGCTCC AAGGGCCTCC 60
 TGCAATAGGG CGCGGTAGAG ACCCGGACCC GCGCCGTGCT CTTGCCGTTT CGTGCGCTC 120
 CGCCCGGGCC CGGCTCAGCC AGGCCCCGCG GTGAGCCATG ATTGCGCTCG GGGCTCCCA 180
 GTGCGTGGT CTGCTGACGC TGCTCGTCCG CGCTGTCCTT CGGTGTCAGG GCCAGGATGT 240
 CCAGGAGGCT GGCAGCTGTG TGCAGGATGG GCAGAGGTAT AATGATAAGG ATGTGTGGAA 300
 GCCGGAGCCC TGCCGGATCT GTGTCTGTGA CACTGGGACT GTCTCTGCG ACGACATAAT 360
 CTGTGAAGAC GTGAAAGACT GCTCAGCCC TGAGATCCCC TTCGGAGAGT GCTGCCCAT 420
 CTGCCCAACT GACCTGCCCA CTGCCAGTGG GCAACAGGA CCAAAGGGAC AGAAAGGAGA 480
 ACCTGGAGAC ATCAAGGATA TTGTAGGACC CAAAGGACCT CTTGGGCCTC AGGACCTGC 540

AGGGGAACAA GGACCCAGAG GGGATCGTGG TGACAAAGGT GAAAAAGGTG CCCCTGGACC 600
 TCGTGGCAGA GATGGAGAAC CTGGGACCCC TGGAAATCCT GCGCCCTGTC GTCTCCCGG 660
 CCCCCCTGGT CCCCTGTGCT TTGGTGGAAA CTITGCTGCC CAGATGGCTG GAGGATTTGA 720
 5 TGAAAAAGCT GGTGGCCGCC AGTTGGGAGT AATGCAAGGA CCAATGGGCC CCATGGGACC 780
 TCGAGGACCT CCAGGCCCTG CAGGTGTCTC TGGGCTCAA GGATTTCAG GCAATCTCGG 840
 TGAACCTGGT GAACCTGGTG TCTCTGGTCC CATGGGTCCC CGTGGTCTC CTGGTCCCC 900
 TGGAAAGCTT GGTGATGATG GTGAAGCTGG AAAACCTGGA AAAGCTGGTG AAAGGGGTCC 960
 GCCTGGTCTT CAGGTGTCTC GTGGTTTCCC AGGAACCCCA GGCCTTCTG GTGTCAAAGG 1020
 10 TCACAGAGGT TATCCAGGCC TGGACGGTGC TAAGGGAGAG GCGGGTGCTC CTGGTGTGAA 1080
 GGGTGAGAGT GGTTCCTCCG GTGAGAACGG ATCTCCGGGC CCAATGGGTC CTCGTGGCCT 1140
 GCCTGGTGAA AGAGGACGGA CTGGCCCTGC TGGCGCTGCG GGTGCCCGAG GCAACGATGG 1200
 TCAGCCAGGC CCCGAGGTC CTCCGGGTCC TGTGGTCTT GCTGGTGGTC CTGGCTTCCC 1260
 TGGTGCTCTT GGAGCCAAGG GTGAAGCCCG CCCCACTGGT GCGCGTGGTC CTGAAGGTGC 1320
 15 TCAAGTCTCT CGCGTGAAC CTGGTACTCC TGGGTCCCCT GGGCTGCTG GTGCTCCCG 1380
 TAACCTGGA ACAGATGGAA TTCTGGAGC CAAAGGATCT GCTGGTGTCT CTGGCATTGC 1440
 TGGTGCTCTT GGTCTCCCTG GGGCACGGGG TCCTCTGGC CCTCAAGGTG CAACTGGTCC 1500
 TCTGGGCCCG AAAGGTGATG CGGGTGAACC TGGTATTGCT GGCTTCAAAG GTGAACAAGG 1560
 CCCCAGGGA GAACCTGGCC CTGCTGGCCC CCAGGGAGCC CTGGACCCG CTGGTGAAGA 1620
 AGGAAGAGA GGTGCCCTG GAGAGCCTGG TGGCGTTGGG CCCATCGGTC CCCCTGGAGA 1680
 20 AAGAGGTGCT CCCGAAACC GCGGTTTCCC AGGTCAAGAT GGTCTGGCAG GTCCCAAGGG 1740
 AGCCCTGGA GAGCGAGGGC CCAAGTGTCT TGCTGGCCCC AAGGGAGCCA ACGGTGACCC 1800
 TGGCGTCTT GGAGAACCTG GCCTTCTGAG AGCCCGGGGT CTCACTGGCC GCCCTGGTGA 1860
 TGCTGGTCTT CAAGGCAAAG TTGGCCCTTC TGGAGCCCTT GGTGAAGATG GTGCTCTG 1920
 25 ACCTCAGGT CTCAAGGGG CTGCTGGGCA GCCTGGTGT ATGGGTTTCC CTGGCCCCAA 1980
 AGGTGCCAAG GGTGAGCTG GCAAAAGCTGG TGAGAAGGGA CTGCTGGTG CTCCTGGTCT 2040
 GAGGGGTCTT CTTGGCAAAG ATGGTGAGAC AGGTGCTGCA GGACCCCTG GCCCTGCTGG 2100
 ACCTGCTCTT GAACGAGGCG AGCAGGGTGC TCCTGGGCCA TCTGGGTTCC AGGGAATTCC 2160
 TGGCCCTCTT GGTCCCCCAG GTGAAGGTGG AAAACAGGT GACCAGGGTG TTCCCGGTGA 2220
 AGCTGAGGCC CTTGGCTCG TGGGTCCCAG GGGTGAACGA GGTTCCTCAG GTGAACGTGG 2280
 30 CTCTCCCGGT GCCCAGGGCC TCCAGGGTCC CCGTGGCTC CCCGGCACTC CTGGCACTGA 2340
 TGGTCCCAA GGTGCATCTG GCCCAGCAGG CCCCTCTGGC GCACAGGGCC CTCAGGTCT 2400
 TCAGGGAATG CTTGGCAGA GGGGAGCAGC TGGTATCGT GGGCCCAAAG GCGACAGGGG 2460
 TGACGTTGGT GAGAAAGGCC CTGAGGGAGC CCCTGGAAAG GATGGTGGAG GAGGCTGAC 2520
 AGGTCCCATT GGGCCCTCTG GCCCAGCTGG TGCTAACGGC GAGAAGGGAG AAGTTGGACC 2580
 35 TCCTGGTCTT CCAGGAAGTG CTGGTCTCG TGGCGCTCCG GGTGAACGTG GAGAGACTGG 2640
 CCCCCCGGA CCAGCGGAT TTGCTGGGCC TCCTGGTCTT GATGGCCAGC CTGGGGCCAA 2700
 GGGTGAGCAA GGAGAGGCCG GCCAGAAAGG CGATGCTGGT GCGCCCTGTC CTCAGGGCCC 2760
 CTCTGGGACA CTGGGGCTC AGGGTCTTAC TGGAGTACT GGTCTTAAAG GAGCCGAGG 2820
 TGCCCAAGGC CCCCCGGGAG CCACTGGATT CCCTGGAGCT GCTGGCCCGG TTGGACCCCC 2880
 40 AGGTCCCGT GCCCAGGGCC TCCACCTGAG GACCCCTGGT TCCCTCTGGA AAGATGGTCC 2940
 CAAAGGTGCT CGAGGAGACA GCGGCCCCCC TGGCCGAGCT GGTGAACCCG GCCTCCAAGG 3000
 TCCTGTGGA CCCCCCTGGC AGAAGGGAGA GCCTGGAGAT GACGCTCCCT CTGGTGCCGA 3060
 AGGTCCACCA CTTGGCCAGG GTCTGGCTGG TCAGAGAGGC ATCGTGGGTC TGCTGGGGA 3120
 45 ACGTGGTGAG AGAGGATTCC CTGGCTTCCC TGGCCCATCG GGTGAGCCCG GCAAGCAGGG 3180
 TGCTCTGGA GCATCTGGAG ACAGAGGTCC TCCTGGCCCC GTGGGTCTC CTGGCTGAC 3240
 GGGTCTGCA GGTGAACCCG GACGAGAGGG AAGCCCCGGT GCTGATGGCC CCCTGGCAG 3300
 AGATGGCGCT GCTGGAGTCA AGGGTATCG TGGTGAAGT GGTGCTGTGG GAGCTCTGG 3360
 AGCCCTGGG CCGCTGGCT CCCCTGGGCC CGCTGGTCCA CTGGCAAGC AAGGAGACAG 3420
 50 AGGAGAAGCT GGTGCACAAG GCCCATGGG ACCCTCAGGA CCAGCTGGAG CCCGGGGAAT 3480
 CCAGGTCTCT CAAGGCCCA GAGGTGACAA AGGAGAGGCT GGAGAGCCTG GCGAGAGAGG 3540
 CCTGAAGGGA CACCGTGGCT TCACTGGTCT GCAGGGTCTG CCGGGCCCTC CTGGCTCTTC 3600
 TGGAGACCAA GGTGCTTCTG GTCTGTCTGG TCCTTCTGGC CTAAGAGGTC CTCTGGCCC 3660
 CGTGGTCCC TGTGGCAAAG ATGGTGCTAA TGAATCCCT GGCCCCATTG GGCCTCTGG 3720
 55 TCCCCGTGGA CGATCAGGCG AAACCGGTCC TGCTGGTCTT CTGGAAATC CTGGGCCCCC 3780
 TGGTCTCCA GGTCCCCCTG GCGCTGGCAT CGACATGTCC GCTTTGCTG GCTTAGGCC 3840
 GAGAGAGAAG GCGCCCGACC CCCTGCAGTA CATGCGGGCC GACCAGGAG CCGGTGGCCT 3900
 GAGACAGCAT GACGCCGAGG TGGATGCCAC ACTCAAGTCC CTCACAACC AGATTGAGAG 3960
 CATCCGAGC CCGGAGGCT CCGCAAGAA CCCTGCTGC ACCTGAGAG ACCTGAAACT 4020
 60 CTGCCACCT GAGTGAAGA GTGGAGACTA CTGGATTGAC CCAACCAAG GCTGCACCT 4080
 GGACGCCATG AAGGTTTTCT GCAACATGGA GACTGGCGAG ACTTGCTCT ACCCAATCC 4140
 AGCAAACGTT CCAAGAAGA ACTGGTGGAG CAGCAAGAGC AAGGAGAAGA AACACATCTG 4200
 GTTTGAGAA ACCATCAATG GTGGCTTCCA TTTCAGTAT GGAGATGACA ATCTGGTCTC 4260
 CAACACTGCC AACGTCCAGA TGACCTTCT ACCTGCTGC ACCTGAGAG ACCTGAAACT 4320
 65 CATCACTAC CACTGCAAGA ACAGCATTGC CTATCTGGAC GAAGCAGCTG GCAACCTCAA 4380
 GAAGGCCCTG CTCATCCAGG GCTCCAATGA CGTGAGATC CCGGCAGAGG GCAATAGCAG 4440
 GTTCACGTAC ACTGCCCTGA AGGATGGCTG CACGAAACAT ACCGTAAGT GGGGCAAGAC 4500
 TGTATCGAG TACCGTCAAC AGAAGACCTC ACCTCTCCC ATCATGACA TTGACCCAT 4560
 GGACATAGGA GGGCCCGAG AGGAATTCCG TGTGGACATA GGGCCGGTCT GCTTCTGTA 4620
 70 AAAACCTGAA CCCAGAAACA ACACAATCCG TTGCAAAACC AAAGGACCCA AGTACTTTCC 4680
 AATCTCAGTC ACTTAGGAC TCTGCACTGA ATGGCTGACC TGACCTGATG TCCATTATC 4740
 CCACCTCTC ACAGTTCGGA CTTTCTCCC CTCTTTTCT AAGAGACCTG AACTGGGCG 4800
 ACTGCAAAAT AAAATCTCGG TGTCTATT TTTTATTGTC TTCTGTAAG ACCTTCGGGT 4860
 CAAGGCAGAG GCAGGAAACT AACTGGTGTG AGTCAAATGC CCCCTGATG ACTGCCCCCA 4920
 75 GCCCAGGCCA GAAGACCTCC CTTAGGTGC CGGGCCGAGG AACTGTGTGT GTCTACACA 4980
 ATGGTGCTAT TCTGTGTCAA ACACCTCTGT ATTTTAAAA ACATCAATTG ATATTAATAA 5040
 TGAAGGATT ATTGGAAGT

SEQ ID NO:124 PFJ1Protein sequence:

Protein Accession #: NP_001835.2

1 11 21 31 41 51
 5 MIRLGAPOSLLVLLTLVAAYLRCCQGDVQEAGSCVQDQQR YNDKDVWKPEPCRICVCDTG 60
 TVLCDDICE DVKDCLSPEI PFGECCPICP TDLATASQGP GKPGQKGEPPG DIKDIVGPKG 120
 PPGPQQPAGE QGPRGDRGDK GEKGAAPGPRG RDGEPGTGN PGPPGPPGPP GPPGLGGNFA 180
 AQMAGGFDEK AGGAQLGVQM GPMGPMGPRG PPGPAGAPGP QGFQGNPGEF GEPGVSGPMG 240
 10 PRGPPGPPGK PGDDGEAGKP GKAGERGPPG PQGARGFPPT PGLPGVKGHR GYPGLDGAKEG 300
 EAGAPGVKGE SGSPGENGSP GPMGPRGLPG ERGRTGPAGA AGARGNDGQP GPAGPPGPVG 360
 PAGGPFPGA PKAGEAGPT GARGPEGAQG PRGEPGTGS PGPAGASGNP GTDGIPIGAKG 420
 SAGAPGLAGA PGFPGPRGPP GPQGATGPLG PKGQTGEPGI AGFKGEQGPKE GEPGPAGPQG 480
 APGPAGEEGK RGARGEPGGV GPIPPGERG APGNRGFPQG DGLAGPKGAP GERGPSGLAG 540
 PKGANGDPGR PGEPGLPGAR GLTGRPGDAG PQGKVGPSGA PGEDGRFPGP GPQARGGQPG 600
 15 VMGFPKPGA NGEFGKAGEK GLPGAFLRG LPGKDGETGA AGPFPAGPA GERGEQGAEP 660
 PSFGQLLPGP PGPPGEGGKP GDQGVPEAG APGLVGRPRG RGFPGERGSP GAQGLQGPGR 720
 LPGTPTDGP KGASGPAGPP GAQGPPLQG MPGERGAAGI AGPKGDRGDV GEKGPEGAPG 780
 KDGGRLTGP IGPFPAGAN GEKGEVGPFG PAGSAGARGA PGERGETGPP GPAGFAGPFG 840
 ADGQGAKEG QEAGQKQDA GAPGQGPSG APGPGPTGV TGPKGARGAQ GPPGATGFP 900
 20 AAGRVPFPGS NGNPFPFP GPSPKDGPKG ARGDSGPPGR ACEPGLQGPA GPPGEKGEFG 960
 DDGSPGAEGP PGPGLAGQR GIVGLPQRG ERGFPGLPGP SGEPGKQGP GASGDRGPPG 1020
 PVGPPLTGP AGEFPGREGSP GADGPPGRDG AAGVKGDRGE TGAVGAFGAP GPPSPGPAG 1080
 PTGKQDRGE AGAQQPMGPS GPAGARGIQG PQGPRGDKGE AGEFGERGLK GHRGFTGLQG 1140
 25 LPGPPPSGD QGASGPAGPS GPRGPPFVG PSKDGANGI PGIPPGPR GRSGETGPAG 1200
 PPGNPPGPPG PGPPGPDIM SAFAGLGPKE KGPDLQYMR ADQAAGGLRQ HDAEVDATLK 1260
 SLNNQIESR SPESGRKNPA RTCDRLKCH PEWKSQDQYWI DPNQGGCTLD MKVFCNMTG 1320
 ETCVYPPAN VPKNWVSSK SKEKKHIWFG ETINGGFHFS YGDDNLAPNT ANVQMTFLRL 1380
 30 LSTEGSQNT YHCKNSIAYL DEAGNLKKA LLIQGSNDVE IRAEGNSRFT YTALKDGCTK 1440
 HTGKWGKTVI EYRSQKTSRL PIIDAPMDI GGPEQEFQVD IGPVCF

SEQ ID NO:125 PFH9 DNA SEQUENCE

Nucleic Acid Accession #: NM_005084

Coding sequence: 162-1487 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 40 GCTGGTCCGA GGCTCCGAGT GCTGTCGGCG AGAAGCAGTC GGGTTTGGAG CGCTTGGGTC 60
 GCGTTGGTGC GCGGTGGAAAC GCGCCCAAGG ACCCCAGTTC CCGCGAGCAG CTCGCGCGCG 120
 CGCCTGAGAG ACTAAGCTGA AACTGCTGCT CAGCTCCCAA GATGGTGCCA CCCAAATTGC 180
 ATGTGCTTTT CTGCTCTGCG GGCTGCTGCG CTGTGGTTTA TCCTTTTGAAC TGGCAATACA 240
 TAAATCCTGT TGCCCATATG AAATCATCAG CATGGGTCAA CAAAATACAA GTACTGATGG 300
 45 CTGCTGCAAG CTTTGGCCAA ACTAAATCC CCGGGGAAAA TGGGCCTTAT TCCGTTGGTT 360
 GTACAGACTT AATGTTTGT CACACTAATA AGGGCACCTT CTTCGGTTTA TATTATCCAT 420
 CCCAAGATAA TGATCGCCTT GACACCCTTT GGATCCCAAA TAAAGAATAT TTTTGGGGTC 480
 TTAGCAAAAT TCTTGAACA CACTGGCTTA TGGCAACAT TTTGAGGTTA CTCTTGGTT 540
 CAATGACAACT TCTGCAAAAC TGGAAATCCC CTCTGAGGCC TGGTGAAAAA TATCCACTTG 600
 50 TTGTTTTTTC TCATGGTCTT GGGGCATTCA GGACACTTTA TTCTGCTATT GGCATTGACC 660
 TGGCATCTCA TGGGTTTATA GTTGTGCTG TAGAACACAG AGATAGATCT GCATCTGCAA 720
 CTACTATTT CAAGGACCAA TCTGCTGAG AAATAGGGGA CAAGTCTGG CTCTACCTTA 780
 GAACCTGAA ACAAGAGGAG GAGACACATA TACGAAATGA GCAGGTACGG CAAAGAGCAA 840
 AAGAATGTC CCAAGCTCTC AGTCTGATTC TTGACATTGA TCATGGAAAG CCAGTGAAAG 900
 55 ATGCATTAGA TTAAAGTTT GATATGGAAC AACTGAAGGA CTCTATTGAT AGGGAAAAAA 960
 TAGCAGTAAT TGGACATTCT TTTGGTGGAG CAACGGTTAT TCAGACTCTT AGTGAAGATC 1020
 AGAGATTGAG ATGTGGTATT GCCCTGGATG CATGGATGTT TCCACTGGGT GATGAAGTAT 1080
 ATTCCAGAA TCTCAGCCC CTCTTTTTTA TCAACTCTGA ATATTTCAA TATCCTGCTA 1140
 ATATCATAAA AATGAAAAAA TGCTACTCAC CTGATAAAGA AAGAAAGATG ATTACAATCA 1200
 60 GGGGTTCAGT CCACCAGAA TTTGCTGACT TCACCTTTGC AACTGGCAAA ATAATTGGAC 1260
 ACATGCTCAA ATTTAAAGGA GACATAGATT CAAATGTAGC TATTGATCTT AGCAACAAAG 1320
 CTTCATTAGC ATCTTACAA AAGCATTAG GACTTCATAA AGATTTGAT CAGTGCGACT 1380
 GCTTGATTGA AGGAGATGAT GAGAACTTA TTCCAGGGAC CAACATTAAC ACAACCAATC 1440
 AACACATCAT GTTACAGAAC TCTCAGGAA TAGAGAAATA CAATTAGGAT TAAATAGGT 1500
 TTTT

SEQ ID NO:126 PFH9 Protein sequence:

Protein Accession #: NP_005075.1

1 11 21 31 41 51
 70 MYPKLVHVF CLCGCLAVVY PFDWQYINPV AHMKSSAWVN KIQVLMMAAS FGQTKIPRGN 60
 GPYSVGCTDL MFDHTNKGTF LRLYPSQDN DRLDTLWIPN KEYFWGLSKF LGTHWLMGNI 120
 75 LRLLFSGMTT PANWNSPLRP GEKYPVVFS HGLGAFRTLY SAIGIDLASH GFIVAAVEHR 180
 DRASATYFF KDQSAEIGD KSWLYLRTLK QEEETHIRNE QVRQRAKECS QALSILIDID 240
 HGKPVKNALD LKFDMEQLKD SIDREKIAVI GHSFGGATVI QTLSEDQRFR CGIALDAWMF 300
 PLGDEVYSRI PQLFFINSE YFYYPANIK MKKCYSPDKE RKMITRGSV HQNFADFTFA 360
 TGIUHGMLK LKGDIDSNVA IDLSNKASLA FLQKHLGLHK DFDQWDCLIE GDDENLIPGT 420
 NINTNTQHIM LQNSSGIEKY N

SEQ ID NO:127 PFH8 DNA SEQUENCE

5 Nucleic Acid Accession #: NM_015900
Coding sequence: 32-1402 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

10 CACGAGCGGC ACGAGGATTT CCAGCTCAGC GATGCCCCCA GGTCCCTGGG AGAGCTGCTT 60
CTGGGTGGGG GGCCTCATTT TGTGGCTCAG CGTTGGAAGT TCAGGGGATG CACCTCCTAC 120
CCCACAGCCA AAGTGGCTG ACTTCCAGAG CGCCAACCTT TTTGAAGGCA CCGATCTCAA 180
AGTCCAGTTT TCCTCTTTG TCCTTCGAA TCCTAGCTGT GGCACGCTAG TAGAAGGAAAG 240
CAGTGACCTC CAAAACTCTG GGTTCATG CACTCTGGGA ACCAAACTAA TTATCCATGG 300
15 ATTCAGGGTT TTAGGAACAA AGCCTTCTG GATTGACACA TTTATTAGAA CCCTTCTGCG 360
TGCAACGAAT GCTAATGTGA TTGCCGTGGA CTGATTAT GGGTCTACAG GAGTCTACTT 420
CTCAGCTGTG AAAAATGTGA TTAAGTTGAG CCTCGAGATC TCCCTTTTCC TCAATAAACT 480
CCTGGTGTCT GGTGTGTCGG AATCCTCAAT CCACATCATT GGTGTTAGCC TGGGGGCCCA 540
CGTTGGGGGC ATGTGGGGAC AGCTTTCGG AGGCCAGCTG GGACAGATCA CAGGCCTGGA 600
20 CCCCCTGGA CTGAGTACA CCAGGGCCAG TGTGGAAGAG CGTTGGATG CTGAGATGC 660
CCTCTTCGTG GAAGCCATCC ACACAGACAC CGACAATTG GGTATTCGGA TTCCCGTTGG 720
ACATGTGGAC TACTTCGTCA ACGGAGGCCA AGACCAACCT GGTGCCCCA CCTTCTTTA 780
CGCAGGTTAT AGTTATCTGA TCTGTGATCA CATGAGGGCT GTGCACCTCT ACATCAGCGC 840
CCTGGAGAAT TCCTGTCCAC TGATGGCCTT TCCTGTGCC AGCTACAAGG CCTTCTCTGC 900
25 TGGACGCTGT CTGGATTGCT TTAACCTTT TCTGCTTTC TGCCCAAGGA TAGGACTGGT 960
GGAACAAGGT GGTGTCAAGA TAGAGCCGCT CCCCAGGAA GTGAAAGTCT ACCTCCTGAC 1020
TACTTCCAGT GCTCCGACT GCATGCATCA CAGCCTCGTG GAGTTTCACT TGAAGGAACT 1080
GAGAAACAAG GACACCAACA TCGAGGTAC CTTCCTTAGC AGTAACATCA CCTCTTCATC 1140
TAAGATCACC ATACCTAAGC AGCAACGCTA TGGGAAAGGA ATCATAGCCC ATGCCACCCC 1200
30 ACAATGCCAG ATAAACCAAG TGAATTCAA GTTTCAGTCT TCCAACCGAG TTTGAAAAA 1260
AGACCGGACT ACCATTATTG GGAAGTTCTG CACTGCCCTT TIGCTGTCA ATGACAGAGA 1320
AAAGATGGTC TGCTTACCTG AACCAGTGAA CTTACAAGCA AGTGTGACTG TTTCTGTGA 1380
CCTGAAGATA GCCTGTGTGT AGTTTAACT GGGCAGGACA CATCTCCCTG CATTTTITTT 1440
35 TTTTITTTTT GAGAGAGAGG TGTGATGAGG GATGTGTGTG TGCAGCTTAT TGTAGACCAT 1500
TACTACTAAG GAGAAAAAGCA AAGCTCTTTC TTATTTTCTT CATAATCAGC TACCTGGAG 1560
GGGAGGGAGA ACTCATTTTA CAGAACTTGG TTTCTTTGCG GATCTTATG TACATACCCA 1620
TTTAGCTTTT CCGATGCATA CTAACTGCA CTTCCTTTAT CTCCTTGGGC ATTCTGACTT 1680
AGGATTCAAT AGAAACATGT ACAGGGTAAA CAATTTTTTA AAAATAAAAC TTCATTGGAGT 1740
40 AAAAAAAAAA AAAAAAAAAA

SEQ ID NO:128 PFH8 Protein sequence:
Protein Accession #: NP_056984.1

45 1 11 21 31 41 51

MPPGPWESCF WVGGLLWLS VGSSGDAPPT POPKADFQS ANLFEGTDLK VQFLFVPSN 60
PSCGQLVEGS SDLQNSGFNA TLGTLIIHG FRVLGTPSW IDTFIRLLR ATNANVAVD 120
50 WYGSTGVYF SAVKNVILS LEISLFLNKL LVLGVSESSI HIIGVSLGAH VGMVMVQLFG 180
GQLGQITGLD PAGPEYTRAS VEERLDAGDA LFVEAIHDT DNLGIRIPVG HVDYFVNGGQ 240
DQPGCPITFY AGYSYLICDH MRVHLVISA LENSCLMAF PCASYKAFLA GRCLDCFNPF 300
LLSCPRIQLV EQGGVKIEPL PKEVKVYLLT TSSAPYCMH SLVEFHLKEL RNKDTNIEVT 360
FLSSNITSS KITIPKQRY GKGIHAHATP QCQINQVKF FQSSNRVWKK DRTTIIGKFC 420
55 TALLPVNDRE KMWCLPEPVN LQASVTVSCD LKIACV

SEQ ID NO:129 PFH7 DNA SEQUENCE

60 Nucleic Acid Accession #: NM_014384
Coding sequence: 89-1336 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

65 CGTTGCCGGG TCOCAGGTCC CGCCAGTGC AGCGCAACGG AGGTGGAAGG CGTTCAGACT 60
CTTAGCTGAA CGCGGAGCTG CGGCGGCTAT GCTGTGGAGC GGCTGCCGGC GTTTCGGGGC 120
GCGCTCCGC TGCTGCCCG GCGGTCTCCG GGTCTCTGTC CAGACCGGCC ACCGGAGCTT 180
GACCTCCTGC ATCGACCTTT CCATGGGACT TAATGAAGAG CAGAAAGAAT TTCAAAAAGT 240
70 GGCCTTTGAC TTGCTGCCCC GAGAGATGGC TCCTAAATATG GCAGAGTGGG ACCAGAAGGA 300
GCTGTTCCTA GTGGATGTGA TGCGGAAGGC AGCCACGCTA GGCTTCGGAG GGGTCTACAT 360
ACAAACAGAT GTGGGCGGGT CTGGGCTGTC ACCTCTTAT ACCTCTGTCA TTTTGAAGC 420
CTTGCTTACA GGCTGCACCA GCACCACAGC CTATATAAGC ATCCACAACA TGTGTGCTG 480
GATGATTGAT AGCTTCGGAA ATGAGGAACA GAGGCACAAA TTTTGCCAC CGCTCTGTAC 540
CATGGAGAAG TTGCTTCTCT ACTGCTCAC TGAACACAGG AGTGGGAGTG ATGCTGCTC 600
75 TCTTCTGACC TCCGTAAGA AACAGGGAGA TCATTACATC CTCAATGGCT CCAAGGCCTT 660
CATCATGGT GCTGTGTGAGT CAGACATCTA TGTGTCATG TGCCGAACAG GAGGACACG 720
CCCCAAGGGC ATCTCATGCA TAGTTGTGTA GAAGGGGACC CCTGGCTCA GCTTTGCCAA 780
GAAGGAGAAA AAGTGGGGT GGAACCTCCA GCAACACGGA GCTGTGATCT TCGAAGACTG 840
TGCTGTCCCT GTGGCCAACA GAATTGGGAG CGAGGGGCAG GGCTTCTCA TTGCCGTGAG 900

AGGACTGAAC GGAGGGAGGA TCAATATTGC TTCCTGCTCC CTGGGGGCTG CCCACGCCTC 960
 TGTCATCCTC ACCCGAGACC ACCTCAATGT CCGGAAGCAG TTTGGAGAGC CTCTGGCCAG 1020
 TAACCAGTAC TTGCAATTC CACTGGCTGA TATGGCAACA AGGCTGGTGG CCGCGCGGCT 1080
 GATGGTCCG AATGCAGCAG TGGCTCTGCA GGAGGAGAGG AAGGATGCAG TGGCCTTGTTG 1140
 CTCCATGGCC AAGCTCTTTG CTACAGATGA ATGCTTTGCC ATCTGCAACC AGGCCTTGCA 1200
 GATGCACGGG GGCTACGGCT ACCTGAAGGA TTACGCTGTT CAGCAGTACG TGCGGGGACTC 1260
 CAGGGTCCAC CAGATTCTAG AAGGTAGCAA TGAAGTGATG AGGATACTGA TCTCTAGAAG 1320
 CCTGCTTCAG GAGTAGAACC CACACTTGTT CTGGCCTGGT GTTCAGTGCG ACTGCAGTCA 1380
 GTGTTGAGTG GTGCCATGTG GGCCGCTCTA TTCAAAGGA ATCATGGATT AGACCCAAGG 1440
 GCTGAGCTCC TCTAGGGCAG GACCTGCACC CTGTGTGTTG GCACCAGCAT CGGGTCTTGG 1500
 ACTGGGGCAG AATCCCCAGT GGAACCGGAA GAGCTGGACT GATGAGAAAC ATCAGAAGAA 1560
 CACATACTAC CTGTGTTTCC TAATGCCAGA AGGGTGACCA GTGAAGATTG ACCGTCAAAC 1620
 CATGAAAGTC CTTTCTTGGA TCCACTTTAT CTTGATTAGT CTGCATTTTA CTAGTTCAC 1680
 GGATCCCTCC TCTAGGGGCC TGGGGACTTT CACTGATGCT CTCCTGATT CTAGAGCAAA 1740
 GGTGTGGGAA GGGGAAATGG AGGAATGCC TCCTGTCTGT GTCGTTCTCT GTGCCACAGC 1800
 TACAGTGCA GAAGGTTTCT CTGATAGCA CACCTCTGAA TGTAATCAT GATAAAATGG 1860
 ATATTGGAA ACTTACTCCT AAGCTGTGAT GTAGGGTGT TTTCTACTTC TGGACTGCCT 1920
 CAATATCAAG GGCTGAGACT TTTGAATGTT GAATATTCGT TGGGTTTCAT GTTAAGACGC 1980
 CTGTGGTCCA GGAGTGCTAT TCAGTGTTTC TGTCTCTGAT AAACACTTTG AATATTTTTT 2040
 TGTGTTTTTG TTTCCTTTT TGAAGCTGTT CCTCCTTTTA AATATTTTTA ATCAGATTGA 2100
 TAAATCTAT CCTCATCCA CCTCTGGTTC TACTATAGTT GATTTTTATT TTAATGTTT 2160
 AATTGATTT GATTAAACAC TTAAGTGAT TTTGAATAA TAAACTCTC GTCCAATTG 2220
 GCTTTTAAAA AAAAAAAA

SEQ ID NO:130 PFH7 Protein sequence:
 Protein Accession #: NP_055199.1

1 11 21 31 41 51
 | | | | |
 MLWSGCRRFG ARLGCLPGGL RVLVQTGHRSLTSCIDPSMG LNEEQKEFQK VAFDFAAREM 60
 APNMAEWDQK ELFPVDVMRK AAQLGFGVY IQTDVGGSGSL SRLDTSVIFE ALATGCTSTT 120
 AYISIHNMCA WMDSFGNEE QRHKFCPLC TMEKFASYCL TEPGSGSDAA SLLTSKQKQ 180
 DHYILNKSKA FISGAGESDI YVVMCRGTGP GPKGISCIVV EKGTPGLSFG KKEKKVGNWS 240
 QPTRAVIFED CAVPVANRIG SEQQGLIAV RGLNGGRINI ASCSLGAHA SVILTRDHLN 300
 VRKQFGEPLA SNQYLQFLA DMATRLVAAR LMVRNAAVAL QEERKDAVAL CSMAKLFATD 360
 ECFALCNQAL QMHGGYGLK DYAVQYVVRD SRVHQILEGS NEVMRILISR SLLQE

SEQ ID NO:131 PFH6 DNA SEQUENCE

Nucleic Acid Accession #: NM_013989
 Coding sequence: 707-1105 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 GCCTGCAGAG AGAGGCACTT TGCAACCACAG ACAGATAGCA AGAAGGGAAA GACAGAGAGT 60
 GAGAAAAAAG AGGAGTCACT CGCTCCTGGG GAAGGGAGAG AGTGAGACTG GGAGAAAGAG 120
 AAGCACAGAA AGTGTGTGTA AAACGGAGTA AAGAAAGAAA AAAAAAAAC TACCCTTAAA 180
 GCACATTAAA AAAAAAAGAA CTCTGGCAAT TCAAGAAAGA AACAGGCTAC GTTTAAAGAG 240
 CATAGAGACA ATGAAAGGCT AAAGAAAATT TAAAAATCTC TGCCACAGTC TCATAGGTGC 300
 TTGGAATGA AAGTAGAAT GCCTGTCTTT AACGGACTCT GACAGAGGTA ACTGGATTAG 360
 GGACGAGTAC GCCAGCTTTT TTTTITTTTT TTTTITTTTT TTTAACATCT TAAATCCTGA 420
 AAAAAAAGAA AAAAAAAGAA AAAAGGCAGC AGCTCCGAAT TGAATGAATT GATGGGCACA 480
 CTCAACTGC TGGGCTGGAG AGACTGGACT TAGTCTTGCC ATTTCTGCTT CTTTGAAAGA 540
 GGAGACAACCT TGGGCTTCCT TTTAATTAG TTTTITTTCC CCTTCTCCCC CAACCCCAA 600
 CCTTCCCCT TACCTCCCC ACCCCCTTTA TCACCACCCC CCTTTTAAAT AAGAGGGTGA 660
 AGGGGAACCA GAGCGCACAA GGGAACTGAC TCAGGAGGCA GAGAAGATGG GCATCCTCAG 720
 CGTAGACTTG CTGATCACAC TGCAAAATCT GCCAGTITTT TTCTCCAACCT GCCTCTTCCT 780
 GGCTCTCTAT GACTCGGTCA TTCTGCTCAA GCACGTGGTG CTGCTGTTGA GCCGCTCCAA 840
 GTCCACTCGC GGAGAGTGGC GGGCGATGCT GACCTCAGAG GGAAGTGGCT CGCTCTGGAA 900
 GAGCTTCTCT CTCGATGCTT ACAAACAGGT GAAATTGGGT GAGGATGCC CCAATTCAG 960
 TGTGGTGATG GTCTCAGTA CAGAAGGAGG TGACAACAGT GGCAATGGTA CCCAGGAGAA 1020
 GATAGCTGAG GGAGCCACAT GCCACCTTCT TGACTTTGCC AGCCTGAGC GCCCACTAGT 1080
 GGTCAACTTT TGCTCAGCCA CTGACCTCC TTTCACGAGC CAGCTGCCAG CCTTCCGCAA 1140
 ACTGGTGAAA GAGTTCTCT CAGTGGCTGA CTCTCTGCTG GTCTACATTG ATGAGGCTCA 1200
 TCCATCAGAT GGCTGGGCGA TACCGGGGGA CTCCTCTTTG TCTTTGAGG TGAAGAAGCA 1260
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 AGCCTTTGCA CTGTGTGTGA TTGTGCAGAG ACAGAAAATT GCTTATCTGG GAGGAAAGGG 1440
 CCCCTTCTCC TACAACCTTC AAGAAGTCCG GCATTGGCTG GAGAAGAATT TCAGCAAGAG 1500
 ATGAAAGAAA ACTAGATTAG CTGGTTAAAG GTATGATTAT AAGAGAGCTT ATTTGTTTAA 1560
 AAGTTTATAT AAAGGCAAGG AAATTAAGAA CTGAATCCAT ATTTCAACAG AGCCCTATTG 1620
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 TCTTTTCACT ACTCAATGGT CATTGGGCTG AGTAAGTAAC CATATCACTT CTCTTCTTAG 1740
 TAAAAAGCCC TATGTGAAAA GATCCCAAGA TGGAGAGGAA GAAACGCTAA TTCAGCATGT 1800
 GTTCATTCTG CATTGAGAAAG GAAGTGATAC ATCTGATGCA TGCTTTGAGA CCAGAAGAAA 1860
 AGACTTACCT GAATAATTAC TACATTAGGG AAGCTACTGT CTACGTTAAG ATAAAGGGTA 1920

TTGCCTTGGC TCTATTGGC ATGGATGGAG CCCAGTTGGA AAATTCCTAA ATATTACAAC 1980
 AAGTCCTTGA ACCCAGGCCA TGTGGTTAGA CGTTGGTGT AAGGTTAGAC CTTATGTTAG 2040
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 5 ATTATTGGTA TATTGTAGA TACCGAGAAT GATCCCTCAG TCTGAGAGGT TAGAATGATC 2160
 ATCTGTAATC TGAGGGTTAA TTTCTAGGCA GGTGGAGAGA GTGGTAAAAA AGAAATGAAA 2220
 TTGACAAGCT AGGAAAGAGG AGGCAGAAAG ATTTGGAAAA TTCACAGAGT TTCACCTTA 2280
 AGCTGTAGAG AGTGGGTGAC ATTGTGTAGC CACGGAAACA TAGAAACATA CACAAGGCCA 2340
 GAAAAAGAAG AAGGAGCTCA ACTAAAGTG GCATAGAGAA TACACATATA AAAACAATAT 2400
 10 ATTTGTCATA TGCTCCTAGA GAGGAGAAAG GGGTGATTGA AAGAAAAAAA AATACTTAAA 2460
 TATTGTAAAT TGTGAGGGGT TCTTTTGGGA AATAATTACT TTTGAACCAT GTATGTGGTA 2520
 TGTATATTTT CAGTGGGTTA ATTATACCCC ATGATACCTA TTAAGGAAA ACCAGTGGGT 2580
 CTGGTGGTG TGTCTTTT CTCCCATTC CTACAATTTC TATGTGGCC AAGTCATTCC 2640
 TAATCTGGT CTCTATAGCA GTGTCTCTC TGAATGCTGA GCTGAAGAAA TTATACGTAC 2700
 15 ATACACACAT ACATACATAC ATACAAATAT ATGTATATAT ATCTCAGCT GCTGCGGGAG 2760
 GTAGGTACCA TGGGCATTCA GCACAGCCTT GATTTCCTCC CAAAGTAGGT GAGCTATAGT 2820
 GAAGAATAGG TGCAACAAAA CAAGCTTACT TCCATTGCAA AATAGAAGAA GAGGAAGTTA 2880
 GAGATAATTG TGATCAATCA TTTGGAGGC TTTGTTATA GGCAACCCCG GTATATCAT 2940
 GGAATTCCA TTGACATTG AATTGGACT TGGATCTCC CTGGTCCCA TTAGCTGAGG 3000
 20 TTTAGTAATC TAAAGTCCCT ATAGTATATG ATTATAATGC TATTTAAAAA AATATATATA 3060
 TAAAAATATT TTTCTTTT AAAATAGACA CTATAGTTT ACCCATAAGT AATATTTAAA 3120
 GATTATAGCT CCCAAAAAGAA TGGACCAACC ACTTTCGTAT CATAATTCT TTTTGGTAAA 3180
 TATGAGACTA TTATGAAATC ATAGTATATG ATTGTATTTA AAGGTACAAT CAAAGGATCT 3240
 TTTGTCCATT CCATTAATAA CTGAATAAAA AATAAATAAA ATGGATAGAA AAAAATAAAA 3300
 25 GTTGAATAAT CATCTTAAA CTAGTTGCT GAAATGAGAA AAGAGTGAGA ACTAGGTGTG 3360
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 CAGCTGGTAT ATTTGTGAAA TATTAAGCT CCATTGGGAC TGATTTTCA TGGCAACATC 3480
 AGCTTTCTAA TGTCTAAAT TCTATAAAAA CCACCCACAA AGAAACAAAG CAAATTTTCA 3540
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 30 AACTTCTACA TTCAAGGGCT TATCTGTC CCATTGATT TTTAACCTCA AAATGGGTGTG 3660
 AGATTACTG TGGAAACCTA AAGCAGTAAA ATAAAAAACC TGGTTGCAGC ACATTCACAC 3720
 TGTGTCTCT AAAATTCCTC TTTTCTCT ATGTACGATA AAGTAACAGT ATGTCAGATA 3780
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 35 AATTCTCCCT GAGGTAGCC CAATGGAGAA ATGAAGCAGA GGAAGGAAAC ATAGAAAGAC 3960
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 GTGGAAGGGC CAATGGAGAA AATGAATGGA CAAAGCTCAG GAATCCCTAC GCTATGTAGA 4080
 ATGTTCTGG TGTATCAGG GTTAAGCCCT GTAATTATGT AACCTATTTA TCGCAACATG 4140
 AATTTTATG TGTCTGTG ATGTATCTT TTATGAAATT AACAAGAACT CATTATTTTG 4200
 40 AGGTAGAGGA AAATCAATGC TTTATCTGAT ATGCTGAGAA ATTATTAGAT TGCCAATACT 4260
 CATGTGCGT TCGAATGTT TATAAGGTT GTTCTTTGA AGAATTGTAG TTCTTAGTCC 4320
 CACAGGAAAA TGTGTATCTA TTTATATATC ATAGTATAAA TCTATGATAT ATTTATATCA 4380
 TATATAAAG ATCTGATTTT CTCTTAGT CCCTAATCAT GTTCTCCCA TAGGCTGTGT 4440
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 45 TTCCAAGAA ATTTAGATA TTATCATAAC ATCTGGGTCT ACTCAAAAC TATTGTTTG 4560
 AAAGACTAT GCTTGGACC TATCAAAAA TGACTTTAT TATGCTTAG TGAATAACT 4620
 AGTGGGATCA ACTGATATT TCTGAATGG GCATGAATGG AGATGCCCGC ACAGTAATGT 4680
 AGAAATGTT CATACAGCTA TTAATATGTA ACTGACCTCC TTAGAGGCG AGTAGTAACT 4740
 GTTCTACTT TGTATAGCTA AGTGACAGTC ACTTAACCTA CATGACTTC TTTTTCACA 4800
 50 TTGGGTCTCT GGTCTGTGT CTTCACCTCA TTTATAGCAC GTCTCTTGA TTTTGGTAG 4860
 TATCAACTTC CCAGTGATCT GTTCAGTTAA GTTCTCTCC CGTTAACCAAG GAAGTGCTTA 4920
 TTCTCATC ACAGTGGGAA GAATAGCCTA TTGTCTTTCA TTTGCTTGA GTGTATTTA 4980
 CTATTGGGC TCTGAAATAA AAATTATGAA ATATGGTGAG GTCACATGT GGTGCTGCT 5040
 TGTGCTAAG AATTCTAGGA GGGCAGGTTA GGAGACAGTT ATGTATGGCC TTTCGGGAAA 5100
 55 ATTCAAGGG TGGGATTACA AGGTGTTC TCAGGCATGC CCCTATGGGC CCTATGTGA 5160
 AGCAAGAAGA ATTGACTGAT TTACAGGACT TCTCTTATG TCAATCTTAA GAGGATGGAT 5220
 GAATCTGGAC ATTTGTTCCA CCCGACCTCT GACTGATGGT TTGGAATAA ACTTTAATTA 5280
 GGATCATATG ACCATTGAAA AAGGAAAAAT GTAGACTCTG ACTTCCGTCC CACTGAAGGA 5340
 TTAATGAAAA CCTTACTAG CATTAGAGC TTTTCAGAAC ATCCCACTG TCATGTGCT 5400
 60 CAGCAGTGA GACTGCAAGT AAGGCTTTA ATTTAGGAG GTTTTTTTT TTTTTTTT 5460
 TTCCCTAAA TGGTATGGCC AAAAGTCAGA GTTAAAAAT ATATAGTTAG ATTCEAACT 5520
 CCTCCTCAC TCTAAAAATA GAATCCAAAC CCACTCTCA TATATGCTTC CAGAATGGGG 5580
 CTTAAGTACC AATCTCTGCT TTGCAATGGG CACAATCTTG GTCATGCTCT GAGGCTCTCT 5640
 AAGAAAAAG AGGATCTAGG ATGGGAGAGC TAGAAAGTTG CTAAGTGGGA AGAACAAGGC 5700
 65 CCTGAGGGGT TGGTCTACCA ATCTGGGAAG ATTTGAAAAA AAACCTCTCG CAAGTGAAGG 5760
 AAGGCTGAAG GCTGCTGCAA GTCAATGAGT GACTTTAGGA TGAGCAAAAC ATTGGGCCAC 5820
 TTCTAATGC CCTATGTGTA TAGTACCAGA AGCAAGGTCT CAGACTTAAC AGACCCAGCT 5880
 CTGTTCAGG GTGAGTCTGA ACCAATAGAA AGCAACATG TGCAGATATC CAAACAAGAC 5940
 TGCTCATGA AGTCGGGCT GGTACCCGT CTTAGGCAGC AACAGCAGAG CTCACGGGAG 6000
 70 CTTATTCAT ATTACTGAG ACTTGAAGA CCCAGCAGAT GTTAAATGAA GTCACATTT 6060
 TGGCTCAAC CCTCCACTC TCCCTCTCC CTCAAAAAAGC CAACAGGTAA ACACATAAAT 6120
 GAAAGAAACC CACAGAAGG GATGGAAAT AAAGAAAAAT CTCTCAAGAC TTCTCCAGGC 6180
 CCATGTCACT GGTCAAGGT GTTTTATGT GTATTAGGAT TGGGGATGT GAAGAAATAA 6240
 GTATCCAGTA CTTTATAACC AAAGCAATTA AATGATATTG GGGTAGGAA TGTGGCCAG 6300
 75 TTTTGTAGT TTTTGGCAT ACATTGTAC CCAGACCTCA CTAAGCCCA AGTAATCGG 6360
 CGCCCGAAG AGGGAGACAG AGATGTGCA GAGTTGACCC AGTGTGCGGA TGATAACTAC 6420
 TGACGAAAGA GTGATGACC TCAGTTAGT GTTGGATGA GTCACATTAG TTTGCTCTC 6480
 CCCATCTTG TCTCCTGGC AAGGAGAATA TGCGGACAT GATGCTAAG GCGCTGGTA 6540
 AATGTGGTA GAATGCACGC GTGCATATG TACACATATG TGCTTCTAG TTGCAGAAAA 6600
 TGAAGTCTT TGGGAGATA TCAAGTAAAA GAGTGTTATC ATATTGGTG TGAAGTCTAT 6660

GTGTGCTTAT ACAATTGTTT CTTGTATTTT AATAAACTTT GAATAAAAGA ATAAAAAAAA 6720
AAAAAAAAAAAA AAAAA

5 SEQ ID NO:132 PFH6 Protein sequence;
Protein Accession #: NP_054844.1

1 11 21 31 41 51
| | | | |
10 MGILSVDLLI TLQILPVFFS NCLFLALYDS VILLKHVVLL LSRKSKSTRGE WRRMLTSEGL 60
RCVWKSFLLD AYKQVKLGED APNSSVVHVS STEGGDNNGN GTQEKIAEGA TCHLLDFASP 120
ERPLVNVFSG ATXPPFISQL PAFRKLVEEF SSVADFLVY IDEAHPSDGW AIPGDSLSLF 180
EVKKHQNQED RCAAQQLLE RFLPPQCRV VADRMNNAN IAYGVAERFV CIVQRQKIAY 240
15 LGGKGPFSYN LQEVHRHWLEK NFSKRXXKTR LAG

20 Nucleic Acid Accession #: NM_001141
Coding sequence: 72-2102 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | |
25 CAGGCGTGTG CCAGGGGGAG CCCCCTCTG CAGCCCTGTG CGCCGTAGAG AGCTGGACTT 60
AGGCTGGCAG CATGGCCGAG TTCAGGGTCA GGGTGTCCAC CGGAGAAGCC TTCGGGGCTG 120
GCACATGGGA CAAAGTGTCT GTCAGCATCG TGGGGAACCG GGGAGAGAGC CCCCCTCTG 180
CCCTGGACAA TCTCGGCAAG GAGTTCACCTG CGGGCGCTGA GGAGGACTTC CAGGTGACGC 240
TCCCGGAGGA CGTAGGCCGA GTGCTGCTGC TGGCGGTGCA CAAGGGCGCC CAGTGTGTC 300
30 CCTGCTGGG GCCCTGGCC CCGGATGCCT GGTCTGCCC CTGGTTCCAG CTGACACCGC 360
CGCGGGGGGG CCACCTCTCT TTCCTCTGCT ACCAGTGGCT GGAGGGGGCG GGGACCTGG 420
TGCTGCAGGA GGGTACAGCC AAGGTGTCTT GGGCAGACCA CCACCTGTG CTCCAGCAAC 480
AGCGCCAGGA GGAGCTTCAG GCCCGGCAGG AGATGTACCA GTGGAAGGCT TACAACCCAG 540
GTGGCTCTCA CTGCTGGAT GAAAAGACAG TGGGAAGACTT GGAGTCAAT ATCAAACTACT 600
35 CCACAGCCAA GAATGCCAAC TTTTATCTAC AAGCTGGCTC TGCTTTGCA GAGATGAAAA 660
TCAAGGGGTT GCTGGACCCG AAGGGGCTCT GGAGGAGTCT GAATGAGATG AAAAGGATCT 720
TCAACTCCG GAGGACCCCA GCAGCTGAGC ACGCATTGA GCACTGGCAG GAGGATGCCT 780
TCTTCGCTC CAGTTCCTG AATGGTCTCA ACCCTGTCT GATCCGCCGC TGCTACTACC 840
TCCCAAAGAA CTTCCTCTG ACTGATGCCA TGGTGGCTC ATTTGTTGGT CCTGGGACCA 900
40 GCTTGACAGC TGAGCTAGAG AAGGGCTCCC TGTTCTGGT GGATCACGGC ATCTCTCTG 960
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CCGCCCCAAA CAGCCCCAT TCCTGCCCCA CTGATGACAA GTGGGACTGG TTGCTGGCCA 1140
AGACCTGGT GCGCAATGCC GAGTTCCTCT TCCATGAGGC CCTCACGCAC CTGCTGCACT 1200
45 CACATCTGCT CCGTGAGTTC TACCCCTGG CTACCTGCG TCAGCTGCC CACTGCCACC 1260
CTCTCTCAA GCTGCTGATC CCGCACACCC GATACACCT GCACATCAAC ACACTCGCCC 1320
GGGAGCTGCT TATCGTGCCA GGGCAGGTGG TGGACAGGTC CACAGGCATC GGCATTGAAG 1380
GCTTCTCTGA GTGATACAG AGGAACATGA AGCAGCTGAA CTATTCTCT CTGTGTCTGC 1440
CTGAGGATAT CCGGACCCGA GGAGTTGAAG ACATCCCAGG CTACTACTAC CGTGATGATG 1500
50 GGATGCAAG GTGGGTGCA GTGGAACGCT TTGTCTCTGA AATCATCGGT ATCTACTACC 1560
CAAGTGATGA GTCTGTCAA GATGACAGAG AGTCCAGGC CTGGGTGAGA GAGATCTCT 1620
CCAAGGGCTT CCTAAACAG GAGAGCTCAG GTATCCCTTC CTACTGGAG ACCCGGGAAG 1680
CCTGGTGGA GTATGTACAC ATGGTGATAT TCACCTGCTC AGCCAAGCAT GCGGCTGTCA 1740
GTGCAGGCA GTTTGACTCC TGTGCTTGA TGCCCAACCT GCCACCCAGC ATGCAGCTGC 1800
55 CACCAACCC CACCAAGGC CTGGCAACAT GCGAGGGCTT CATAGCCACC CTCCACCTG 1860
TCAATGCCAC ATGTGATGTC ATCCTTGCTC TCTGTTGCT GAGCAAGGAG CCTGGAGACC 1920
AAAGGCCCTT GGGCACCCT CCGGATGAGC ACTTACAGA GGAGGGCCCT CGGCGGAGCA 1980
TCGCCACCTT CCAGAGCCGC CTGGCCCAAG TCTCGAGGG CATCCAGGAG CGGAACCGGG 2040
60 GCCTGGTGT GGCCTACACC TACCTAGACC CTCCCCTCAT CGAGAACAGC GTCTCCATCT 2100
AATCCCAAG GGAACACAGG CCCAGATGAC ATCCCTTTGA CCACATCGCT CTAGGATAAC 2160
TGGCACCCAG AGAAAAGGAC TCCTCAGAAA AAACAGGCC CCATGTGCTT CTCTGGGAC 2220
AACCAGACTT TGTAACCTAC CCCCACCAAC ATACACACAC ACAAACACAG AAACAAAATC 2280
AAAACAGAGA AAGCAGAAAA TCTACCAAGA ACAGAGTCTC AGGACAGAAC CACTGATCT 2340
65 TTGGAGGCT CCAAGCCTCA AAGTGCCCGC AGAGCCCACT TTGAGGGTTT TGCTAGTTGG 2400
TTTGTGTTT CGTTTACAGC CGTGGGGGA AGCACAATA CCCGCCAG GGCCCACTAG 2460
CATCCACTGA TTGGACCTTA TGGTACCCA ACTCAAGGAC AGCCACCAAG AAGTGGCTGC 2520
CAAAGAGACT GGGCGCAGTG GCTCATGCC ATAATCCAG CACTTTGGGA GATGGAGGCG 2580
70 GGAATAATCA TTGAGGTCAG AAGTTCAAGG CCAGCCTGGA CGACATAGCG AGACTCCACC 2640
TCTACCAAAA AATAAAATT AAAAAACAAA AAAAAAAAAA AAAAA

75 SEQ ID NO:134 PFH5 Protein sequence;
Protein Accession #: NP_001132.1

1 11 21 31 41 51
| | | | |
MAEFRVRVST GEAFGAGTWD KVSIVGTR GESPLPLDN LGKEFTAGAE EDFQVTLPED 60
VGRVILLRVH KAPPVPLLLG PLAPDAWFCR WFQLTTPRGG HLLFPYQWL EGAGTLVLQE 120
GTAKVSWADH HPVLQQQRQE ELQARQEMYQ WKAYNPGWPH CLDEKTVEDL ELNRYSTAK 180

NANFYLAQGS AFAEMKIKGL LDRKGLWRS L NEMKRIFNFR RTPAAEHAF E HWQEDAFFAS 240
 QFLNGLNPVL IRCHYLKPN FVPTDAMVAS LLGPGTSLQA ELEKGSFLV DHGLSGIQT 300
 NVINGKPKQS AAPMTLLYQS PGCGPLLPLA IQLSQTGPN SPIFLPTDDK WDWLLAKTWV 360
 RNAEFSFHEA LTHLLHSHLL PEVFTLATLR QLPCHPLFK LLIPHTRYTL HINTLARELL 420
 IVPGQVVDRS TGIGIEGFE LIQRNMKQLN YSLLCLPEDI RTRGVEDIPG YYYRDDGMQI 480
 WGAVERFVSE IIGIYPSDE SVQDDRELQA WVREIFSKGF LNQESSGIPS SLETREALVQ 540
 YVTMVIPTCS AKHAAVSAGQ FDSCAWMPNL PPSMQLPPT SKGLATCEGF IATLPPVNAT 600
 CDVILALWLL SKEPGDQRL GTYPDEHFE EAPRRSIATF QSRLAQISRG IQERNRGLVL 660
 PPTYLDPLI ENSVSI

SEQ ID NO:135 PFH4 DNA SEQUENCE

Nucleic Acid Accession #: NM_002742

Coding sequence: 236-2974 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GAATTCCTTC TCTCTCTC CTGCGCCTTC TCTCGCCCTC CTCTCTCTC CTCGCCCTCC 60
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 TTTTCCTGCT GGGCTCTCGG AGAAAGAAGC TCTGGCTCA GCGGCTGCAA AACTTTCTTG 180
 CTGCGCGGCC GCCAGCCCC GCCCTCCGCT GCCCGGCCCT GCGCCCCGCC GAGCGATGAG 240
 CGCCCTCCCG GTCTGCGGCC CGCCAGTCC GCTGCTGCC GTGGCGCGCG CAGCTGCCGC 300
 AGCGCGCGCC GCACTCGTCC CAGGGTCCGG GCCCGGCCCG GCGCGTCTT TGGTCTCTGT 360
 CGCGGCCCGG GTCGGGGGCA TCTGTTCCA TCTGCAGATC GGCCTGAGCC GTGAGCCGGT 420
 GCTGCTGCTG CAGGACTCGT CCGGGGACTA CAGCCTGGCG CAGCTCCGCG AGATGGCTTG 480
 CTCCATTGTC GACCAAGATG TCCCTGAATG TGGTTTCTAC GGAATGTATG ATAAGATCCT 540
 GCTTTTTCGC CATGACCCTA CCTCTGAAAA CATCTTCAG CTGGTGAAAG CGGCCAGTGA 600
 TATCCAGGAA GGCATCTTA TTGAAGTGGT CTTGTACAGT TCCGCCACCT TTGAAGACTT 660
 TCAGATTGCT CCCACGCTC TCTTTGTICA TTCATACAGA GCTCCAGCTT TCTGTGATCA 720
 CTGTGGAGAA ATGCTGTGGG GGCTGGTACG TCAAGGTCTT AAATGTGAAG GGTGTGGTCT 780
 GAATTACCAT AAGAGATGTG CATTTAAAT ACCCAACAAT TGCAGCGGTG TGAGGCGGAG 840
 AAGGCTCTCA AAGCTTTCCT TCACTGGGGT CAGCACCATC CGCAGATCAT CTGCTGAAC 900
 CTCTACAAGT GCCCTGATG AGCCCTTCT GCAAAAAATCA CCATCAGAGT CGTTTATTGG 960
 TCGAGAGAAG AGGTCAAAT CTCAATCATA CATTGGACGA CCAATTCACC TTGACAAGAT 1020
 TTTGATGCTT AAAGTAAAG TGCCGCACAC ATTTGTATC CACTCTACA CCCGCGCCAC 1080
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 AGATTGCAGA TTCAACTGCC ATAAACGTTG TGCACCGAAA GTACCAACA ACTGCTTGG 1200
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 TGGCGTTGGT GCAGATGTGG CCAGGATGTG GGAGATAGCC ATCCAGCATG CCCTTATGCC 1860
 CGTCATTCCC AAGGGCTCCT CCGTGGGTAC AGGAACCAAC TTGCACAGAG ATATCTCTGT 1920
 GAGTATTCCA GTATCAAAAT GCCAGATTCA AGAAAATGTG GACATCAGCA CAGTATATCA 1980
 GATTTTCTCT GATGAAGTAC TGGGTCTGG ACAGTTTGGG ATTGTTTATG GAGGAAAAA 2040
 TCGTAAAAAC GGAAGAAGATG TAGCTATTAA AATCATTGAC AAATTACGAT TTCCAACAAA 2100
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 CCATGGAGAC ATGCTGGAAA TGATCTGTG AAGTGAAAAG GGCAGTTGC CAGAGCATAT 2280
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 AGTGTGGGT ACCCCGCTT ACCTGGCTCC TGAGGTCTTA AGGAACAAGG GCTAATATCG 2520
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 CACTGTGGAA CTAATAAATA CATACGGTCA GGTTAACAT TTGCTTGA GAAGTCCAT 3060
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 TAAGAGACAG AATGTATCTG TGAAGTAGTT CTGTTTGGTG TGTCCCATG GTGTTGTCAT 3360
 TGTAACAAAA CTCTGAAGA GTCGATTATT TCCAGTGTTC TATGAACAAC TCCAAAACCC 3420
 ATGTGGGAAA AAAATGAATG AGGAGGGTAG GGAATAAAAT CCTAAGACAC AAATGCATGA 3480
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 ACTCAAGACA ATGCACCTAG CTGTGCAAGA CTAAGTGTCT TTAAGCCTAA ATGCCTTAGA 3600
 AATGTAACCT GCCATATATA ACAGATACAT TTCCCTCTTT CTTATAATAC TCTGTTGATC 3660

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 ATTCTTGTC AAAAAAAAAA AA

5 SEQ ID NO:136 PFH4 Protein sequence:
 Protein Accession #: NP_002733.1

10 1 11 21 31 41 51
 MSAPPVLRPF SPILLVAAAA AAAAAALVPG SGPGAPFLA PVAAPVGGIS FHLQIGLSRE 60
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 SDIQEGDLIE VVLSRSATFE DFQIRPHALF VIHSYRAPAFD DHCGEMLWGL VRQGLKCEGC 180
 GLNYHKRCFA KIPNNCSGVR RRRLSNVSLT GVSIRTSSA ELSTAPDEP LLQKSPSESF 240
 15 IGRKRSNSQ SYIGRPIHLD KILMSKVVP HTFVHSYTR PTVQCYCKKL LKGLFRQGLQ 300
 CKDCRFNCHK RCAPKVPNNC LGEVTINGDL LSPGAESDVV MEEGSDDDNS ERNSGLMDDM 360
 EAMVQDAEM AMAECQNSG EMQDPDPDE DANRTISPST SNNPLMRVV QSVKHTKRKS 420
 STVMKEGWMV HYTSKDTLRK RHYWRDLSKC ITLFQNDTGS RYYKEIPSE ILSLEPVKTS 480
 ALIPNGANPH CFETITANVV YYVGENVVNP SSPSPNNVL TSGVGADVAR MWEIAIQHAL 540
 20 MPVKGSSV GTGTNLHRDI SVSISVSNQC IQENVDISTV YQIFDEVLG SQFGIVYGG 600
 KHRKTGRDVA IKIDKLRFP TKQESQLRNE VALQNLHHP GVVNLECMFE TPERVFFVME 660
 KLHGDMLEMI LSSEKGRLEP HITKFLITQI LVALRHLHFK NVHCDLKPE NVLLASADPF 720
 PQVKLCDGFI ARIIGKFSR RSVVGTPAYL APEVLNRKGY NRSIDMWSVG VHYVSLSGT 780
 25 FPFNEDEDIH DQIQNAAFMY PPNPWKEISH EADILNNLL QVKMRKRYSV DKTLSPWVWQ 840
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 EMKALGERVS IL

30 SEQ ID NO:137 PFH3 DNA SEQUENCE

Nucleic Acid Accession #: X95425
 Coding sequence: 712-3825 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 AATGGTCAGT CAATACATTA TAACATAATA CACCAAATGC TAGAATAGAA GGGGAGGGGG 60
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 40 TTGCTTTTG CTGCTGCTC TCCTGTTTTT CATTCCTCAC ATTTTCTCAA TCCTCTTTCT 240
 TTATCCTTAG CCACCTGCT TTTTCTCTC TTTTAAAAA AATCGGAGAT TTCGTCTTAA 300
 AATGATTGT CTTCCTTACC TTCGTCCATT TCAACACTGA AGGCTGCAAA GAACTTCACC 360
 TTTCCTTAG TGGATTATTA AAATCTCTAA TCCGTAAAAA GTCTTTTGA AAGGCAAAAG 420
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 45 ACTAATATTT CATTTAACC ACCAAAAAGG GAGGCGGAGA GGAGCCAGAA GCAAACTTCA 540
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 GACCCCAAGG GGGGACAAGG AGGACTCCCG AGTCTCCCTT CTCCGCTCTC CGAGACCGAA 660
 GAGGTGAGCT GAGCCGCTCG GGACAGCGGC ACCGGAGGAG GCTCGGAGAA GATCGGGGGC 720
 TCGGGGCCCC GGGGTGCGGG ACACCGCGCG CCCCCAAGCG GCGGCGGCGA CACCCCATC 780
 50 ACCCAGCGT CCTGCGCGG CTGCTACTCT GCACCTCGAC GGGCTCCCT CTGGACGTGC 840
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 55 TCAGAAATCT TCATAGAAT CAAATTTACC CTGCGGACT GCAACAGCCT TCCTGGAGGA 1140
 CTGGGGACCT GTAAGGAAAC CTTTAATATG TATTACTTTG AGTCAGATGA TCAGAAATGG 1200
 AGAAACATCA AGGAAAAACCA ATACATCAAA ATTGATACCA TTGCTGCCGA TGAAGCTTT 1260
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 60 GTTCTGTGC GTGTATACTA TAAAAAATGC CTTCTGTGG TACGACACTT GGCTGTCTTC 1440
 CCTGACACCA TCACTGGAGC TGATTCTTCC CAATTGCTCG AAGTGTACAG CTCCTGTGTC 1500
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 65 GTGTGCAGAG CTGGGTCTT CAAAGCCTCA CCTACATCC AGAGCTGCGG CAAATGTCCA 1680
 CCTCACAGTT ATACCATGA GGAAGCTTCA ACCTCTGTG TCTGTAAAA GGATTATTTC 1740
 AGGAGAGAGT CTGATCCACC CACAATGGCA TGCACAAGAC CCCCCTCTGC TCCTCGGAAT 1800
 GCCATCTCAA ATGTTAATGA AACTAGTGTCT TTCTGGAAT GGATTCGCCC TGCTGACACT 1860
 GGTGGAAGGA AAGACGTGTC ATATTATAT GCATGCAAGA AGTGCAACT CCATGCAGGT 1920
 70 GTGTGTGAGG AGTGTGGCGG TCATGTCAGG TACCTCCCC GGCAAGCGG CCTGAAAAAC 1980
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 GTGAATGGAG TGTCCGACT GAGCCAGGA GCCCGGCAGT ATGTGTCTGT AAATGTAAAC 2100
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 75 ATCAAGCATT TTGAAAGGA CCAAGAGACC AGTACACGA TTATCAAAAT TAAAGAGACA 2280
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CTGCCAGGAG TAAGAACTTA CATTGATCCA CATACCTATG AGGATCCCAA TCAAGCTGTC 2700
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 5 GAAGCAAGTA TCATGGGACA GTTGTGATCAT CCTAACATCA TCCATTTAGA AGGTGTGGTG 2940
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 ATCTCTGAG GAATGAAGTA CCTTCTGAC ATGGGCTATG TGCATAGAGA TCTTGCTGCC 3120
 AGAAACATCT TAATCAACAG TAACCTTGTG TGCAAAAGTGT CTGACTTTGG ACTTTCCTGG 3180
 10 GTACTGGAAG ATGATCCCGA GGCAGCCTAC ACCACAAGGG GAGGAAAAAT TCCAATCAGA 3240
 TGGACTGCCC CAGAAGCAAT AGCTTTCCTA AAGTTTACTT CTGCCAGTGA TGTCTGGAGT 3300
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 15 AAGTTTGTAG AAATAGTCAA CATGTTGGAC AAGCTGATAC GTAACCCAAG TAGTCTGAAG 3540
 ACGCTGGTTA ATGCATCCTG CAGAGTATCT AATTTATTGG CAGAACATAG CCCACTAGGA 3600
 TCTGGGGCCT ACAGATCAGT AGGTGAATGG CTAGAGGCAA TCAAGATGGG CCGGTATACA 3660
 GAGATTTTCA TGAAAAATGG ATACAGTTCA ATGGACGCTG TGGCTCAGGT GACCTTGGAG 3720
 GATTGAGAC GGCCTGGAGT GACTCTGTG GGTCAACAGA AGAAGATCAT GAACAGCCTT 3780
 20 CAAGAAATGA AGGTGCACT GGTAAACGGA ATGGTCCCAT TGTAACTTCA TGAAATGTC 3840
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25 SEQ ID NO:138 PFH3 Protein sequence:
 Protein Accession #: CAA64700.1

30 1 11 21 31 41 51
 MRSGPRGAG HRRPPSGGGD TPITPASLAG CYSAPRRAPL WTCLLLCAAL RTLLASPSNE 60
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 35 EGASRIEFL KFTLRDCNSL PGGLGTCKET FMYFYFESDD QNGRNIKENQ YIKIDTIAAD 180
 ESFTELDLDG RVMKLNTEVR DVGPLSKGF YLAFQDVGAC IALVSVRVYY KKCPSVVRHL 240
 AVFEDITIGA DSQLLEVSG SCVNHSVTDE PPKMHCSAEG EWLVPIGKCM CKAGYEEKNG 300
 TCQVCRPGFF KASPHIQSCG KCPHYSYTHE EASTSCVCEK DYFRRESPP TMACTRPSSA 360
 PRNAISNVNE TSVFLEWIPP ADTGGRKDVS YYIACKKCNH HAGVCEECGG HVRYPRLQSG 420
 40 LKNTSVMMVD LLAHTNITYFE IEAVNGVSDL SPGARQYVSV NVTINQAAPS PVTNVKKGKI 480
 AKNSISLSWQ EPDRPNGIUL EYEIKHFEKD QETSYTIKS KETTITAEGE KPASVYVFQI 540
 RARTAAGYGV FSRRFEFETT PVFAASSDQS QIPVIAVSVT VGVILLAVVI GVLLSGSCCE 600
 CGCGRASSLC AVAHPILIWR CGYSKAKQDP EEEKMHFHNG HIKLPGVRTY IDPHTYEDPN 660
 QAVHEFAKEI EASCITIERV IGAGEFGEVC SGRLKLPGRK ELPVAIKTLK VGYTEKQRRD 720
 45 FLGEASIMGQ FDHPNIHLE GVVTKSKPVM IVTEYMENG SLDTLKKNNG QFTVIQLVGM 780
 LRGISAGMKY LSDMGYVHRD LAARNILNS NLVCKVSDFG LSRVLEDDPE AAYTTRGGKI 840
 PIRWTAPEAI AFRKFTSASD VWSYGIVMWE VVSYGERPYW EMTNQDVIKA VEEGYRLPSP 900
 MDCPAALYQL MLDWQWKERN SRPKFDEIVN MLDKLRNPS SLKTLVNASC RVSNLLAEHS 960
 50 PLGSGAYRSV GEWLFAIKMG RYTEIFMENG YSSMDAVAQV TLEDLRLRGV TLVGHQKKIM 1020
 NSLQEMKVQL VNGMVPIL

55 Nucleic Acid Accession #: NM_016029
 Coding sequence: 78-1097 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
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 65 TGACTGGAGC CTCGAGTGA ATTGGTGAGG AGCTGGCTTA CCAATTGTCT AAACATAGGAG 300
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 70 ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTG CTGACAAAA TGTGTTCTGC 600
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 75 GCAATAATGG AGACCAGTCC CACAAGATGA CAACCACTCG TTGTGTGCGG CTGATGTTAA 900
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 CATATTTGTG CAAATACATG CCAACCTGGG CCGTGGTGGT AACCAACAAG ATGGGGAAGA 1020
 AAAGGATTGA GAATTTTAA AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080
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 AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200

ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
AGATTGCCAT GAATCTTGCA AA

5

SEQ ID NO:140 PFH2 Protein sequence:
Protein Accession #: NP_057113.1

1 11 21 31 41 51
10 | | | | |
MNWELLWLL VLCALLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVVWVTGASS 60
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ATKAVLQEFGR IDILVNNGG MSQRSLCMDT SLDVYRKIE LNYLGTVSLT KCVLPHEMER 180
15 KQGKIVTVNS ILGIISVPLS IGYCASKHAL RGFENGLRTE LATYPGIHVS NICPGPVQSN 240
IVENSLAGEV TKITGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISEQP FLVVTYLWQY 300
MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD

20

SEQ ID NO:141 PFH1 DNA SEQUENCE

Nucleic Acid Accession #: NM_021614
Coding sequence: 1-1740 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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30 TCCTCAGCCC CCGAGATCGT GGTGTCTAAG CCGAGGCACA ACAACTCCAA CAACCTGGCG 240
CTCTATGGAA CCGGCGCGCG AGGCAGCACT GGAGGAGGCG GCGCGCGTGG CCGGAGCGGG 300
CACGGCAGCA GCAGTGGCAC CAAGTCCAGC AAAAAAGAAA ACCAGAACAT CGGCTACAAG 360
CTGGGCCACC GCGCGCCCTT GTTCGAAAAG CGCAAGCGGC TCAGCGACTA CGCGCTCATC 420
TTCGGCATGT TCGGCATCGT GGTCAATGGT ATCGAGACCG AGCTGTCTGT GGGCGCCTAC 480
35 GACAAGGCGT CGCTGTATTC CTTAGCTCTG AAATGCCTTA TCAGTCTCTC CACGATCATC 540
CTGCTCGGTC TGATCATCGT GTACCACGCC AGGGAATAC AGTTGTTTAT GGTGGACAAT 600
GGAGCAGATG ACTGGAGAAT AGCCATGACT TATGAGCGTA TTTTCTTCAT CTGCTTGAA 660
ATACTGGTGT GTGCTATTCA TCCCATACCT GGGGAATTATA CATTCACATG GACGCGCCGG 720
CTGCGCTTCT CCTATGCCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTTATCTATA 780
40 CCAATGTCTT TAAGACTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAAACTTTTC 840
ACTGATGCTT CCTCTAGAAG CATTGGAGCA CTTAATAAGA TAACTTCAA TACACGTTTT 900
GTTATGAAGA CTTAATGAC TATATGCCCA GGAACGTGAC TCTTGGTTTT TAGTATCTCA 960
TTATGGATAA TTGCCGATG GACTGTCCGA GCTTGTGAAA GGTACCATGA TCAACAGGAT 1020
GTTACTAGCA ACTTCTCTGG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCCATTGGT 1080
45 TATGGTGACA TGGTACTTAA CACATACTGT GGAAGAAGGAG TCTGCTTACT TACTGGAATT 1140
ATGGGTGCTG GTTGCACAGC CCTGGTGGTA GCTGTAGTGG CAAGGAAGCT AGAAGTTACC 1200
AAAGCAGAAA AACACGTGCA CAATTTTCAT ATGGATACTC AGCTGACTAA AAGAGTAAAA 1260
AATGCAGCTG CCAATGTACT CAGGGAAACA TGGCTAATTT ACAAATAAC AAAGCTAGTG 1320
AAAAAGATAG ATCATGCAAA AGTAAGAAAA CATCAACGAA AATTCCTGCA AGCTATTTCAT 1380
50 CAATTAAGAA GTGTAATAAT GGAGCAGAGG AAAGTGAATG ACCAAGCAAA CACTTTGGTG 1440
GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATTT CTGACTTAAA CGAAAGGAGT 1500
GAAGACTTCG AGAAGAGGAT TGTACCCCTG GAAACAAAAC TAGAGACTTT GATTGGTAGC 1560
ATCCACGCCC TCCCTGGGCT CATAAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTCATT 1620
GAGGCTCAGA TGGAGAGCTA CGACAAGCAC GTCACCTTACA ATGCTGAGCG GTCCCGGTCC 1680
55 TGTCCAGGA GCGGCGGTC CTCTCCACA GCACCACCA CTTTCATCAGA GAGTAGCTAG

55

SEQ ID NO:142 PFH1 Protein sequence:
Protein Accession #: NP_067627

1 11 21 31 41 51
60 | | | | |
MSSCRYNGGV MRPLSNLSAS RRNLHEMDSE AQPLQPPASV GGGGASSPS AAAAAAAVS 60
SSAPEIVVSK PEHNNNNLA LYGTTGGGST GGGGGGGSG HGSSSGTKSS KKKNNQIGYK 120
65 LGHRRALFEK RKRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180
LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFFICLE ILVCAIHPI GNYTFTWTAR 240
LAFSYAPSTT TADVDIISI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRF 300
VMKTLMTICP GTVLLVFSIS LWIAAWTVR ACERYHDQDD VTSNFLGAMW LISITFLSIG 360
YDGMVNTYCK GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNFMD MDTQLTKRVK 420
70 NAAANVLRST WLJYKNTKLV KKIDHAKVRK HQRKFLQAIH QLRSVKMEQR KLNDQANTLV 480
DLAKTQNMV DMISDLNERS EDFEKRIVTL ETKLETIGS IHALPGLISQ TIRQQQRDFI 540
EAQMESYDKH VTYNAERSRS SSRRRSSST APPTSSESS

75

SEQ ID NO:143 PF69 DNA SEQUENCE

Nucleic Acid Accession #: AL110139, coding region is FGENESH predicted
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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| | | | |
 ATGCGCGCGG TGCCGCTGCC CGCCCCGCTC CTGCGCTGC TGCTGCTCGC GCTCCTGGCC 60
 GCTCCCGCCG CCCGCGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
 CGCGAGTCCG GGCCACCGCC CGGCCCGGGG CCCGGGAACA CCACCCGGTT TGGGTCTGGG 180
 GCGGCGGGCG GCAGCGGCAG CTCCAGCTCC AACAGCAGTG GCGACGCCIT GGTGACCCGC 240
 ATTTCCATCC TCCTCCGCGA CTAACCCACC CTCAAGGCAG CCGTGATCGT GGCCTTCGCC 300
 TTTACCAACC TCCTCATCGC CTGCTGCTG CTGCGCGTCT TCAGGTGCGG AAAGAGGTTA 360
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGA AATGGCGCCA 420
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 GATGGCAGAT GCCAGAAGAT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
 TGTGAGAGGC TCACAGGTTC CATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT 1860
 TCCCCCGAC AGCCCTGTT TCTGTCCAG CCCTGA

SEQ ID NO:144 PFG9 Protein sequence:

Protein Accession #: none available, FGENSEH predicted

40
 45
 50

| | | | |
 1 11 21 31 41 51
 MRVPLPAPL LPLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60
 AAGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FILLIACLL LRVFRSGKRL 120
 KKTRKYDIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGQCILLTVP 180
 VPPFILDID LPARCSGRPD GGRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSVGGV 240
 ETKTNVMYKT PAFSCVSGIC SDCHWQARFH VTTMELLPP FGHFFKVPPT STPHGFRQLQ 300
 LNLMEKLDSS ALRRNTRAPS ARCLPLVLA MAEAESDLPN PWWHFSATGS PIKTLTYQTM 360
 STLGLDVFCG AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESQFPHIL RLLRECPPLS 420
 THPVRLARS ARGQASLTGR RVFRPRQSL HGGGAGTAT CLLVLKILL RPHLDLFYK 480
 ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHAHEPV KRGPSQLR HTCPGWGITH 540
 ANLQTPDQ GQEGPREDTV HPGDLDGVA NFYLEEGFQ DGRQCKMVLV SEEGPPSLTG 600
 CERLTGSHHF SSSHSKWSFL SPRQPLFLSR P

SEQ ID NO:145 PFG6 DNA SEQUENCE

55
 Nucleic Acid Accession #: NM_013427
 Coding sequence: 875-3799 (underlined sequences correspond to start and stop codons)

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 65
 70
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| | | | |
 1 11 21 31 41 51
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 GTCTCCTGAA GCTCCCTCTT CCACGGAGAG CGCTGAGCGC CGCCGGGAAT TCCATCCAC 120
 CGTGGGCACG CAGTCTTTGG AGGTCCCGGG CGCAGCACGC TCGGTGTCC CACACTGCAG 180
 CAAGACAGAG ACCCGCGGGG AACCTTGAGC TTGGAACAAC CCTTGAGCCT CTGCAGTCGG 240
 AAGAGTGGGC GCAGCAGCCC AGCGGAGGCC AGGCGCGCAA CCTCGGGGCG CGGGGCAAGG 300
 AGAGAGTGA GGGAGGCCA GCTCAGGCGC CCGGCTCAGG AGCGGGAGGA AGTTCTCGCG 360
 GCGCCGGGAG CGCGGTGGAC GCGCCCTGGG CGCACGCCCA GGCAGCCTTC TCCCTGGCCC 420
 TCGGGACTGT CTTGGGGCGG CAAGGAGGAG CTGCTGGAG TCTTAGAGGC CATCCAGAGC 480
 CAGCGAGCAG GAGGCTGCG TCTCCGCT CAGCTAGGAA GGGGAGTGG CGCTGGCAGG 540
 CTGGAGCTGG GAACCCAGCG AGCGCTGAC CTTCCTCTC CTCTCTCTGA CCTCTTTCG 600
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 GCGCGTAGC TGGGCTTTGC TCTCCACCGC CTGGGCAAA CCCCGGGCCA GCCCCGCTG 780
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 GGAGGAGGTG GTCCTCAGT GCAGCCCGCG CGAGATGTC GCGCAGAGCC TGCTCCACAG 900
 CGTCTTCTC TGTTCTCTCG CCGCTTCAAG TAGCGCGGCC TCGGCAAGG GCTTCTCAA 960
 GAGGAAGCTG CGCCAGACCC GCAGCCTGGA CCCGCCCTG ATCGGCGGCT GCGGAGGCGA 1020
 CGAGCGGGCG GCGGAGGCGA GTGCGCGGG AGCCACGGCG GCGCCCTCT ACTCCCATC 1080
 ACTCCAGCC GAGAGTCTG GCGCTCGCTT GCGCTCCTT TCCCGGGGTC GCGCCCCAG 1140
 GGCCACCAGG CTACCGCTC CTGACCTCT TTGCTGCTC TTCTCCACAC CCAGCACCCC 1200

GCAGGAGAAG TCACCATCCG GCAGCTTTCA CTTGACTAT GAGGTTCCTC TGGGTCCGG 1260
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 5 TCCTAGGAGG TGGCTCCAGC AGAGGAAGTT CCAGTCCCA CCGACAGTC GCGGGCACCC 1440
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 GCGGCTGAGG TCAGTCCCA TCCAGAGTCT CTCAGAGCTG GAGAGGGCCC GGCTGCAGGA 1560
 AGTGCCCTTTT TATCAGTTGC AACAGGACTG TGACCTGAGC TGTGAGATCA CCATTCCCAA 1620
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 10 AAACAAAGAC AAGAAATTC TCCACAGGC ATTTGGAATG CCTTATCCC AAGTCATTGC 1740
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 TGAATTTGTG GCTTCCCTCC TCCCATTTGG AAATAAAAGA CAAAACAAAG AACTCTCAAG 1860
 CAGTAACCTA TCTCTCAGCT CAACCTCAGA AACACCGAAT GAGTCAACGT CCCCACAC 1920
 CCGGAAACCG GCTCCTCGGG CTAGGAGGAG GGGTGCCATG TCAGTGGATT CTATCACC 1980
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 15 TCAAAGTAAA AAGGAAAAAG CCAGAGATAA GAAACTCAGT CTGAATCTTA TTTACAGACA 2100
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 20 CATCAACACT TCTTTGTGG AGCCGGAGGA ACAGCTGGGC ACCTTGACG TCCTCATATA 2400
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 25 TGTTGTGCAA AAGATGATTG AAAATTATGA AGCCTGTTT ATGGTTCCCC CAGATCTCCA 2700
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 30 CCGGGGGGGC TCGGAGAAGC TTTACAGAGT GCCAGGGCAG TTTATGCTGG TGGGCCACTT 3000
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 AGGAATGACA GGTTCCTCTG GAGACATTTT TGAAGCAGC TCCCTAAGAG CCGGGCCCTG 3180
 TCCCTTTTCT CAAGGGAAAC TGTCCCAAAA TTGGCTCCTG TGGCAGGGGA GCCCCGAGA 3240
 35 GCTGGACAGC GACACGAGG GGGCTCGGAG GACTCAGGCC GCAGCCCCCG GCACGGAGGG 3300
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 CAGCGAGAGT GAGCTGGATG TGGCCGGGCT GCAGAGCCGG GCCACACCTC AGTGCCAAAG 3480
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 40 GCCCGGGGCA GCGGCAAGCT GGATCCAGGG GCCCCCGGAA GCGGTGGAGA CACCCACGGA 3600
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 45 CCTCACGCC AGGGGGGACC GTGGGTGGTG GCCACTGGCA CACTTAGTGT TCTTCTTCA 3900
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 55 AATACGTTT CAGGAAAAATG CTAATCTGA TAGATTACGA AATATATTT TAGAAGTTGT 4500
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 GTTGCTCCG CACGTTTACA TCAAATTCAG TTTTATATAG GCCATATATA ATATATATT 4620
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 60 TTAAGAATCT ACACAGATA TCAAATTAT AGAACATGTT TTTCCCTT GCCCATAAT 4740
 CAGTATTGCG CAAATTCAT GCAATTCCTT AAAAATAA TCACATTGTT AAAAGGCCTA 4800
 CAGCTTTGTA CTACATTGT GCCAAAGGCT GAGGAAATGT TTTCTTCA ATTTTATGT 4860
 GTATTGTAAA ATGTTCTACC GTACTTTAGT AGTTTGAAGT TTCAAGTGC ATAATATT 4920
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 65 AAAGTGTATT ATAAAAAAG ATTTTITTTT TTTAAACAT GCTACTCTA ATTTTCATGT 5040
 TGGTGATGAA ATTCCAGTG GTGTTTCTTA AGTTTCTATC TTGTGCCATG ATGAATAAAA 5100
 AGTTAAGCAA AAAAAAAAAA AAAAAAAAAA AAA

SEQ ID NO:146 PFG6 Protein sequence:
 Protein Accession #: NP_038286.1

1 11 21 31 41 51
 75 MSAQSLHSV FSCSSPASS AASAKGFSKR KLRQTRSLDP ALIGCGSDE AGAEGSARGA 60
 TAGRLYSPSL PAESLGRPLA SSSRGPPPPA TRLPPLPLC SSFSTPTPQ EKSPSGSFH 120
 DYEVLGRGG LKKSMAWDL SVLAGPASSR SASSILCSSG GGPNGIFASP RRWLQQRKFQ 180
 SPDPGRHPY VVWKSEGDFT WNSMGRSVR LRSVPQISLS ELERARLQEV PFYQLQQDCD 240
 LSCQITPKD GQKRKKSIRK KLSLKGKEKN KDKFIPQAF GMPLSQVIAN DRAYKLKQDL 300
 QRDEQKASD FVASLLPFGN KRQNKELSS NSSLSSTSET PNESTSPNTP EPAPRRARRG 360

AMSVDSITDL DDNQSRILEA LQLSLPAEAQ SKKEKARDKK LSLNPIYRQV PRLVDSCCQH 420
 LEKHGLQTVG IFRVGSKKR VRQLREEFDR GIDVSLIEEE SVHIDVAALLK EFLRDMPPDL 480
 LTRELYTAFI NTLLEPEEQ LGTLQLLIYL LPPCNCOTLH RLLQFLSIVA RHADDNISKD 540
 GQEVGTGNKMT SLNLATIFGP NLLHKQKSSD KEFSVQSSAR AEESTAIIV VQKMIENYEA 600
 LFMVPPDLQN EVLISLLETD PDVVYLLRR KASQSSSPDM LQSEVSFVSG GRHSSTDSNK 660
 ASSGDIPYD NNSPVLERS LLAMQEDAAP GGSEKLYRVP GQFMLVGHLS SSKSRESSPG 720
 PRLGKDLSEE PFDIWTGTHS TLKSGSKDPG MTGSSGDIFE SSSLRAGPCS LSQGNLSPNW 780
 PRWQGSFAEL DSDTQGAARRT QAAAPATEGR AHPAVSRACS TPHVQVAGKA ERPTARSEQY 840
 LTLSGAHDLS ESELDVAGLQ SRATPQCQRH HSGRDRDKRP PFPYGPQKP AAAAAWIQGP 900
 PEGVETPTDQ GGQAAREEQ VTQKKLSSAN SLPAGEQDSP RLGDAGWLDW QRRERWQIWEL 960
 LSTDNPDALP ETLV

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SEQ ID NO:147 PFG4 DNA SEQUENCE

Nucleic Acid Accession #: NM_002202

Coding sequence: 240-1289 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
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 CTTAAATTGG ACTCCTAGAT CCGCGAGGGC GCGCGCAGC CGAGCAGCGG CTCTTTCAGC 120
 ATTGGCAACC CCAGGGGCCA ATATTTCCTA CTAGGCCACA GCTCCAGCAT CCTCTCTGTG 180
 GGCTGTTTAC CAAGCTGTACA ACCACCATTT CACTGTGGAC ATTACTCCCT CTTACAGATA 240
 TGGGAGACAT GGGAGATCCA CCAAAAAAAA AACGTCTGAT TTCCCTATGT GTTGGTTGCG 300
 GCAATCAGAT TCACGATCAG TATATTCTGA GGGTTTCTCC GATTTTGGAA TGGCATGCGG 360
 CATGTTTGAA ATGTGCGGAG TGAATCAGT ATTTGGACGA GAGCTGTACA TGCTTTGTTA 420
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 AGTGCAACAT CGGCTTCAGC AAGAACGACT TCGTGATGCG TGCCCGCTCC AAGGTGTATC 540
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 CCGCAAACCC GCGGCCAGAT GCGCTCATGA AGGAGCAACT GGTAGAGATG ACGGGCCTCA 900
 GTCCCGGTGT GATCCGGGTC TGGTTTCAAA ACAAGCGGTG CAAGGACAAG AAGCGAAGCA 960
 TCATGATGAA GCAACTCCAG CAGCAGCAGC CCAATGACAA AACTAATATC CAGGGGATGA 1020
 CAGGAATCC CATGGTGGCT GCCAGTCCAG AGAGACACGA CGGTGGCTTA CAGGCTAACC 1080
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 AATTATGCT CTAATTCAT GTGTTTGTG TTTTCTTAA ATATTATGT AAATCAAGC 2340
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SEQ ID NO:148 PFG4 Protein sequence:

Protein Accession #: NP_002193.1

70

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1 11 21 31 41 51
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 EDGLFCRADH DVVERASLGA GDPLSPLHPA RPLQMAAEPI SARQPALRPH VHKQPEKTR 180
 VRTVLNEKQL HTLRTCYAA PRPDALMKEQ LVEMTGLSPR VIRVWFQNK RCKDKRSIMM 240
 KQLQQQPNQ KTNIGMTGT PMVAASPERH DGGQLQNPVE VQSYQPPWKV LSDFALQSDI 300
 DQPARQQLVN FSEGGPGSNS TGSEVASMSS QLPDTPNSMV ASPIEA

SEQ ID NO:149 PFG2 DNA SEQUENCE

Nucleic Acid Accession #: NM_0011172

Coding sequence: 39-1103 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
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 10 TGATAGGAGC CCCGTCTCA CAAGGGCAGA AAAGAAAAGG AGTGGAGCAT GGTCCCGCTG 180
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 TTGGAGATTG GAGTTTACT CCAGTCCCCA AAGATGATCT CTACAACAAC CTGATAGTGA 300
 ATCCACGCTC AGTGGGTCTT GCCAACCAGG AACTGGCTGA GGTGGTTAGC AGAGCTGTGT 360
 CAGATGGCTA CAGCTGTGTC AACTGGGAG GAGACCACAG CCTGGCAATC GGTACCATTA 420
 GTGGCCATGC CCGACACTGC CCAGACCTTT GTGTGCTCG GGTGATGCC CATGCTGACA 480
 15 TCAACACACC CTTTACCCT TCATCAGGAA ATCTCCATGG ACAGCCAGTT TCATTCTCC 540
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 20 TGAGTTTGA TATTGCTCA TTGACCTTA CACTGGCTCC AGCCACAGGA ACTCCTGTTG 840
 TCGGGGACT AACCTATCGA GAAGGCATGT ATATTGCTGA GGAAATACAC AATACAGGGT 900
 TGCTATCAGC ACTGGATCTT GTTGAAGTCA ATCTCAGTT GGCCACCTCA GAGGAAGAGG 960
 CGAAGACTAC AGCTAACCTG GCAGTAGATG TGATTGCTTC AAGCTTTGGT CAGACAAGAG 1020
 AAGGAGGGCA TATTGTCTAT GACCAACTTC CTACTCCAG TTACCAGAT GAATCAGAAA 1080
 25 ATCAAGACCG TGTGAGAAIT TGGAGACAC TGTGCACTGA CATGTTTCAC AACAGGCATT 1140
 CCAGAATTAT GAGGCATTGA GGGGATAGAT GAATACTAAA TGGTGTCTG GGTCAATACT 1200
 GCCTTAATGA GAACATTTAC ACATTCTCAC AATTGTAAGG TTCCCTCTCT ATTTTGGTGA 1260
 CCAATACTAC TGTAAATGTA TTTGGTTTTT TGCAGTTTAC AGGGTATTAA TATGCTACAG 1320
 TACTATGTAA ATTTAAAGAA GTCATAAACA GCATTATTA CCTTGGTATA TCATACTGGT 1380
 30 CTGTGTCTG TGTGTCCTC ACATTAAAGT GGTTTTTCAT CTTTCTCTCC TCCTCCACA 1440
 GCCTGGCTAT ACAGTGCATC CTGAACTGT CAGCCACAG CAGCAATATG CTTATTCTAT 1500
 CCACATCCCT AACATCATGC ATTCACAAGG TCAAAGTTCT GGTCCACAAA CCTTCCCTA 1560
 TAGAAGTTCA ATGGCTGGCA AAGAATTTGT AGTAAACCAG GCCTCCAGG ATGGCAGCT 1620
 CCAGTAAGAT GATAATGGAA AGCAGCAGCT TGTGGTTGT CACTCTACAA AGAGAAGCAA 1680
 35 AGTGGGAGT AGTACGAAGT TTGGATAACC TTCTTCTAA ACATTGGGG GTTAGACCTG 1740
 GGACCACGGC TGGATACTCT GAGGCTGTAT GTTGTATCAC ACAGCCACTT AGCAGGAAGT 1800
 ATCTATAAGG TTTTATGCT GTCACTTAGG GATAACACTG TCTACCTCAC AGAAATGTTA 1860
 AACTGAGACA ATAAAACCCA AAGCAT

SEQ ID NO:150 PFG2 Protein sequence:

Protein Accession #: NP_001163.1

45 1 11 21 31 41 51
 MSIRGSLRL LQTRVHSILK KSVHSVAVIG APFSQGGKRR GVEHGPAAIR EAGLMKRLSS 60
 LGCHLKDIFD LSFTVPKDD LYNLNIVNPR SVGLANQELA EVVSRAVSDG YSCVTLGGDH 120
 SLAIGTISGH ARHCPDLV VVDAHADINT PLTSSGNLH GQPVSELLRE LQDKVPQLPG 180
 50 FSWIKPCISS ASIVYGLRD VDPPEHFLK NYDIQYFSMR DIDRLGIQKV MERTFDLLIG 240
 KRQRPHLSF DIDAFDPTLA PATGTPVVGG LTYREGMYIA EEIHNTGLLS ALDLVEVNPQ 300
 LATSEEAKT TANLAVDVIA SSFGQTRREG HIVYDQLPTP SSPDESENQA RVRI

SEQ ID NO:151 PFG1 DNA SEQUENCE

Nucleic Acid Accession #: NM_017906

Coding sequence: 80-1255 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 AATTATATAT TTTTACTCTA TGTITCTCTA CATGTTTTT TCTTCCGTT GCTGGCGGAA 60
 GAGGCACGTG CGCTGCTGAA TGGAGCTGGT CGCTGGTTGC TACGAGCAGG TCCTCTTTGG 120
 GTTCGGTGTA CACCCGGAGC CCAAGGCTTG CGCGACCAC GAGCAATGGA CTCTGTGGC 180
 65 TGACTTCACT CACCATGCTC AACTGCCTC CTGTGCAGCA GTAGCTGTAA ATAGTCGTTT 240
 TGTGGTCACT GGGAGCAAAG ATGAAACAAT TCACATTTAT GACATGAAAA AGAAGATTGA 300
 GCATGGGGCT CTAGTGCAATC ACAGTGGTAC AATAACTTGC CTGAAATTCT ATGGCAACAG 360
 GCATTTAATC AGTGGAGCGG AAGATGGACT CATCTGTATC TGGGATGCAA AGAAATGGGA 420
 ATGCCTGAAG TCAATTAAAG CTCACAAAGG ACAGGTGACC TTCTTTCTTA TTCACCCATC 480
 70 TGGCAAGTTG GCCCTGTCGG TTGGTACAGA TAAAACTTTA AGAACGTGGA ATCTTGTTGA 540
 AGGAAGATCA GCATTCATAA AAAATATAAA ACAAAATGCT CACATAGTAG AATGGTCCCC 600
 AAGAGGAGAG CAGTATGTAG TTATCATACA GAATAAATA GACATCTATC AGCTTGACAC 660
 TGCATCAATT AGTGGACCA TCACAAATGA AAAGAGAAAT TCCTCTGTTA AATTCTTTT 720
 AGAGTCTGTC CTTCGAGTGG CTGGAGATGA AGAAGTTATA AGGTTTTTT ACTGTGATTC 780
 75 ACTAGTGTGC CTCTGCGAAT TTAAGCTCA TGAACACAGG GTAAAGGACA TGTTCAGTTT 840
 TGAATTTCCA GAGCATCATG TTATTGTTT AGCATCGAGT GATGGTTTCA TCAAAATGTG 900
 GAAAGCTTAAG CAGGATAAGA AAGTTCCCCC ATCTTTACTC TGTGAAATAA ACTAATATGC 960
 CAGGCTGACG TGTCTTGAAG TGTGGCTAGA CAAAGTGGCA GACATGAAAA GCCTTCTCC 1020
 AGCTGCAGAG CCTTCTCTG TAAGTAAAGA ACAGTCAAAA ATTGGCAAAA AGGAGCCTGG 1080
 TGACACAGTG CACAAGAAG AAAAGCGGTC AAAACCTAAC ACAAGAAAAA GCGGTTTAAC 1140

AGGTGACAGT AAGAAAGCAA CAAAAGAAAG TGGCCTGATA TCAACCAAGA AGAGGAAAAAT 1200
 GGTAGAAATG TTGGAAAAGA AGAGGAAAAA GAAGAAAATA AAAACAATGC AGTGAATCAC 1260
 AGATGTCTCC TGAAAGAACT CTTTAGATG AAATCATTCT ACTCAAATGT ACCTTAATTT 1320
 TTTTITTTCC CTGAGTAAAA GCAAGAAATT TCTTCCTTG GAAAAAATAT ATATATTAAA 1380
 AAACCACTTT TAGATGGTTT TTTTAAAAA AAAAAAAAAA ACTGGTAAAA TTACTTTTGG 1440
 CAGACAGTGT TTTATGAATT ATGTATCATG TTGATATATA ATATGTTAAT GTGTCATGTA 1500
 ATTTTACTT TGTACAAAGC AAATAAGAT CTTTCTCAA AAAAAAAAAA AAAA

SEQ ID NO:152 PFG1 Protein sequence;
 Protein Accession #: NP_060376.1

1 11 21 31 41 51
 MELVAGCYEQ VLFQFAVHPE PKACGDHEQW TLVADFTHIA HTASLSAVAV NSRFVVTGSK 60
 DETHIYDMK KKHGALVH HSGITTCCLKF YGNRHLISGA EDGLICIWDA KWWECLKSIK 120
 AHKGQVTFLS IHPGKLALS VGTDKTLRTW NLVEGRSAFI KNKQNAHIV EWSPRGEQYV 180
 VIIQNKIDYI QLDIASISGT ITNEKRISV KFLSESVLAV AGDEEVIRFF DCDSLVCLCE 240
 FKAHENRVKD MFSFEIPEHH VIVSASSDGF IKMWKLKQDK KVPSSLCEI NTNARLTCLG 300
 VWLDKVVADMK SLPPAAEPSV VSKEQSKIGK KEPGDTVHKE EKRSKPNTKK RGLTGDSKKA 360
 TKESGLISTK KRKMVEMLEK KRKKKKIKTM Q

SEQ ID NO:153 PFD6 DNA SEQUENCE

Nucleic Acid Accession #: NM_014668
 Coding sequence: 110-2953

(underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GATGTCCTGG ACATGCTCTG GCTGGCTAAT CTCCATGTTT TAGCCGACTG AAAATACGGT 60
 GGCCAAAGTGG ATGGTGTGCT TATTTGCACT CTAAGAAAT TTCTTTTGA TGTGGCAGAA 120
 AATCGAGGAT GTGGAGTGGG GACCCAGAC TTAATGGAG CTGGAGGGTC TGCCTTGCAAT 180
 CCTGATCTTC AGTGGGATGG ACCCGCATGG GGAGTCTCTG CCGAGGTCTT TGAGGTACTG 240
 TGACCTGCGA TTGATAAACT CCTCCTGCTT GGTGAGAACA GCCTTGGAGC AGGAGCTGGG 300
 CTGGCTGCC TACTTTGTGA GCAACGAGGT TCCCTTGGAG AAGGGGGCTA GGAACGAGGC 360
 CTTGAGAGAT GATGCTGAGA AGCTGAGCAG CACAGACAAC GAGGATGAGG AGCTGGGGAC 420
 AGAAGGCTCT ACCTCGGAGA AGAGAAGCCC CATGAAAAGG GAGAGGTCCC GCTCCACGA 480
 CTCAGCATCC TCATCCCTCT CTCCAAGGC TTCCGGTTCA GCGCTCGTG GCGAGTCTTC 540
 GGCTCAGCCC ACAGCACTCC CCCAGGGAGA GCATGCCAGG TCGCCCCAGC CCCGTGGCCC 600
 CGCAGAGGAG GGCAGAGGCC CTGGTGAGAA ACAGAGGCC CCGGCAAGTC AGGGGCCACC 660
 CTCGGCCATC AGCAGGCACA GTCCCGGGCC GACGCCCCAG CCCAGCTGTA GCCTCAGGAC 720
 CGGCCAGAGG AGCGTCGAGG TGTCGGTCACT CCGTCTGTC TCCAGCTGT CCTCCTCTCT 780
 GGGCTCATCC TCCTCATCCG TGGCGCCCGC TGCCGGCAGC TGGTCTCTGC AGGCCTCCCA 840
 GTGCTCTCTG ACCAAGGCTC GCGCCAGCC ACCCATGTCT TCTTGCCCA AGCTCGTGTA 900
 CGACATGGCT GTGTCCACTG ACAGCAGTGG CCTGCCCAAG GCGGCTCTCC TCTGCGCTCT 960
 CCCCTCGGTC ATGTGGGCGA GCTCTTCCG CCCCTGCTC AGCAAGACCA TGACATCCAC 1020
 CGAGCAGTCC CTCTACTGCA GGCAGTGGAC GGTGCCCGG CCCAGCCACA TGGACTACGG 1080
 CAACCGGGCC GAGGGCCCGG TGGACGGCTT CCACCCCGC AGGCTCTCTC TCAGCGGCC 1140
 CCCTCAGATC GGAAGACAG GTGCTACCT GCAGTCTCTC AGTGTCTGT CCAGGATGCT 1200
 TGTTCCGGCT ACAGAGTGG ATGTCTATGA CGAGGAGGAG ATCAATATCA ACCTCAGAGA 1260
 AGAATCTGAC TGGCATTATC TCCAGCTTAG CGACCCCTGG CCAGACCTGG AGCTGTTCAA 1320
 GAAGTTGCC TTTGACTACA TCATTACGA CCCGAAGTAT GAAGATGCCA GCCTGATTG 1380
 TTGCACTAT CAGGGTATAA AGAGTGAAGA CAGAGGGATG TCCCGAAGC CGGAGGACCT 1440
 TTATGTGCGG CGTCAGACGG CACGATGAG ACTGTCCAAG TACGAGCGT ACAACACTTA 1500
 CCACCACTGT GAGCAGTGCC ACCAGTACAT GGGCTTCCAC CCCGCTACC AGCTGTATGA 1560
 GTCCACCTGT CACGCTTTG CTTTCTCTTA CTCCATGCTA GGAGAGGAGA TCCAGCTGCA 1620
 CTTATCATC CCCAAGTCCA AGGACACCA CTTTGTCTT AGCCAACCTG GAGGCCAGCT 1680
 GGAGAGCATG CGACTACCCC TCGTGACAGA CAAGAGCCAT GAATATATAA AAAGTCCGAC 1740
 ATCACTCCA ACCACGGGCC GTCACGAACA TGGGCTCTT AATCTGTACC ACGCAATGGA 1800
 CGGTGCCAGC CATTTGCACG TGCTGGTTGT CAAGGAATAC GAGATGGCAA TTTATAAGAA 1860
 ATATTGGCCC AACCACATCA TGCTGGTGCT CCCCAGTATC TTCAACAGTG CTGGAGTTGG 1920
 TGCTGCTCAT TTCTCATCA AGGAGCTGTC CTACATAAC CTGGAGCTCG AGCGGAACCG 1980
 GCAGGAGGAG CTGGGAATCA AGCCGAGGA CATCTGGCCT TTCAATGTGA TCTCTGATGA 2040
 CTCTGCGTG ATGTGGAACG TGGTGGATGT CAACTGTCT GGGGAGAGAA GCAGGGAGTT 2100
 CTCTGGTCT GAAAGGAACG TGCTTTTGA GCACATCATG CAGCACATCG AGGCGGGCCC 2160
 CGACATCATG CACTACGCCC TGCTGGGCT GCGGAAGTGG TCCAGCAAGA CCCGGGCCAG 2220
 CGAGGTGCAA GAGCCCTTCT CCCGCTGCCA CTGACACAAC TTATCATCC TGAACGTGGA 2280
 CCTGACCCAG AACGTGCAGT ACAACAGAA CCGGTTCTGT TGTGACGATG TAGACTTCAA 2340
 CCTCGGGGTG CACAGCGCCG GCCTCTGCT CTGCCGTTT AACCGCTTCA GCGTGATGAA 2400
 GAAGCAGATC GTGGTGGCG GGCACAGGTC CTTCCACATC ACATCCAAGG TGTCTGATA 2460
 CTCTGCCGCG GTCTGCGCG CCCAGTACAT CTGTGCCCG GACAGCAAGC ACACGTTCT 2520
 CGCAGCGCCC GCCAGCTCC TGCTGGAGAA GTTCTGTCAG CACCACAGCC ACCTTCTT 2580
 CCCGCTGCTT CTGAAGAAC ATGACACCC AGTGCTGTCT GTCGACTGTT ACCTGAACT 2640
 GGGATCTCAG ATTCTGTTT GCTATGTGAG CTCCAGGCC CACTCTTAA ACATCAGCTG 2700
 CTGGGACTGT CTGTTGAGT GGCTGCTGCT GTACCTCTGT GACTCTTTT TGGGAGCTAG 2760
 CTTTITGAAA AAGTTTCATT TTCTGAAAGG TCGACGTTG TGTGTCATCT GTCAGGACCG 2820
 GAGCTCACTG CGCCAGACGG TCGTCCGCT GGAGCTCGAG GACGAGTGGC AGTTCGGCT 2880

GCGGATGAG TTCCAGACCG CCAATGCCAG GGAAGACCGG CCGCTCTTT TTCTGACGGG 2940
 ACGACACATC TAAGGAAGAC AGCGGCGAGT TTTCTGAAGA GATGAGTGCT CAGAGCCCTC 3000
 ATGCTGTGTA GGCTAAAGGG AGGCTCGGAA CGGTGGGGCG TTGACTGGA ATGGACCCCA 3060
 GGGACTGTCC AGGTGCAGCC CTTCTAGTA CACATGGGCC CCCGAGGCCG TGGTCTGGG 3120
 AGCCAGGAAG ACTCCGAGT GGGTGAGAAT GAAAACTTGA GACTCCCAAG TTCTGGGCCA 3180
 GCGCATGTCT CTGGGCTGTT TAAAGCCCA TTTCACGAGG AACAAAGATT TACTTCCTGT 3240
 CCTGCCATTC GTGTGCTTCC ATGGACAAAC CTGATTTTTT TCTCTTAGTT CTAAAGAATC 3300
 TTGGGTATTT TTGAGCGGT GCCAGTATTT CAGTAGATGG GATTTTCAGC AAGTAGGTTT 3360
 CCCTGTAACC TCCTACAAAG CAATATTCCA AAGGAACATT TAACTGTAA AGGCTGGAGA 3420
 CAAGAAAAAA TAAGTAGATC GTTTTAATAA CAATTATTTA ATTGCTATA AGTTTGCTGT 3480
 TTCAGAGGCT AGCCCAAAGG CATCAAAATTT AATAAAGTTA AACAAATTTA TTACTTCAG 3540
 AGCAAAATATG ATCTTATTTA AATAATATAG GGTAAATACC CTACCTCTTA GAAAGGGCAA 3600
 AAATGCAAGG AAGCTTCTTT TAAACTAAA AGGGTTTTTT GGGGGGGGAG TTGGCGGGGA 3660
 GGAAATAAGG CTAACAGAGG TTGACCTAAA ATTAGCTTA CAAAGGAGAA AGGACCACAT 3720
 TGCTTACTTG AACACAGCAA TGAACAACAA CAAAGTGATA TATAAATAG TTGATGAGAA 3780
 CTAGACTTAT GACTGTAGTT TACTAGAGTT TAGTTTTTCT TIGCTGAAGT AGCTCATTTT 3840
 CTCTTACTAA TGTTTGGTTC CTCAGGGAAG AATCTCACTT GACTAGAGAG GAGGTGGGAA 3900
 CAGAAGAGAG AAGGAGGAGG GGAGATGTAT TTCTTAGGGC TCACCCCTTC ACAGACTGAC 3960
 AGAATGGTTT TGTTTGTGTT TGTTTGTGTT TTGAGATGGA CTCTAGCTCT 4020
 GTCACCCAGG CTGGAGTGCA GTGGTGCGAT CTCGGCTCAC TGCAAGCTCC GCCTCCCGGG 4080
 TTCTACCAT TCTCTGCTC CAGCCTCCCG AGTAGCTGGG ACTACAGGCG CCCACCACCA 4140
 CGCCCGGCTA ATTTTGTGA TTTTGTAGTA GAGACGGGGT TTCACCATGT TAGCCAGGAT 4200
 GGTCTCGATC TCCTGACCTC GTGATCCGCC CGCCTCGGCC TCCCAAAGTG CTGGGATTAC 4260
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 CATGCCCCGG CGCCTGGACA GTGATCATCT TGTTCACTCT GTTCAGTCTT TCTTGTGTG 4380
 ATTGGAATTA TTCATCCCTT TTGAAAGATG AGAAGGTGGA GATGCAAGA GTCTACCTTT 4440
 CCAAGTTCTC ACTGCTGAAA AGAGCTAGAA GCACAGTICA AAGTTCTGGC TTCTGGACTC 4500
 TGCACTCCAG GTCTCCCTTC TCCACTTGC CTACCTCAA TGCCACACTG TTTTGAAGT 4560
 GGCCATAAC TTGAAGGAAA AGTTTAAAGA CAGTTCAATT TAATCATCAG AATGCATTCT 4620
 TTTTCTTTC GGAGACGGAG TTTCATCTT GCTGCCAGG CTGGAGTGCA ATGGTGCAAT 4680
 GATCTCGGCT CACTGCAACC TCTGCTCCT GGGTTCAAAGT GATTCTCCAG CCTCAGCCTC 4740
 CCGAGTAGCT GGGATTATGG GCGCCACCA CCATGCCAG CTAATTTTGT TATTTTTTTT 4800
 TTTTAGTAGA GATGGGTTT CGCCAGGTTG GCCAGGCTGG TCTTGGAAC TCCTGGCCTC 4860
 AGGTGATCTG CCCACCTCAT CCTCCAAAAG TGCTGGGATT ACAGGCATGA GCCACTGCCG 4920
 CTGGCCCTAG AATGCATTCT TACACATCTA TCCTAGACAT TTATAAGCAC TCTAATGGAT 4980
 AACACTCAA GAATAATGA TTGTAAGAAG TGATGCCGAA GAGTTGATGT CAATCTTTT 5040
 TTCTTAAGAA AAAAAGTCCG CGAGTATTA ATATTTAGAT CAATGTTTAT AAAATGATTA 5100
 CTTTGTATAT CTCATTATTC CTATTTTGA ATAAAACTG ACCTTCTTTA ATCATATACT 5160
 TGCTTTTGT AAATAGCAGC TTTTGTGCA TTCTCCAC TTTATTAGT AATTAAAT 5220
 GGAAAAAAC CTCAAACCTA TATCTTGTG TGTTCAGTC TTATAATAA AACTTATAAT 5280
 GCATG

45 SEQ ID NO:154 PFD6 Protein sequence:
 Protein Accession #: NP_055483.1

1 11 21 31 41 51
 50 MWQKIEDVEW RPQTYLELEG LPCILIFSGM DPHGESLPRS LRYCDLRLIN SSCLVRTALE 60
 QELGLAAFYF SNEVPLEKGA RNEALESDAE KLSSTDNEDE ELGTEGSTSE KRSPMKRERS 120
 RSHDSASSSL SSKASGSAIG GESSAQPTAL PQGEHARSPO PRGPAEEGRA PGEKQRPAS 180
 QGPSPAISRH SPGPTPQDC SLRTGQRSVQ VSVTSSCSQL SSSSGSSSS VAPAAAGTWVL 240
 55 QASQCSLTKA CRQPPVFLP KLVDYDMVST DSSGLPKAAS LLPSPVMWA SSFRPLLSKT 300
 MTSTEQSLYY RQWTVPRPSH MDYGNRAEGR VDGFIHPRLL LSGPPQIGKT GAYLQLSVL 360
 SRMLVRLTEV DVYDEEINI NLREESDWHY LQLSDPWPDL ELFKKLPFDY IHDPKYEDA 420
 SLICSHYQGI KSEDRGMSRK PEDLYVRRQT ARMRLSKYAA YNTYIHCEQC HQYMGFHPRY 480
 QLYESTLHAF AFSYSMLGEE IQLHFIPKS KEHIFVFSQP GGQLESMLRP LVTDKSHEYI 540
 60 KSPITFTPTG RHEHGLFNLY HAMDGASHLH VLVVKEYEMA IYKKYWPNHI MLVLPISFNS 600
 AGVGAHFLI KELSYHNLLE ERNRQEELGI KPQDIWPFIV ISDDSCVMWN VVDVNSAGER 660
 SREFSWSERN VSLKHMOMHI EAAPDIMHYA LLGLRKWSSK TRASEVQEPF SRCHVHNFI 720
 LNVDLTONVQ YNQNRFLCDD VDFNLRVHSA GLLLCRFNRF SVMKKQIVVG GHRSHFITSK 780
 VSDNSAAVVP AQYICAPDSK HTFLAAPAQL LLEKFLQHHS HLFPLSLKN HDHPVLSVDC 840
 65 YLNLGSQISV CYVSSRPDSL NISCSDLLFS GLLLYLDCSF VGASFLKKFH FLKGATLCVI 900
 CQDRSSLRQT VVRLELEDEW QFRLRDERQT ANAREDRPLF FLTGRHI

SEQ ID NO:155 PFC6 DNA SEQUENCE

70 Nucleic Acid Accession #: NM_000522
 Coding sequence: 1-1167 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 75 ATGACAGCCT CCGTGCTCTT CCACCCCGCG TGGATCGAGC CCACCGTCAT GTTCTCTAC 60
 GACAACGGCG GCGGCTGGT GGCCGACGAG CTCAACAAGA ACATGGAAGG GCGGCGGCG 120
 GCTGCAGCAG CGGCTGCAGC GCGGCGGCT GCGGCGGCGG GGGCGGGGGG CTTCCCCAC 180
 CCGCGGCTG CCGCGGCAGG GGGCAACTTC TCGGTGGCGG CCGCGGCGCG GGCTGCGCG 240
 CGCGCGGCGG CCAACACCTG CCGCAACCTG ATGGCGCAAC CGCGCGCTTT GCGGCCAGGA 300
 GCGCGCTCGC CTACAGCAG CGCCCCCGG GAGGCGCCCC CGTGGCTGCG CGCGCTGCT 360

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10
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CGCGCGGCTG CCGCTGCAGC CGCGCGCGCC GCGCGCGCGT CGTCTCGGG AGTCCCGGC 420
 CCGGCGGGCC CGCGCGCGCC AGAGGCGGCC AAGCAATGCA GCCCTGCTC GGCAGCGGCG 480
 CAGAGCTCGT CGGGGCGCGC GCGCGTGCCT TATGGCTACT TCGGCAGCGG CTAACACCCG 540
 TGGGCGCGCA TGGGCGCGCC CCGCAACGCC ATCAAGTCGT GCCCGCAGCC CCCCTCGGCC 600
 GCGCGCGCGC CCGCTTTCGC GGACAAGTAC ATGGATACCG CCGGCCAGC TGCCGAGGAG 660
 TTCAGTCCC GCGCTAAGGA GTTCGCGTTC TACCACCAGG GCTACGCAGC CGGGCCTTAC 720
 CACCACCATC AGCCCATGCC TGGCTACCTG GATATGCCAG TGGTGCCGGG CCTCGGGGGC 780
 CCGGCGAGT CGCGCCACGA ACCCTTGGGT CTTCCTATGG AAAGCTACCA GCCTGGGGC 840
 CTGCCAACG GCTGGAACGG CCAAAATGTAC TGCCCAAAG AGCAGGCGCA GCCTCCCCAC 900
 CTCTGGAAGT CCACTCTGCC CGACGTGGTC TCCATCCCT CGGATGCCAG CTCCTATAGG 960
 AGGGGAGAA AGAAGCGCGT GCCTTATACC AAGGTGCAAT TAAAGAACT TGAACGGGAA 1020
 TACGCCACGA ATAAATTCAT TACTAAGGAC AAACGGAGGC GGATATCAGC CACGACGAAT 1080
 CTCTCTGAGC GGCAGGTCAC AATCTGGTTC CAGAACAGGA GGGTAAAGA GAAAAAAGTC 1140
 ATCAACAAAC TGA AACAC TAGTTAA

SEQ ID NO:156 PFC6 Protein sequence:
 Protein Accession #: NP_000513.1

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30

1 11 21 31 41 51
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 MTASVLLHPR WIEPTVMFLY DNGGGLVADE LNKMEGAAA AAAAAAAAAA AGAGGGGFPH 60
 PAAAAAGGNF SVAIAAAAAA AAAANQCRNL MAHPAPLAPG AASAYSSAPG EAPPSAAAAA 120
 AAAAAA AAAASSSGPG PAGPAAEAA KQCSFCSAAA QSSGPAALP YGYFGSGYYP 180
 CARMGPPPA IKSCPQPSA AAAAAFADKY MDTAGPAAEE FSSRAKEFAF YHQGYAAGPY 240
 HHHQMPGVL DMPVVPGLGG PGESRHEPLG LPMESYQPPA LPNGWNGQMY CPKEQAQPPH 300
 LWKSTLPDVV SHPSDASSYR RGRKKRVPT KVLKELERE YATNKFITKD KRRRISATTN 360
 LSRQVTIWF QNRRVKEKV INKLKITS

SEQ ID NO:157 PFA3 DNA SEQUENCE

Nucleic Acid Accession #: AW102723
 Coding sequence: 523-2676 (underlined sequences correspond to start and stop codons)

35
40
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60
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70
75

1 11 21 31 41 51
 | | | | |
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 TTCTTACACT TTCTCTGCGC TAGAGCAGCG AGCAGCTGG AACAGACCCA GCGCGAGGAC 180
 ACCTGTGGGG GAGGAGGCGC CTGGAGGAGC TTAGAGACCC CAGCGGCGCG TGATCTCACC 240
 ATGTGCGGAT TTGCGAGGCG CGCCCTGGAG CTGCTAGAGA TCGGAAGCA CAGCCCCGAG 300
 GTGTGCGAAG CCACCAAGAC TCGGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCGG 360
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 TACCAAGTGT CTGGAATTGA TAGTGGCTTC TGTTTGTGAG TCTCATATAA GAACTACAGC 480
 TCATCAGGAG GAGATCGCAG CAGGGTAAGA GACACCAACA CCAATGTTCTG CACGAAGCTC 540
 AAGGATCTCA AGATACAGG AGAGTGTCTT TTCTCTTAC TGGCACCAGG TCAAGTTCCT 600
 AACGAGTCTT CAGAGGAGGC AGCAGGAAGC TCAGAGAGCT GCAAAGCAAC CGTGCCCATC 660
 TGTCAGACA TTCTGAGAA GAACATACAA GAAAGTCTTC CTCAAGAAAA AACCAAGTCG 720
 AGCCGAGTCT ATCTGACAC TTTGGCAGAG AGTATTGCA AACTGATTTT CCCAGAGTTT 780
 GAAACGCTGA ATGTGCACT TCAGAGACA TTGCAAAAGC AAAAAATAA AGAAAGCAGG 840
 AAATCTTTGG AAAGAGAAGA CTTTGA AAAA ACAATTGCAG AGCAAGCAGT GCAGCAGAGT 900
 CCAGTGGAGT TATCAAGAAA TCTTTGGTG AAGAGGTTT TAAATATGT TACGAGGAAG 960
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 CCTCTGAAA CAGAGCAGCC ATTGCCAAGA AGCAGGAAAA AGGGGCAGCT TGAGGACGCC 1080
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 AGAACCACT CCTGATTCT TCCCGGCATC ATAAAGGCAG CTGCTCAGT ATTATATGAA 1200
 ACGGAAGTGG AAGTGTCTGT AATGCTTCCC TGCTTCCATA ATGATTGCAG CGAGTTTGTG 1260
 AATCAGCCCT ACTTGTGTGA CTCCGTTTAC ATGAAAAGCA CCAAGCCATC CCTGTCCCCC 1320
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 CATTTCATGT TTGACAAAGA TATGACAATT CTGCAATTG GCAATGGCAT CAGAAGGCTG 1440
 ATGAACAGGA GAGACTTTCA AGGAAAGCCT AATTTGAAT ACTTTGAAAT TCTGACTCCA 1500
 AAAATCAACC AGACCTTTAG CGGGATCATG ACTATGTTGA ATATGCAGTT TGTGTACGA 1560
 GTGAGGAGAT GGGCAAACTC TGTGAAGAAA TCTTCAAGGG TTATGGACCT CAAAGGCCAA 1620
 ATGATCTACA TTGTTGAATC CAGTGCAATC TTGTTTTGG GGTCAACCTG TGTGGACAGA 1680
 TTAGAAGATT TTACAGGACG AGGCTCTAC CTCTCAGACA TCCCAATCA CAATGCACTG 1740
 AGGGATGTGG TCTTAATAGG GGAACAAGCC CGAGCTCAAG ATGGCCTGAA GAAGAGGCTG 1800
 GGGAACTGAG AAGTACCTT TGAAGCAAGCC CACCAAGCCC TGGAGGAGGA GAAGAAAAAG 1860
 ACAGTAGACC TTCTGTGCTC CATATTCCC TGTGAGGTTG CTCAGCAGCT GTGGCAAGGG 1920
 CAAGTTGTGC AAGCAAGAA GTTCAGTAAT GTCACCATGC TCTTCTCAGA CATCGTTGG 1980
 TTCACTGCCA TGTGCTCCCA GTGCTCACCG CTGAGGTCA TCACCATGCT CAATGCACTG 2040
 TACACTCGCT TCGACAGCA GTGTGGAGAG CTGGATGTCT ACAAGGTGGA GACCAATTGC 2100
 ATGCTATTG TGTGGCTTGG GGGATTACAC AAAGAGAGTG ATACTCATGC GTTTCAGATA 2160
 GGCCTGATGG CCCTGAAGAT GATGGAGCTC TGTATGAAG TTATGTCTCC CATGGAGAA 2220
 CCTATCAAGA TGCGAATTGG ACTGCACCTT GGATCAGTTT TTGCTGGCGT CGTTGGAGTT 2280
 AAAATGCCCC GTTACTGTCT TTTTGAAGAC AATGTCACT TGGTAACAA ATTTGAGTCC 2340
 TGCAGTGTAC CAGGAAAAAT CAATGTCAAG CCAACAACCT ACAGATTACT CAAAGACTGT 2400
 CCGTGTATTG TGTATTCCCC TCGATCAAGG GAGGAACCTC CACCAAACTT CCTAGTGAA 2460
 ATCCCCGGA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAAACTC AAAACCATGC 2520

TTCCAAAAGA AAGATGTGGA AGATGCAAGC CAATTTTTTA GGCAAAGCAT CAGGAATAGA 2580
 TTAGCAACCT ATATACCTAT TTATAAGTCT TTGGGGTTTG ACTCATTGAA GATGTGTAGA 2640
 GCCTCTGAAA GCACCTTTAGG GATTGTAGAT GGCTAAACAAG CAGTATTAAG ATTTCAGGAG 2700
 CCAAGTCACA ATCTTTCTCC TGTTTAACAT GACAAAATGT ACTCACTTCA GTACTTCAGC 2760
 TCTTCAAGAA AAAAAAAAAA ACCTTAAAAA GCTACTTTTG TGGGAGTATT TCTATTATAT 2820
 AACCAGCACT TACTACCTGT ACTCAAAATT CAGCACCTTG TACATATATC AGATAATTGT 2880
 AGTCAATTGT ACAAACCTGAT GGAGTCACCT GCAATCTCAT ATCCTGGTGG AATGCCATGG 2940
 TTATTAAGT GTGTTTGTGA TAGTTGTCGT CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3000
 AAAA

SEQ ID NO:158 PFA3 Protein sequence
 Protein Accession #: NP_000847.1

1 11 21 31 41 51
 MFCTKLKDLK ITGECPSLL APGQVPNESS EEAAGSSESC KATVPICQDI PEKNIQESLP 60
 QRKTSRSRVY LHTLAESICK LIFPEFERLN VALQRTLAKH KIKESRKSLE REDFEKTAE 120
 QAVQSPVEL SKNLLVKRFL KYVTRKMKTS LGWLEAPLKI FKQLQYPSET EQPLFRSRKK 180
 GQLEDASILC LDKEDDFLHV YFFPKRTTS LILPGIIKAA AHVLYETEVE VSLMPPCFHN 240
 DCSEFVNQPY LLYSVHMKST KPSLSPSKPQ SSLVPTSLF CKTFPHFMF DKDMTILQFG 300
 NGIRRLMNRD DFQGGKPNFEY FEILTPKINQ TFGIMTMLN MQFVVRVRW DNSVKKSSRV 360
 MDLKGMIYI VESSAILFLG SPCVDRLEDF TGRGLYLSDI PIHNLARDV LIGEQAQAD 420
 GLKKRLGLKL ATLEQAQHAL EEEKKKTVDL LCSIFPCEVA QQLWQQQVVQ AKKFSNVTML 480
 FSDIVGFTAI CSQCSPLQVI TMLNLYTRF DQCGGELDVY KVETIAMPV WLGGHLKESD 540
 THAVQIALMA LKMMELSDV MSPHGEPIKM RIGLHSGSVF AGVVGVKMPR YCLFGNNVTL 600
 ANKFESCVP RKINVSPTTY RLLKDCPGFV FIPRSREELP PNFSEIPGI CHFLDAYQQG 660
 TNSKPCFKK DVEDASQFFR QSIRNRLATY IPIYKSLGFD SLKMCRASES TLGIVDG

SEQ ID NO:159 PFA1 DNA SEQUENCE

Nucleic Acid Accession #: NM_004362
 Coding sequence: 102-1934 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGCGGGCGGG ACTGGTCTGA AGAGACGCGG GGACAAAGTG GCAACGACTT GGACATCTGA 60
 GCTGTCACTG CCGAAACAG GCCGCAAGAG AGATAATCAA TATGCAATTTT CAAGCCTTTT 120
 GGCTATGTTT GGGTCTCTG TCTATCTCAA TTAATGCAGA ATTTATGGAT GATGATGTTG 180
 AGACGGAAGA CTTTGAAGAA AATTCAGAAG AAATTGATGT TAATGAAAGT GAACTTTCCT 240
 CAGAGATTAA ATATAAGACA CCTCAACCTA TAGGAGAAGT ATATTTTGCA GAAACTTTTG 300
 ATAGTGAAGG GTTGGCTGGA TGGGTCTTAT CAAAAGCAAA GAAAGATGAC ATGGATGAGG 360
 AAATTTCAAT ATACGATGGA AGATGGGAAA TTGAAGAGTT GAAAGAAAAC CAGGTACCTG 420
 GTGACAGAGG ACTGGTATTA AAATCTAGAG CAAAGCATCA TGCAATATCT GCTGTATTAG 480
 CAAACCAATT CATTTTGTCT GATAAACCTT TGATAGTTCA ATATGAAGTA AATTTTCAAG 540
 ATGGTATTGA TTGTGGAGGT GCATACATTA AACTCCTAGC AGACACTGAT GATTTGATTG 600
 TGGAAAACTT TTATGATAAA ACATCCTATA TCATTATGTT TGGACCAGAT AAATGTGGAG 660
 AAGATTATAA ACTTCATTTT ATCTTCAGAC ATAAACATCC CAAAACCTGGA GTTTTCGAAG 720
 AGAAACATGC CAAACCTCCA GATGTAGACC TTAATAAGTT CTTTACAGAC AGGAAGACTC 780
 ATCTTTATAC CCTTGTGATG AATCCAGATG ACACATTGGA GGTGTGATGT GATCAACAG 840
 TTGTAACAAA AGGAAGCCTC CTAGAGGATG TGGTTCCTCC TATCAAACTT CCAAAGAAA 900
 TTGAAGATCC CAATGATAAA AAACCTGAGG AATGGGATGA AAGAGCAAAA ATTCCTGATC 960
 CTCTGCCGT CAAACCAGAA GACTGGGATG AAAGTGAAAC TGCCCAATAA GAAGATTCAA 1020
 GTGTGTTTAA ACCTGCTGGC TGGCTTGATG ATGAACCAAA ATTTATCCCT GATCCTAATG 1080
 CTGAAAAACC TGATGACTGG AATGAAGACA CGGATGGAGA ATGGGAGGCA CCTCAGATTG 1140
 TTAATCCAGC ATGTCCGATT GGGTGTGGTG AGTGGAAACC TCCCATGATA GATAACCCAA 1200
 AATACAAAGG AGTATGGAGA CCTCCACTGG TCGATAATCC TAACATCAG GGAATCTGGA 1260
 GTCTCGAAA AATTCCTAAT CCAGATTATT TCGAAGATGA TCATCCATTT CTTCGACTT 1320
 CTTTCAGTGC TCTTGGTTTA GAGCTTGGT CTATGACCTC TGATATCTAC TTGATAATT 1380
 TTATTATCTG TTGCGAAAAG GAAGTAGCAG ATCACTGGGC TGCAGATGTT TGGAGATGGA 1440
 AAATAATGAT AGCAAATGCT AATAAGCCTG GTGTATTAAA ACAGTTAATG GCAGCTGCTG 1500
 AAGGGCACCT ATGGCTTTGG TTGATTTATC TTGTGACAGC AGGAGTGCCA ATAGCATTAA 1560
 TTACTTCATT TTGTGGCCA AGAAAAAGTA AGAAAAACA TAAAGATACA GAGTATAAAA 1620
 AAACCGACAT ATGTATACCA CAAACAAAAG GAGTACTAGA GCAAGAAGAA AAGGAAGAGA 1680
 AAGCAGCCTT GGAACCAACA ATGGACCTGG AAGAGGAAAA AAAGCAAAAT GATGGTGAAA 1740
 TGCTTGAAAA AGAAGAGGAA AGTGAACCTG AGGAAAAGAG TGAAGAAGAA ATTGAAATCA 1800
 TAGAAGGGCA AGAAGAAAGT AATCAATCAA ATAAGTCTGG GTCAGAGGAT GAGATGAAAG 1860
 AAGCAGATGA GAGCACAGGA TCTGGAGATG GGCCGATAAA GTCAGTACGC AAAAGAAGAG 1920
 TACGAAAGGA CTAAACTAGA TGAATATT TTTAATTCCT GAGAGGATGT TTGGCATTGT 1980
 AAAAAATCAGC ATGCCAGACC TGAACCTTAA TCAGTCTGCA CATCCTGTTT CTAATATCTA 2040
 GCAACATTAT ATCTTTCAG ACAATTATTT TAGTCTCTCA TTTCCGAGGA AAAAGAAGCA 2100
 ACTTTGAAGT TACCTCATCT TTGAATTTAG AATAAAAGTG GCACATTACA TATCGGATCT 2160
 AAGAGATTAA TACCATTAGA AGTTACACAG TTTTAGTTGT TTGGAGATAG TTTTGGTTTG 2220
 TACAGAACAA AATAATATGT AGCAGCTTCA TTGCTATTGG AAAAAATCAG TATTGGAATT 2280
 TCCACTTAAA TGGCTATACA ACAATATAAC TGGTAGTTCT ATAATAAAAA TGAGCATATG 2340
 TTCTGTGTGT AAGAGCTAAA TGCAATAAAG TTTCTGTATG GTTGTGTTAT TCTATCAACA 2400
 ATTGAAAGTG TTGATATAGA CCAACATTTA CCTAGTTTGT GTCAAATTAT AGTTACAGTG 2460
 AGTTGTTTGC TTAATTTATA GATTCTTTTA AGGACATGCC TTGTCATAA AATCACTGGA 2520

TTATATTGCA GCATATTTTA CATTTGAATA CAAGGATAAT GGGTTTTATC AAAACAAAAT 2580
 GATGTACAGA TTTTITTTTCA AGTTTTTATA GTTGCTTTAT GCCAGAGTGG TTTACCCCAT 2640
 TCACAAAATT TCTTATGCAT ACATTGCTAT TGAAAAATAA ATTTAAATAT TTTTTCATCC 2700
 TGAAAAAAA

SEQ ID NO:160 PFA1 Protein sequence:
 Protein Accession #: NP_004353.1

1 11 21 31 41 51
 | | | | |
 MHFQAFWLCL GLLFISINAE FMDDDVETED FEENSEEIDV NESELSSEIK YKTPQPIGEV 60
 YFAETFDSEGR LAGWVLSKAK KDDMDDEEISI YDGRWEIEEL KENQVPGDRG LVLKSRKHH 120
 AISAVLAKPF IFADKPLIVQ YEYVNFQDGD CGGAYIKLLA DTDDLLENF YDKTSYIMF 180
 GPDKCGEDYK LHFIFRHKHP KTGVFEEKHA KPPDVLKKF FTDRKTHLYT LVMNPDPTFE 240
 VLVDQTVVNN GSLLEDVPPP IKPPKEIEDP NDKKPEEWE RAKIPDPSAV KPEDWDESEP 300
 AQIEDSSVK PAGWLDDEPK FIPDPNAEKP DDWNEDTDGE WEAPQLNPA CRIGCGEWP 360
 PMIDNPKYKG VWRPPLVDNP NYQGIWSPRK IPNPDYFEDD HPFLTSTSA LGLELWSMTS 420
 DIYFDNFIC SEKEVADHWA ADGWRWKIMI ANANKPGVLK QLMAAAEHP WLWLYLVTA 480
 GVPALITSF CWPRKVKKKH KDTEYKKTDI CIPQTKGVLE QEEKEEKAAL EKPMDLSEEK 540
 KQNDGEMLEK EEESEPEEKS EEEIEIEQG EESNQSNKSG SEDEMKEADE STGSGDGP 600
 SVRKRRVRKD

SEQ ID NO:161 PEZ9 DNA SEQUENCE

Nucleic Acid Accession #: NM_005932
 Coding sequence: 75-2216 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 GCGGAGCGCG CGCTCCACG GAAAGCAGCA GGGCAGGGAT CTGCGTTGGA GGAAGGGACT 60
 GCTCTGGTGC TAGAATGCTG TGCCTCGGAA GGCTGGGCGG CTGGGAGGCC AGAGCAGCAG 120
 CTCTGCCGCC CGCCCGGCGG GGCCGGGAA GCCTCGAAGC CGGATCCGG GCCCGAAGGG 180
 TCAGCACCAG CTGGTCTCCC GTGGGCGCGG CCTTCAATGT CAAGCCCCAG GGCAGCCGCT 240
 TGGACCTGTT CGGCGAGCGG GCGCGTCTTT TTGGAGTTCC TGAGCTGAGT GCCCAGAAG 300
 GATTTCATAT TGCACAAGAA AAAGCCTTGA GAAAGACAGA ATTGCTGTG GACCGTGCA 360
 GTTCCACCCC ACCTGGGCCC CAGACCGTGC TGATCTTCGA TGAGCTCTCG GATTCTTAT 420
 GCAGAGTGGC CGACTGTGCT GATTITGTGA AAATCGCTCA CCCTGAGCCA GCATTACAG 480
 AAGCTGCGGA AGAAGCTGT AGAAGTATTG GCACCATGGT AGAGAAGTTG AACACAAATG 540
 TGGATTATA TCAAAAGTTG CAAAAATTAC TAGCTGATAA AAAACTTGTG GATTCCCTTG 600
 ATCCAGAAAC AAGGCGAGTG GCTGAACGTG TTATGTTTGA TTTTGAAAT AGTGGAAATCC 660
 ATCTAGACAA ACAAAGCGT AAAAGAGCAG TGGACCTCAA TGTTAAATC TTGGATTGTA 720
 GTAGTACATT TCTTATGGGA ACCAATTTC CCAACAAGAT TGAGAAGCAT CTCTTACCAG 780
 AACACATTCG TCGTAACCTT ACATCTGCTG GGGATCATAT CATAATTGAT GGTCTCCACG 840
 CAGAATCACC AGATGACTTG GTGCGAGAAG CTGCTTATAA AATTTTCTT TATCCCAATG 900
 CTGGTCAATT GAAATGTTTA GAAGAATTGC TCAGCAGCAG AGATCTTCTG GCAAAGTTGG 960
 TGGGGTATTC CACGTTTTCT CACAGGGCTC TCCAAGGAAC GATAGCTAAA AATCCAGAGA 1020
 CTGTCATGCA GTTCTTGAA AAACATCTG ACAAACCTTC TGAAAGAACT CTGAAAGATT 1080
 TTGAGATGAT ACAGGGGATG AAAATGAAAC TGAATGCTCA AAATTCGAA GTAATGCCCT 1140
 GGGACCCCCC TTACTACAGT GGTGTGATTC GTGCAGAAAG GTATAATATT GAGCCACGCC 1200
 TATATGCCCC GTTTTCTCT CTGGAGCAT GCATGGAAGG CTTGAATATT TTGCTTAA 1260
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 ATGTCGGAAA ACTGGCTGTT GTTCATGAAT CTGAAGGATT GTTGGGGTAC ATTACTGTG 1380
 ATTTTITICA GCGAGCAGAC AAACACATC AGGATTGCCA TTCACTATC CGTGGAGGCA 1440
 GACTAAAGGA AGATGGAGAC TATCAACTCC CACTGTGAGT TCTTATGCTG AATCTTCCCC 1500
 GTTCCTCAAG GAGTCTCCA ACTTGTCTAA CTCTGGCAT GATGGAAAT CTTTCCATG 1560
 AAATGGGACA TGCCATGCAT TCAATGCTAG GACGTACTCG TTACCAACAC GTCAGTGGGA 1620
 CCAGGTGCC TACTGATTTT GCTGAGGTTC CTCTATTCT GATGGAGTAC TTTGCAATG 1680
 ATATCGAGT AGTTAACCAA TTGCCAGAC ATTATCAGAC TGGACAGCCA CTGCCAAAA 1740
 ATATGGTGTC TCGTCTTTGT GAATCTAAAA AGGTTTGTGC TGCAGCTGAT ATGCAACTTC 1800
 AGGTCTTTA TGCCACTCTG GATCAAACTC ACCATGGGAA GCATCCCTG AGGAATTC 1860
 CCACAGACAT TCCTAAGGAA ACACAAGAGA AATCTATGG CCTACCATAT GTTCCAAATA 1920
 CTGCTTGCCA GCTGCGATTG AGCCACCTCG TGGGGTATGG TGCTAGATAT TACTCTTACC 1980
 TCATGTCCAG AGCGGTGCGC TCCATGGTIT GGAAGGAGTG TTTTCTACAG GATCCTTTCA 2040
 ACAGGGCTGC CGGGGAGCGC TATCGCAGGG AGATGCTGGC CCACGGTGA GGCAGGGAGC 2100
 CCATGCTCAT GGTGGAAGGT ATGCTTCAGA AGTGTCTTC TGTTGATGAC TTCGTAAGTG 2160
 CCCTCGTTTC CGACTTGGAT CTGGACTTCG AAACCTTCT CATGGATICT GAATAAAAGA 2220
 AACACTCTAC ACCTCTAATC AAGGTCATGT AGTAATGACT TTGTTATAAA TGCTACAGCT 2280
 GTGAGAGCTT GTTCTGATT GTTTCATTGT TCGCTCTGT AATTCTGAAA AACTTTAAAC 2340
 TGGTAGAATC TGAATAAAT AATTGTTTTT AATTAATAAA AAAAAAAAAA AA

SEQ ID NO:162 PEZ9 Protein sequence:
 Protein Accession #: NP_005923.1

1 11 21 31 41 51
 | | | | |
 MLCVGRLLGL GARAAALPPR RAGRGSLEAG IRARRVSTW SPVGAAFNVK PQGSRLDLFG 60
 ERARLFGVPE LSAPEGFHIA QEKALRKTEL LVDRACSTPP GPQTVLIFDE LSDSLCRVAD 120

5 LADFKIAHP EPAFREAAEE ACRSIGTMVE KLNTNVDLYQ SLQKLLADKK LVDSLDPETR 180
RVAELFMFDF EISGHIHLDKQ KRKRAVDLNV KILDLSSTFL MGTNFPNKIE KHLLPEHRR 240
NFTSAGDHII IDGLHAESPD DLVREAAKYI FLYPNAGQLK CLELLSSRD LLAKLVGYST 300
FSHRLAQGTI AKNPETVMQF LEKLSDKLSE RILKDFEMIR GMKMKLNAQN SEVMPWDPPY 360
YSGVIRAERY NIEPSLYCPF FSLGACMEGL NILLNRLLGI SLYAEQPAKG EVWSEVDYRKL 420
AVVHSEGLL GYIYCDFFQR ADKPHQDCHF TIRGGRLKED GDYQLPLVVL MLNLPSSRS 480
SPTLLTGMGM ENLFHEMGAH MHSMLGRTRY QHVTGTRCPT DFAEVSILM EYFANDYRVV 540
NQFARHYQTG QPLPKNMVSR LCESKKVCAA ADMQLQVFYA TLDQIYHGKH PLRNSTTDIL 600
10 KETQEKFYGL PYVPNTAWQL RFSLHVGYGA RYYSYLMSRA VASMVWKECF LQDPFNRAAG 660
ERYRREMLAH GGGREPLMV EGMLQKCPV DDFVSALVSD LDLDFTFLM DSE

SEQ ID NO:163 PEZ8 DNA SEQUENCE

15 Nucleic Acid Accession #: AF103907
Coding sequence: none (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
20 ACAGAAGAAA TAGCAAGTGC CGAGAAGCTG GCATCAGAAA AACAGAGGGG AGATTGTGT 60
GGCTGCAGCC GAGGGAGACC AGGAAGATCT GCATGGTGGG AAGGACCTGA TGATACAGAG 120
GAATTACAAC ACATATACTT AGTGTTCCTCA TGAACACCAA GATAAATAAG TGAAGAGCTA 180
GTCCGCTGTG AGTCTCTCTA GTGACACAGG GCTGGATCAC CATCGACGGC ACTTCTGTAG 240
25 TACTCAGTGC AGCAAAGAAA GACTACAGAC ATCTCAATGG CAGGGGTGAG AAATAAGAAA 300
GGCTGCTGAC TTACCATCT GAGGCCACAC ATCTGCTGAA ATGGAGATAA TTAACATCAC 360
TAGAAACAGC AAGATGACAA TATAATGTCT AAGTAGTGAC ATGTTTTTGC ACATTTCCAG 420
CCCCTTTAAA TATCCACACA CACAGGAAGC ACAAAGGAA GCACAGAGAT CCTCGGGAGA 480
AATGCCCGGC CGCCATCTTG GGTATCGAT GAGCCTCGCC CTGTGCCTGG TCCCGCTTGT 540
GAGGGAAGGA CATTAGAAAA TGAATTGATG TGTTCCTTAA AGGATGGGCA GGAAACAGA 600
30 TCCTGTTGTG GATATTATT TGAACGGGAT TACAGATTG AAATGAAGTC ACAAAGTGAG 660
CATTACCAAT GAGAGGAAAA CAGACGAGAA AATCTTGATG GCTTCACAAG ACATGCAACA 720
AACAAAATGG AATAGCTTGA TGACATGAGG CAGCCAAGCT GGGGAGGAGA TAACCACGGG 780
GCAGAGGGTC AGGATTCTGG CCTGCTGTC TAACTGTGC GTTCATAACC AAATCATTTC 840
ATATTICTAA CCTCAAAAAC AAAGCTGTTG TAATATCTGA TCTCTACGGT TCCTCTGGG 900
35 CCAACATTC TCATATATC CAGCCACACT CATTTTAAAT ATTTAGTTC CAGATCTGTA 960
CTGTGACCTT TCTACACTGT AGAATAACAT TACTCATTT GTTCAAAGAC CCTTCGTGTT 1020
GCTGCTAAT ATGACTGTGA CTGTTTTTCC TAAGGAGTGT TCTGGCCAG GGGATCTGTG 1080
AACAGGCTGG GAAGCATCTC AAGATCTTTC CAGGGTTATA CTACTAGCA CACAGCATGA 1140
TCATTACGGA GTGAATTATC TAATCAACAT CATCTCAGT GTCTTTGGCC ATACTGAAAT 1200
40 TCATTTCCTA CTTTGTGCC CATCTCAAG ACCTCAAAAT GTCATTCCAT TAATATCACA 1260
GGATTAACCT TTTTITTTAA CCTGGAAGAA TTCAATGTTA CATGCAGCTA TGGGAATTTA 1320
ATTACATATT TTGTTTCTCA GTGCAAAGAT GACTAAGTCC TTATCCCTC CCTTTGTGTT 1380
GATTTTTTTT CCAGTATAAA GTTAAAAATG TTAGCCTTGT ACTGAGGCTG TATACAGCAC 1440
AGCCTCTCCC CATCCCTCCA GCCTTATCTG TCATCACCAT CAACCCCTCC CATACCACT 1500
45 AAACAAAATC TAACCTGTAA TTCCTTGAAC ATGTCAGGAC ATACATTATT CCTTCTGCCT 1560
GAGAAAGCTC TCCTGTCTCT TTAATCTAG AATGATGTAA AGTTTGAAT AAGTTGACTA 1620
TCTTACTTCA TCAAAAGAA GGCACATAT GAGATTATC ATCAGATGAG ACAGCAAAATA 1680
CTAAAGTGTG AATTGTGATA TAAGAGTTTA GATAAATATA TGAATGCAA GAGCCACAGA 1740
50 GGGAAAGTTT ATGGGGCAGC TTGTAAAGCC TGGGATGTGA AGCAAAGGCA GGGAACTCA 1800
TAGTATCTTA TATAATATC TTCATTCTC TATCTCTATC ACAATATCCA ACAAGCTTTT 1860
CACAGAATTC ATGCAGTGA AATCCCAAAA GGTAACCTTT ATCCATTCCA TGGTGAGTGC 1920
GCTTTAGAAAT TTGTGCAAAAT CATACTGGTC ACTTATCTCA ACTTTGAGAT GTGTTGTGCC 1980
TTGTAGTTAA TTGAAAGAAA TAGGGCACTC TTGTGAGCCA CTTAGGGTT CACTCTGGC 2040
AATAAAGAA TTAACAAGAG CTACTCAGGA CCAAGTTGTA AGAGCTCTGT GTGTGTGTGT 2100
55 GTGTGTGTGT GAGTGTACAT GCCAAAGTGT GCCTCTCTCT CTGACCCAT TATTTCAGAC 2160
TTAAACAAG CATGTTTTC AATGGCACTA TGAGCTGCCA ATGATGTATC ACCACCATAT 2220
CTCATIATTC TCCAGTAAAT GTGATAATA TGTCACTGT TAACATAAAA AAAGTTTGAC 2280
TTCACAAAAG CAGCTGGAAA TGGACAACCA CAATATGCAT AAATCTAACT CCTACCATCA 2340
60 GCTACACACT GCTTGACATA TATGTTAGA AGCACTCGC ATTTGTGGGT TCTCTAAGC 2400
AAAATACTTG CATTAGGTCT CAGCTGGGGC TGTGCATCAG GCGGTTGAG AAATATTCAA 2460
TCTCAGCAG AAGCCAGAAT TTGAATTCCT TCATCTTTA GGAATCATT ACCAGGTTTG 2520
GAGAGGATTC AGACAGCTCA GGTGCTTICA CTAATGTCTC TGAACCTCTG TCCTCTTTG 2580
TGTTTCATGA TAGTCCAATA AATAATGTTA TCTTGAAC TATGCTCATA GGAGAGAATA 2640
65 TAAGAACTCT GAGTGATATC AACATTAGGG ATTCAAAGAA ATATTAGATT TAAGCTCACA 2700
CTGGTCAAAA GGAACCAAGA TACAAAGAAC TCTGAGCTGT CATGCTGCCC ATCTCTGTGA 2760
GCCACAACCA ACAGCAGGAC CCAACGCATG TCTGAGATCC TAAATCAAG GAAACCAAGT 2820
TCATGAGTTC AATCTCTCTA TTATGGATGC TAGCTTCTGG CCATCTCTGG CTCTCTCTT 2880
GACACATATT AGCTTCTAGC CTTTGCTTCC ACGACTTTTA TCTTTTCTCC AACACATCGC 2940
70 TTACCAATCC TCTCTCTGCT CTGTGCTTT GGACTTCCCC ACAAGAAATT CAACGACTCT 3000
CAAGTCTTTT CTTCATCTCC CACCACTAAC CTGAATGCC AGACCCCTAT TTTTATTAAT 3060
TTCCAATAGA TGCTGCTAT GGGCTATATT GCTTTAGATG AACATTAGAT ATTTAAAGCT 3120
CAAGAGGTTT AAAATCCAAC TCATTATCTT CTCTTCTTT CACCTCCCTG CTCTCTCTCC 3180
TATATTACTG ATTGCACTGA ACAGCATGGT CCCCATTGTA GCCATGCAA TGAGAAACCC 3240
75 ACTGGCTCTT TGTGTACAT GCATGCAAGA CTGCTGAAGC CAGAAGGATG ACTGATTACG 3300
CCTCATGTTT GGAGGGGACC ACTCTGGGC CTTCGTGATT GTCAGGAGCA AGACCTGAGA 3360
TGCTCCCTGC CTTCAGGTTC CTCTGCATCT CCCCCTTCTA ATGAAGATCC ATAGAATTTG 3420
CTACATTGTA GAATTCCTAAT TAGGAACTCA CATGTTTAT CTGCCCTATC AATTTTTTAA 3480
ACTTGCTGAA AATTAAGTTT TTCAAAATC TGTCTGTGA AATTACTTTT TCTTACAGTG 3540
TCTTGGCATA CTATATCAAC TTTGATTCTT TGTTACAAC TTTCTTACT TTTTATCACC 3600

AAAGTGGCTT TTATTCTCTT TATTATTATT ATTTTCTTTT ACTACTATAT TACGTTGTGA 3660
 TTATTTTGTG CTCTATAGTA TCAATTATT TGAATTAGTT TCAATTTATT TTTATTGCTG 3720
 ACTTTTAAAA TAAGTGATTC GGGGGGTGGG AGAACAGGGG AGGGAGAGCA TTAGGACAAA 3780
 TACCTAATGC ATGTGGGACT TAAACCTAG ATGATGGGTT GATAGGTGCA GCAAACCACT 3840
 ATGGCACAG TATACCTGTG TAAACAACT ACACATTCTG CACATGTATC CCAGAACGTA 3900
 AAGTAAAAAT TAAAAAAG TGA

PEZ6 Protein sequence:

Protein Accession #: none

SEQ ID NO:164 PEZ6 DNA SEQUENCE

Nucleic Acid Accession #: AB028945

Coding sequence: 1-3765 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 ATGATGATGA ACGTCCCGG CGGAGGAGCG GCCGCGGTGA TGATGACGGG CTACAATAAT 60
 GGTGCGCTGT CCCGGAATTC TCTCTACAGT GACTGCATTA TTGAGGAGAA GACGGTGGTC 120
 CTGCAGAAAA AAGACAATGA GGGCTTTGGA TTCGTGCTTC GAGGGGCCAA AGCTGACACA 180
 CCCATTGAAG AATTACACAC AACACCGGCT TTCCAGCCCT TACAGTACCT GGAGTCCGTG 240
 GATGAAGGTG GGGTGGCGTG GCAAGCCGGA CTAAGGACCG GGGACTTCTT GATTGAGGTT 300
 AACAATGAGA ATGTTGTCAA AGTCGGCCAC AGGCAGGTGG TGAACATGAT CCGGCAGGGA 360
 GGGAAATCAC TGGTCTTAA GGTGGTCACG GTGACCAGGA ATCTGGACCC CGACGACACC 420
 GCCAGGAAGA AAGTCCCCC GCCTCCAAAG CGGGCACCAG CCACAGCCCT CACCTGCGC 480
 TCCAAGTCCA TGACCTCGGA GCTGGAGGAG CTCGTGGATA AAGATAAACG CGAGGAGATA 540
 GTCCCGGCTT CCAAGCCCTC CCGCGCTGCT GAGAACATGG CTGTGGAACC GAGGGTGGCG 600
 ACCATCAAGC AGCGGCCAGC CAGCCGGTGC TTCCCGCGCG GCTCAGACAT GAACTCTGTG 660
 TACGAACGCC ACGGAATGCG CGTGATGACG CCCACTGTTC CTGGGAGCCC AAAAGCCCCG 720
 TTCTGGGCA TCCCTCGAGG TACGATGCGA AGGCAGAAAT CAATAGACAG CAGAATCTTT 780
 CTATCAGGAA TAACAGAGGA AGAGCGGCGA TTTCTGGCTC CTCCAATGCT GAACTTCACC 840
 AGAAGCTGT CCAATGCGGA CACCTCTGAG GACATCCCC CTCCACCGCA GTCTGTGCCC 900
 CCGTCCCCAC CACCACTTTC CCAACCACT TACAAGTCCC CCAAGTCCC AACTCCAAGA 960
 GTCTACGGGA CGATTAAGCC TGCCTCAAT CAGAATTCTG CCGCCAAGGT GTCCCCGCC 1020
 ACCAGGTCG ACACGTGGC CACCATGATG AGGGAGAAGG GGATGTACTT CAGGAGAGAG 1080
 CTGGACCGCT ACTCCTTGA CTCTGAAGAC CTCTACAGTC GGAATGCCGG CCCGCAAGCC 1140
 AACTTCCGCA ACAAGAGAGG CCAGATGCCA GAAAACCCAT ACTCAGAGGT GGGGAAGATC 1200
 GCCAGCAAAG CCGTCTACGT CCCCGCCAAG CCGCCAGGC GGAAGGGGAT GCTGTTGAAG 1260
 CAGTCCAACG TGGAGGACAG CCCCAGAGAG ACGTGCTCCA TCCCTATCCC GACCATCATC 1320
 GTGAAGGAGC CGTCCACCCAG CAGCAGCGGC AAGAGCAGCC AGGGCAGCAG CATGGAGATC 1380
 GACCCCAAGG CCCCAGGACC ACCGAGCCAG CTGCGGCTG ACGAAAGCCT GACCGTCAGC 1440
 AGCCCTTTG CCGCCGCCAT CGCCGAGGCC GTCCGCGACC GTGAGAAGCG GCTGGAAGCC 1500
 AGGAGGAACT CCCCAGCCTT CCTCTCCACA GACCTGGGGG ATGAGGATGT GGGCCTGGGG 1560
 CCACCCGCCC CCAGGACGCG GCCCTCCATG TTCCCGGAGG AGGGGGATT TGTCTACGAG 1620
 GACAGCGCTG ACAGAGCTGT ATCCCCCATG CCGAGTGCCA CGCCAGGGA GCCGAAAAAC 1680
 CATTTCTGGG GTGGCGCCGA GGCCAAGTCT CCGGGTGAGG CTGGGAGGCC GCTGAATTCC 1740
 ACGTCCAAAG CCCAGGGGCC CGAGAGCAGC CCAGCAGTGC CTTCCGAGAG CAGCGGCACA 1800
 GCCGGCCCCG GGAATTATGT CCACCACTC ACAGGGCGGC TGCTTGATCC CAGCTCCCCG 1860
 CTGCGCCTGG CACTCTCCGC AAGGGACCGA GCCATGAAGG AGTCTCAACA GGGACCCAAA 1920
 GGGGAGGCC CCAAGGCCGA CCTCAACAAA CCTCTTTACA TTGATACCAA AATGCGGCC 1980
 AGCCTGGAT CCGGCTTCCC TACGGTACC AGGCAGAAAC CCGGGGAGCC CCGTAGGCGG 2040
 CAGGAGACCG AGAACAGTA CGAGACCGAC CTGGGCCGAG ACCGGAAAGG CGATGACAAG 2100
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 CTGGCATCCG TGGACTTGGG TGAGGATTTT ATTTTACAG AGCCATTGCC TCCTCCCCCTG 2460
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 GACTTAGTGA AGCAGAAGAA AAGCGACACC CCTCAGTCCC CTTGTTGAA CTCCAGCCAA 2580
 CCAACCAACT CTGCAGACAG CAAGAAGCCA GCCAGTCTT CAAACTGTCT GCCTGCCTCA 2640
 TTCTGCGCAC CCCGTGAAAG CTTTGACGCC GTCGCCGACT CTGGGATCGA GGAGGTGGAC 2700
 AGCCGGAGTA GCAGCGACCA CCACCTCGAG ACGACCAACA CTATCTCCAC CGTGTCTAGC 2760
 ATCTCCACCC TGTCTTCCGA AGGTGGAGAG AATGTGGACA CCTGCACAGT CTATGCAGAT 2820
 GGGCAAGCAT TTATGGTGA CAAACCCCA GTACCTCTTA AGCCAAAAAT AAGGCCCATC 2880
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 10 GCCTTTCCCT AGTCTGTGG CCTCTCAGAG GACACCTGAT GCTCACTGC CCCTCTTCT 4260
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 15 CCAAGCAGAT GTCACATGGA GTTAGTCAA GCACAAAGTC ACGATTCCAC AATGGAGGGG 4560
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 40 TGCTGAGCT GCCCATAT TTAGAAAAAT TAAAAATGGT GGTITGGCCA TTAATTTGTC 6060
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 60 AGGTGTGGT TGTGATGCA AACAACAGT GAACACTGTC TGAATTAAC AAAAAGCTGC 7260
 CCGACTTGCA ATCTAATGTA GATTATCTA GGCAATTGGG CCAGCTCTGC CTCTCTAAAA 7320
 CTGACCAGAA AAATCTCTCT CATCGAGTAA ACAGGCTCCT GTCAGTGC TAATCTGCCT 7380
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 65 TTCTCTTTG TCTGGGTGG AAGCAGCGGT GCGCGGAGG GCCAGCCAGA TCCGGACCTT 7560
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 70 AAAACTGTT GTCTTAGTT CCTAAAGTT CTCTACTTT GGCACATTCC CCAAGTTGAGC 7860
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 75 TGGCGAAGTG GAATGTGTT CTGTATTGT AGACAACAT GTACCCATGC AAGTAGGTGA 8160
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 GTGGGGAATC AGAGAATTC CAAACTTGT TCTCAGACT CCGCAGATCT CATCACTTTG 8280
 ATTTCTAATC CATGCTGAT TGGTGATTT GTTTATCGTT CCGTAACTT GTTCTACATT 8340
 CCACAGTCT TACCCTTTTA TGTCAAAT TACAACAAT CCGTGCATT GATTCCACTC 8400
 TGGAACTCTT TTTTCATGCC AATTTGAAA TTTTAATACG AGCCTTCAA TAAACACAGA 8460

AAAGAAAAAA AAAAAAAAAA AAAAAAAAAA

5 SEQ ID NO:165 PEZ6 Protein sequence:
Protein Accession #: BAA82974.1

1 11 21 31 41 51
10 MMMNVPGGGA AAVMMTGYYN GRCPRNSLYS DCIIIEKTVV LQKKDNEGFG FVLRGAKADT 60
PIEEFTPTPA FPALQYLESV DEGGVAWQAG LRTGDFLIEV NNENVVKVGH RQVVMNIRQG 120
GNHLVLKVVT VTRNLDPPDT ARKKAPPPPK RAPTTALTTLR SKSMTSELEE LVDKDKPEEI 180
VPASKPSRAA ENMAVEPRVA TIKQRPSSRC FPAGSDMNSV YERQGIAMVT PTVPGSPKAP 240
15 FLGIPRGTM RQKSIDSRIF LSGITEERQ FLAPPMLKFT RLSMPDTS DIPPPQSV 300
PSPPSPPTT YNCPKSPYPR VYGTIKPAFN QNSAAKVSPA TRSDTVATMM REKGMFYFRE 360
LDYSLDSED LYSRNAGPQA NFRNKRQMP ENPYSEVGKI ASKAVYVPAK PARRKGMLVK 420
QSNVEDSPK TCSIPTTII VKEPSTSSG KSSQGSMEI DPQAPPPSQ LRPDES LTVS 480
SPFAAIIAGA VRDREKRLEA RRNSPAFLST DLGDEDVGLG PPAPRTRPSM FPEGDFADE 540
20 DSAEQLSSPM PSATPREPEN HFVGGAEASA PGEAGRPLNS TSKAQGPSS PAVPASSGT 600
AGPGNYVHPL TGRLLDPSSP LALALSARDR AMKESQQGPK GEAPKADLNK PLYIDTKMRP 660
SLDAGFTVT RQNTGRPLRR QETENKYETD LGRDRKGDDK KNMLIDIMDT SQKSGAGLLM 720
VHTVDATKLD NALQEEDEKA EVEMKPDSSP SEVPEGVSET EGALQISAAP EPTTVPGRTI 780
VAVGSMEEAV ILFRIPIPPP LASVDLDEDF IFTEPLPPPL EFANSFDIPD DRAASVPALS 840
25 DLVKQKKSDT PQSPSLNSQ PTNSADSKKP ASLSNCLPAS FLPPSFDA VADSGIEVD 900
SRSSSDHILE TTSTSTYSS ISTLSSEGE NVDTCVYAD GQAFMVDKPP VPPKPKMKPI 960
IHKSNALYQD ALVEEDVDSEF VIPIPPPPP PGSAQPGMAK VLQPRTSKLW GDVTEIKSPI 1020
LSGPKANVS ELNSILQMN REKLAKPEG LSPMGAKSA SLAPRSPEIM STISGTRSTT 1080
VTFVTRPGTS QPITLQSRPP DYESRTSGTR RAPSPVVSPT EMNKETLPAP LSAATASPS 1140
30 ALSDVFLSPS QPPSGDLFGL NPAGRSRSPS PSILQQPISN KPFTTKPVHL WTKPDVADWL 1200
ESLNLGEHKE AFMDNEIDGS HLPNLQKEDL IDLGVTVRVGH RMNIERALKQ LLDR

SEQ ID NO:166 PEZ4 DNA SEQUENCE

35 Nucleic Acid Accession #: NM_000024
Coding sequence: 220-1461 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
40 ACTGCGAAGC GGCTTCTTCA GAGCACGGGC TGGAACTGGC AGGCACCGCG AGCCCTAGC 60
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GAGGCTTCCA GCGTCCGCT CGCGCCCGC AGAGCCCGC CGTGGTCCG CCCGCTGAGG 180
CGCCCCAGC CAGTGCCTT ACCTGCCAGA CTGCGCGCCA TGGGGCAACC CGGGAACGGC 240
AGCGCTTCT TGCTGGCACC CAATAGAAGC CATGCGCCGG ACCACGACGT CACGCAGCAA 300
45 AGGGACGAGG TGTTGGTGGT GGGCATGGGC ATCGTCAATG CTCTCATGT CTTGGCCATC 360
GTGTTTGGA ATGTGCTGGT CATCACAGCC ATTGCCAAGT TOGAGCGTCT GCAGACGGTC 420
ACCAACTACT TCATCACTTC ACTGGCCTGT GCTGATCTGG TCATGGGCTT GGCAGTGGTG 480
CCCTTTGGG CCGCCCATAT TCTATGAAA ATGTGGACTT TTGGCACTT CTGGTGCAG 540
TITTTGACTT CCAATGATGT GCTGTGCGTC ACGGCCAGCA TTGAGACCCT GTGCGTGATC 600
GCAGTGGATC GCTACTTTGC CATTACTTCA CCTTCAAGT ACCAGAGCCT GCTGACCAAG 660
50 AATAAGCCCC GGGTATCAT TCTGATGGTG TGGATTGTG CAGGCCCTAC CTCTTCTTG 720
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55 AGGCAGTCC AGAAGATTGA CAAATCTGAG GGCCGCTTC ATGTCCAGAA CCTAGCCAG 960
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GAGCACAAG CCCTCAAGAC GTTAGGCATC ATCATGGGCA CTTTCAACCT CTGCTGGCTG 1080
CCCTTCTTCA TCGTTAATAT TGTGATGTG ATCCAGGATA ACCTCATCCG TAAGGAAGTT 1140
TACATCTCC TAAATTTGAT AGGCTATGTC AATTCTGGT TCAATCCCT TATCTACTGC 1200
60 CGGAGCCAG ATTTCAGGAT TGCCTTCCAG GAGCTTCTGT GCCTGCCAG GTCTTCTTG 1260
AAGGCCTATG GGAATGGCTA CTCCAGCAAC GGCAACACAG GGGAGCAGAG TGGATATCAC 1320
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65 AGAACACTAA ACAGACTATT TAACTTGAGG GTAATAAACT TAGAATAAAA TTGTAAAAAT 1560
TGATAGAGA TATGCAGAAG GAAGGGCATC CTCTGCCCTT TTTTATTTT TTAAGCTGTA 1620
AAAAGAGAGA AAACCTATTT GAGTGATTAT TTGTTATTTG TACAGTTCAG TTCCTCTTTG 1680
CATGGAATTT GTAAGTTTAT GTCTAAAGAG CTTAGTCTC AGAGGACCTG AGTCTGCTAT 1740
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70 TGCTGGTAAT TTGATCTGA AGGAGATTTT CCTTCTACA CCCTGGACT TGAGGATTTT 1860
GAGTATCTCG GACCTTTCAG CTGTGAACAT GGACTCTTC CCCACTCTC TTATTGTCTC 1920
ACACGGGTA TTTTAGGCAG GGATTGAGG AGCAGCTTCA GTTGTTTTC CGAGCAAAGG 1980
TCTAAAGTTT ACAGTAAATA AAATGTTTGA CCATG

75 SEQ ID NO:167 PEZ4 Protein sequence:
Protein Accession #: NP_000015.1

1 11 21 31 41 51

5 MGQPGNGSAF LLAPNRSHAP DHDVTQQRDE VVVVGMGIVM SLVLAIVFG NVLVITALAK 60
 FERLQTVINY FITSLACADL VMGLAVVPPG AAHILMKMWT FGNFWCEFMT SIDVLCVTAS 120
 IETLCVIAVD RYFAITSPFK YQSLLTKNKA RVILMVWIV SGLTSFLPIQ MHWYRATHQE 180
 AINCYANETC CDFFTNQAYA IASSIVSFYV PLVIMVFVYS RVFQEAQRQL QKIDKSEGRF 240
 HVQNLSQVEQ DGRTHGLRR SSKFCLKEHK ALKTLGIIMG TFLCWLPPF IVNIVHVIQD 300
 NLIRKEYIIL LNWIGYVNSG FNPLYCRSP DFRIAFQELL CLRRSSLKAY GNGYSSNGNT 360
 GEQSGYHVEQ EKENKLLCED LPGTEDFVGH QGTVPDND SQGRNCSTND SLL

10

Nucleic Acid Accession #: NM_004457
 Coding sequence: 143-2305 (underlined sequences correspond to start and stop codons)

15

1 11 21 31 41 51

20 GAATTCGTTG TTGGGAAGGA CTGGGGAAC AGCTGTAAC¹ TTTGCCACCC TCAGAAGCTG 60
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 GAAACCTTGC TTGTGTGATA CATAGTAAGT CTTTCACTT ATTACTGCTT GCCTGTGTTT 3600

ATATCTGGAT TATCAAAAGC AATAGTGCAC CAATTAAGAT GTGCTCAAAT CAGGACTTAA 3660
 ATCATAGGCA CCACATTTT CATGTCAGAC TAGTTACTTT GTTGATICTC AGTTACTGTA 3720
 GGCATCAAAA GGCAAAAATC A

5

SEQ ID NO:169 PEZ1 Protein sequence:
 Protein Accession #: NP_004448.1

1 11 21 31 41 51
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 NSKPDSAYRS VNSLDGLASV LYPGCDTLDK VFTYAKNKFK NKRLLGTRV LNEEDEVQPN 120
 GKIFKKVILG QYNWLSYEDV FVRAFNFGNG LQMLGQKPKT NIAIFCETRA EWMIAAQACF 180
 MYNQFLVLTLY ATLGGAIVH ALNETEVTNI ITSKEQLQTK LKDIVSLVPR LRHIITVDGK 240
 15 PPTWSDFFPKG IIVHTMAAVE ALGAKASMEN QPHSKPLPSD IAVIMYTSGS TGLPKGVMS 300
 HSNHAGITG MAERIPELGE EDVYIGYLP L AHVLELSAEL VCLSHGCRIG YSSPQTLADQ 360
 SSKIKKGSKG DTSMLKPTLM AAVPEIMDRI YKNVMNKVSE MSSFQRNLF I LAYNYKMEQI 420
 SKGRNTPLCD SFVRKVRSL LGGNIRLLLC GGAPLSATTQ RFMNICFCPP VGGYGLTES 480
 20 AGAGTISEVW DYNTGRVGP LVCCEIKLN WEEGGYFNTD KPHPRGEIL GGQSVTMGY 540
 KNEAKTKADF SEDENQQRWL CTGDIGEFEP DGCLKIIDRK KDLVKLQAGE YVSLGKVEAA 600
 LKNLPLVDNI CAYANSYHSY VIGFVVPNQK ELTELARKKG LKGTWHEELN SCSEMENEVLK 660
 VLSEAAISAS LEKFEIPVKI RLSPEPWTFE TGLVTDAPFL KRKELKTHYQ ADIERMYGRK

25

SEQ ID NO:170 PCQ7 DNA SEQUENCE
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 30 | | | | |
 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GCGCGCTGTG 60
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 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180
 35 GTGTGACGGG CTGCGTGAAT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
 GTCGAAATGT GGCCCAACCT TCTTCCCTCG TGCCAGCGGC ATCCATTGCA TCATTGGTCG 300
 CTTCGGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
 AAACCCCTCTG CTTCGTCCA CCGCCCGCTA CCACTGCAAG AACGGCTCT GTATTGACAA 420
 GAGCTTCATC TGGCATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
 40 AAGTTCTCAA GAACCCGCGA GTGGCCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
 TTACCCCGCA ATCACCATATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
 CTGCTGGAGA CTGCTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
 GCACCCGGCTG CAGCACCCCTG TGCTGCTGTC CCGCTCGGTG GTCTGGGACC ACCCCACCA 720
 CTGCAACGCT ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
 45 GAATGCGTGC GAAGTAGGCT CCCCACCCCTC CTACTCCGAG GCGTTGCTGG ACCAGAGGCC 840
 TGGCTGGTAT GACCTTCTCT CACCGCCCTA CTCCTCTGAC ACGGAATCTC TGAACCAAGC 900
 CGACCTGCCC CCTGACCCCT CCGGTCGCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
 CAGCAGCCCTG CTGAGCGTGG AAGACACAGC CCACAGCCCG GGGCAGCCCT GCCCCACGGA 1020
 GGGCACTGCT GAGCCAGGCG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
 50 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTCCCATTC TAACAATTG 1140
 TGCTCATGGG AAGCTCTTTA AGCACCCTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
 AACTATCTCT TCATTCCCTCT CCTCCCCAG ACTTCAGAGA GTTTTCTTCT GCGTCTCAGT 1260
 TGACATGATC TGTGTGCGCT CTTCCTGTCG AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320
 CACCCCTATT TTTCACATTA TTCTGTCTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
 55 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
 CGCTGGAGCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAATTC CCATTTGAGC 1560
 ATCAAAACCT GCTTTGCACA ATCTATTATT ATGCCCCCG TFCAGCAGAG TCAGTGGCCA 1620
 AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTCCG AACGTTATT TGGTTTGTG 1680
 60 AAGGACTCTG AAACCATCTA CCGTGTATAA ATTCTGGCTT TAGAAATTG CCCAAGAATG 1740
 CTCATTCTGA GAGCTTTCTC CAGCAGCATA TATCATCAGC CTCATCTAA AATAGGCAGG 1800
 GAGCCCTCCC CATGAGTTTA TCCAAAGTCT CAGCTCTTAA AATGCAGGCT GCCAAGACCC 1860
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCACAGCTG 1920
 ACCTGCCCGT AGGCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
 65 GTATGTCCTT GTGGCCACA CCCAGCCTGT CTGTCTCAT CTGTCAGCT CAACACTGGC 2040
 CTCCAAAGTT CCTTAAACAC TTGCAAAGTC CTTTATTACCT GTGCATTGG ACTTGAGGAC 2100
 ACTGGTTTCT ATCACAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220
 GGTCAAGGTC AGGCTCTCTC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
 70 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
 TGAAACAGTG TGTGTGTTT TTCCCTTCTA GTTAAGGGAC TATTATATAG TGTATAGGAA 2400
 AGCTGTCTCT TTTTGTGTTT TTCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460
 ACACCCCTGC CCGCTGAGC CCGCTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
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 75 AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640
 TTCTCTGTGT CAGTCAAGC ACAGGGCCCC CTCTCTGCA GGAATAAGGG GTAAAAAGTT 2700
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 CCACCTCCGG CAGCTGTAC CCAATTCAGAA CTCTTTCCG CAGCTGAAGA AATGTTCACT 2820
 AACCTGTTTG ACCTAAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAG TGGCATTGAG 2880
 TGATCTGTGT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTATCAGAA 2940

	AAGCTAGCCA	CTGGTATTTT	GTTTTGTTTA	AAAAAAAAAA	GAAAGAAAGA	AAGAAAGAAA	3000
	AACGGAAAGG	AACCTAGCTG	CCTGTATCTT	TCATTTTATA	AATAGCACTT	GAGTTATTTT	3060
	CTGAGTAATC	CAATAAGAA	CTTTTGATGA	CAGCCAGAAT	GTGTTAGAAC	TCTGGCTGAA	3120
5	CATTTTCATCT	CCTGTGAGTC	AGAAGGGCTT	TATTTCTCCC	TTTGATGGGG	CCCCTTCTTC	3180
	TTTCTGGTGC	TCTGGAAGTT	GTTTAGAGGA	AAGAAATCTA	ATTTTAATTA	ATTGCGCAGT	3240
	GAGTTAATCT	CACCTCGTTT	TCTGCTTCCA	GGCATCTTAG	GAAAAACAAA	TGGTTTATGT	3300
	AGATAAGGGA	TGCTACTATA	TGCTTTTATA	AAACAAACAG	GGACATTTT	ATTATAGATT	3360
	TGATTTTTTT	AATGAATGTT	TTTAAAAATA	TATAAATAGG	ACACCAAAGC	GGCAGGGTTT	3420
10	TTTTTGGGGG	GAGGGGGTTT	GTTTTCCAAC	TCAAGATGGC	ACATTAGTGG	CCAGCAATAT	3480
	TTTTTAACTC	ATCCAACCA	GGAAGCTTTT	TTATACATGT	CCTAAATCTA	CGCCAACCAG	3540
	AAAAATAGTCT	CATCTCTTTT	TTTCTCAAT	GAGATCCGTG	TTTATTTTA	GCATTAAATT	3600
	AGTTACACTG	TGATGACTGG	CCTATTACCT	GACTCAGCTC	CCTCTACCTT	GAAATGACA	3660
	TTTTTAAAAA	ATGCAACTAA	GTGGTTAATA	GTGTGTGACG	CTCAAAGTTA	ATGTAAACTG	3720
	GAAAGGTTGT	GTGTGCTGTC	TTTTTGTGTT	TTGGTTAGGC	TTGGTTTGT	TTTTTAATTT	3780
15	TTATACTTTC	TAATAAATT	GCAGTTTCAT	TCTTCTGTT	TGTGCAAAWG	GWMCTAMARM	3840
	AAAMAAACAC	AWYTTTGGGG	GGGCTTGGGC	TCGGAACAAA	GTTTTAAACA	CCACTTCGGG	3900
	TGGGCGCGCG	GGGCCACGTC	AGGTACGGCG	ACCACGCGGG	CCCAACCGGG	ACCCACAGAAG	3960
	GAAACCTTGG	CCAAGAAAAA	GGTGGCGAGA	ATTCTCCACA	CCAGAAAAAA	ACGCGCCGGG	4020
20	GGAAACCCGA	GAGTGTTCGG	TAAACCAAC	CCGAAGAGAG	AACCTCAGAAG	CACACAAGCG	4080
	GGACTCAACC	AGGAGGACCC	AAGGGAACCC	GATAGAGTAC	G		

25 SEQ ID NO:171 PCQ7 Protein sequence:
Protein Accession #: none found

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30							
	MWLLGPLCLL	LSSAAESQLL	PGNNFTNECN	IPGNFMCSNG	RCIPGAWQCD	GLPDCFDKSD	60
	EKECKPAKSK	CGPTFFPCAS	GIHICIIGRFR	CNGFEDCPDG	SDEENCTANP	LLCSTARYHC	120
	KNGLCIDKSF	ICDQNNQD	NSDEESCESS	QEPGSGQVVF	TSENQLVYYP	SITYAIIIGSS	180
	VIFVLVVALL	ALVLHHQRKR	NNLMTLPVHR	LQHPVLLSRL	VVLDDPHHCN	VTYVNVNNGIQ	240
35	YVASQAEQNA	SEVGSFPYS	EALLDQRPAP	YDLPPFPYS	DTESLNQADL	PPYRSRSGSA	300
	NSASSQAASS	LLSVEDTSHS	PGQPGPQEGT	AEPRDSEPSQ	GTEEV		

40 SEQ ID NO:172 PEL3 DNA SEQUENCE
Nucleic Acid Accession #: NM_005858.1
Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

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45	GTCAATATGA	ACATTCCAGA	TACCTATCAT	TACTCGATGC	TGTTGATAAC	AGCAAGATGG	60
	CTTTGAACTC	AGGGTCACCA	CCAGCTATTG	GACCTTACTA	TGAAAACCAT	GGATACCAAC	120
	CGGAAACCC	CTATCCCCCA	CAGCCCACATG	TGGTCCCCAC	TGCTACGAG	GTGCATCCGG	180
	CTCAGTACTA	CCCGTCCCC	GTGCCCCAGT	ACGCCCGAG	GSTCCTGACG	CAGGCTTCCA	240
	ACCCCGTCTG	CTGCACGCAG	CCCAAAATCCC	CATCCGGGAC	AGTGTGCACC	TCAAAGACTA	300
	AGAAAGCACT	GTGCATCACC	TTGACCTTGG	GGACCTTCTC	CGTGGGAGCT	GGCTTGGCGG	360
50	CTGGGCTACT	CTGGAAGTTT	ATGGGCAGCA	AGTGCTCCAA	CTCTGGGATA	GAGTGGGACT	420
	CCTCAGGTAC	CTGCATCAAC	CCCTCTAACT	GGTGTGATGG	CGTGTCAAC	TGCCCGCGG	480
	GGGAGGACGA	GAATCGGTGT	GTTCGCTCT	ACGGACCAAA	CTTCATCTCT	CAGATGFACT	540
	CATCTCAGAG	GAAGTCTTGG	CACCTGTGT	GCCAAGACGA	CTGGAACGAG	AACTACGGGC	600
	GGGCGGCTG	CAGGACATG	GGCTATAAGA	ATAATTTT	CTCTAGCCAA	GGAATAGTGG	660
55	ATGACAGCGG	ATCCACCAGC	TTTATGAAAC	TGAACACAAG	TGCCGGCAAT	GTGATATCT	720
	ATAAAAAAT	GTACCAAGT	GATGCTGTT	CTTCAAAAGC	AGTGGTTTCT	TTACGCTGTT	780
	TAGCCTCGCG	GGTCAACTTG	AACTCAAGCC	GCCAGAGCAG	GATCGTGGCG	GGTGAGAGCG	840
	CGCTCCCGGG	GGCCTGGCCC	TGGCAGGTCA	GCCTGCACGT	CCAGAACGTC	CACGTGTGCG	900
60	GAGGCTCCAT	CATCACTCCC	GAGTGGATCG	TGACAGCCGC	CCACTGCGTG	GAAAAACCTC	960
	TTAAACAATCC	ATGGCATTGG	ACGGCATTTG	CGGGGATTTT	GAGACAATCT	TTTATGTTCT	1020
	ATGGAGCCGG	ATACCAAGTA	CAAAAAGTGA	TTTCTCATCC	AAATTAATGAC	TCCAAGACCA	1080
	AGAACAATGA	CATTGCGCTG	ATGAAGCTGC	AGAAGCTCT	GACTTTCAAC	GACCTAGTGA	1140
	AACCACTGTC	TCTGCCCAAC	CCAGGCATGA	TGCTGCAGCC	AGAACAGCTC	TGCTGGATT	1200
	CCGGGTGGGG	GGCCACCGAG	GAGAAAGGGA	AGACCTCAGA	AGTGCTGAAC	GCTGCCAAGG	1260
65	TGCTTCTCAT	TGAGACACAG	AGATGCAACA	GCAGATATGT	CTATGACAAC	CTGATCACAC	1320
	CAGCCATGAT	CTGTGCCCGC	TTCTTGCAAG	GGAACGTGCA	TTCTTGCCAG	GGTGACAGTG	1380
	GAGGCGCTCT	GCTCACTTCG	AACAACAATA	TCTGGTGGCT	GATAGGGGAT	ACRAAGCTGG	1440
	GTCTGGCTG	TGCCAAAGCT	TACAGACCAG	GAGTGTACGG	GAATGTGATG	GTATTCACGG	1500
	ACTGGATTTA	TGACAAATG	AAGGCAACG	GCTAATCCAC	ATGGTCTTCG	TCCTTGACGT	1560
70	CGTTTACAA	GAAAAACAAT	GGGCTGGTTT	TGCTTCCCG	TGATGATTT	ACTCTAGAG	1620
	ATGATTACAG	GGTCACTTCA	TTTTTATTAA	ACAGTGAATC	TGCTGGCTT	TGGCACTCTC	1680
	TGCCATATCT	TGCAGGCTGC	AGTGGCTCCC	CTGCCAGCC	TGCTTCCCT	AACCCCTTGT	1740
	CCGCAAGGGG	TGATGGCCCG	CTGGTGTGCG	GCACTGGCGG	TCAATTGTGG	AAGGAAGAGG	1800
	GTGAGAGCT	GCCTCACTTG	AGATCTTCT	GCTGAGTCTT	TTCCAGGGGC	CAATTTTGGA	1860
75	TGAGAGTGA	GCTGTCACTT	CTCAGCTGCT	GGATGACTTG	AGATGAAAAA	GGAGAGACAT	1920
	GGAAAGGAG	ACAGCCAGGT	GGCACTTCCA	CGGCTGCC	TCTGGGCCCA	CTTGGTAGTG	1980
	TCCCACTCT	ACTTCAACAG	GGGATTTTTC	TGATGGGTTT	TTAGAGCTT	AGCAGCCCTG	2040
	GATGCTGGCC	AGAAATAAAG	GGACCAGCCC	TTTATGGGTG	GTGACGTGTT	AGTCACTTGT	2100
	AAGGGGAACA	GAAACATTTT	TGTTCTTATG	GGGTGAGAA	ATAGACAGTG	CCCTTGGTGC	2160

5 GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
 CATTGGGTGG GGCTCCTGGG AGGAGAGACT AGCCTTCCTC CTCATCCTCC CTGACCCCTGC 2280
 TCCTAGCACC CTGGAGAGTG AATGCCCTTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340
 ATGTCGGCCT CTTCAGGCCT GATAGTCATT GGAATTGAG GTCCATGGGG GAAATCAAGG 2400
 ATGCTCAGTT TAAGGTACAC TGTTCCTATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
 CTGAGTTCAA AGCCATCTTT

10 SEQ ID NO:173 PEL3 Protein sequence:

Protein Accession #: NP_005647.1

15 1 11 21 31 41 51
 MALNSGSPPA IGFYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPFVP QYAPRVLTQA 60
 SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120
 DSSGTCINPS NMGDGVSHCP GGEDENRCVR LYGFNFILQM YSSQRKSWHP VCQDDWNENY 180
 GRAACRDMGY KKNFYSSQGI VDDSGSTFSM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSRIVGGE SALPGAWFWQ VSLHVQNVHV CGGSIITPEW IVTAHCVVEK 300
 20 PLNNFWHHTA FAGILRQSFH FYGAGYQVQK VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360
 VKPVCLFNPNG NMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLIETQRC NSRYVYDNL 420
 TPAMICAGFL QGNVDSQGD SGGPLVTSNN NIWMLIGDTS WSGSCAKAYR PGVYGNVMVF 480
 TDWIYRQMKK NG

25 SEQ ID NO:174 PBJ4 DNA SEQUENCE

Nucleic Acid Accession #: AJ694767
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 CAGAGAGGCT GTATTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60
 GGGGTACAC ATTCCTTCCA TACGGTTGAG CCTCTACCTG CCTGGTGCTG GTCCACAGTTC 120
 35 AGCTTCTTCA TCAATGGTGA TCCCAATGGC AATGAATCCA GTGCTACATA CTTCATCCTA 180
 ATAGGCTTCC CTGCTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCCCATTT GTGCTCCCTC 240
 TACCTTATATG CTGTGCTAGG TAACTTGACA ATCATCTACA TTGTGCGGAC TGAGCAGCAG 300
 CTGCATGAGC CCATGTATAT ATTTCTTTGC ATGCTTTCAG GCATTGACAT CCTCATCTCC 360
 ACCTCATCCA TGCCCAAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTT 420
 40 GATGCTTGTG TGCTACAGAT GTTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480
 CTGCTGGCCA TGGCTTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGCG CCATGCCACA 540
 GTACTTACGT TGCCCTCGTG CACCAAAATT GGTGTGGCTG CTGTGGTGGC GGGGGCTGCA 600
 CTGATGGCAC CCTTTCCTGT CTTCATCAAG CAGCTGCCCT TCTGCCGCTC CAATATCCTT 660
 TCCCATTCCT ACTGCCATCA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720
 45 AATGCTGCTT ATGCTCTTAT CGTCATCATC TCCGCCATTG GCCTGGACTC ACTTCTCATC 780
 TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTGGGCTG TGACACGTGA AGCCCAAGGC 840
 AAGGCATTTG GCACCTTGCGT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC 900
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 50 TTGGCCAATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020
 ACAAGGAGA TTCCGACAGC CATCCTTCGA CTTTTCATG TGGCCACACA CGCTTCAGAG 1080
 CCTTAGGTGT CAGTGATCAA ACTTCTTTTC CATTCAGAGT CCTCTGATTC AGATTTTAAT 1140
 GTTAACATTT TGGAGACAG TATTCAGAAA AAAAATTTCC TTAATAAAAA TACAACCTCAG 1200
 ATCTCTCAA TGTAAACTG GTTGGGGAAT CTCCATTTT TCAATATTAT TTTCTCTTTT 1260
 55 GTTTCTTTCG TACATATAAT TATTAATACC CTGACTAGGT TGTGGTTGGA GGGTTATTAC 1320
 TTTTCATTTT ACCATGCAGT CCAATCTAA ACTGCTTCTA CTGATGGTTT ACAGATTTCT 1380
 GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAGGAAAAA 1440
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 ACTCCCAACC ACATTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG 1560
 60 AAATAATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620
 AGAGTACATT TACTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680
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 TTAGTACCTT CATGTAGCC ATGGGAAAAAT TGATGTTTCA TGGGGATCAG TGAATTAAT 1800
 65 GGGGTACATC AAGTATAAAA ATTAATAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860
 GGAAGAACTG TTAAGAGAC CAACAGGGTA GTGGGTTAGA GATTTCAGA GTCTTACATT 1920
 TTCTARAGGA GGTATTAAAT TTCTTCTCAC TCATCCAGTG TTGATTTTAG GAATTTCTCT 1980
 GCAACAGAAC TCATGGCTTT AATCCCACTA GCTATTGCTT ATTGCTCTGG TCCAATTGCC 2040
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 AGAAAGTCTG CATAGGGCTT ATAGCAAAGT ATTTATTTT AAAAGTTCCA TAGGTGTTTC 2160
 70 TGATAGGCAG TGAGGTTAGG GAGCCACAG TTATGATGGG AAGTATGGAA TGGCAGGTGT 2220
 TGAAGATAAC ATTGGCTTTT TGAGTGTGAC TCGTAGCTGG AAAGTGAGGG AATCTTCAGG 2280
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 75 TACTAAACCA TGTGATCATA TATGTGGTAA GTTTTCATTT CTTTTCATAT CCTCAGGTTT 2520
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 80 TTAATTTTGA GCCATTACTT CCAATGTGAG TGGAAAGTAC ATGTGCAATT TTTATACCTG 2880
 GCTCATAAAA CCTCCCATG TGCAGCCTTT CATGTTGACA TTAATGTGTA CTTGGGAAGC 2940

TATGTGTTAC ACAGAGTTAA TTAACCNAA AGGCCTGGNA ATTTTGTGNN AANNAAACTG 3000
TGGCCNAG GCCCNCAACC CTTTNTNNA ATTTGGCAAN NTCCACTTT GTANTTTGGT 3060
AAGGAGGCCA GTTGATAAG TGAATAATA AGTACTATTG TGTC

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Protein Accession #: SEQ ID NO:175 PBJ4 PROTEIN SEQUENCE
not available, cloned at Eos

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1	11	21	31	41	51	
MVDPNNGNESS	ATYFILIGLP	GLEEAQFWLA	FPLCSLYLIA	VIGNLTIYI	VRTEHSLHEP	60
MYIFLCMLSG	IDILISTSSM	PKMLAIFWPN	STTIQFDACL	LQMPAIHSL	GMESTVLLAM	120
AFDRYVAICH	PLRHATVLT	PRVTKIGVAA	VVRGAALMAP	LPVPIKQLPF	CRSNILSHSY	180
CLHQDVMLKA	CDDIRVNIVY	GLIIVISAIG	LDSLLISFSY	LLILKTLVLG	TREAQAKAFG	240
TCVSHVCAVF	IFYVPFGLS	MVHRFSKRRD	SPLPVILANI	YLLVPFVLNP	IVYGVKTKKEI	300
RQRILRLFHV	ATHASEP					

20

Nucleic Acid Accession #: SEQ ID NO:176 PM72 DNA SEQUENCE
NM_004624.1
Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

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TCGGAGCCTG	CGGAGGGTGG	TGGTGGTGGT	GGTGGTGGCC	CTCGCCCGCC	TCACTCATGC	60
CTCCTCCTCC	TCCTCTCTCC	CTCAGGCGCC	TCGGTGGCGG	TTGGTCGGCG	GTTACGCGGC	120
TGGTGGTCCG	GGCGGCGCGG	GCTCGCTCTC	GGGAGGCGCG	GGGCGGATCT	CGCGGCGCAG	180
CGCGGCGCGG	CGGAGGTGGG	GTCGCGCGGC	GGAGGCGGCT	CGAGCTTCGT	GCTGCGCGCT	240
CGCTCTTGGG	CTCTCGCTCG	CAGGAGGAGT	GTGACTATGT	GCAGATGATC	GAGGTGCAGC	300
ACAAGCAGTG	CCTGAGGAGG	GCCAGCTGGG	AGAATGAGAC	AATAGGCTGC	AGCAAGATGT	360
GGGACAACCT	CAACTGCTGG	CCAGCCACCC	CTCGGGGCCA	GGTAGTGTGT	TTGGCCTGTC	420
CCCTCATCTT	CAAGCTCTTC	TCCTCCATTC	AAGGCCGCAA	TGTAAGCCGC	AGCTGCACCG	480
ACGAAGGCTG	GACGCACCTG	GAGCCTGGCC	CGTACCCCAT	TGCTGTGGT	TTGGATGACA	540
AGGCAGCGAG	TTTGGATGAG	CAGCAGACCA	TGTCTACGG	TTCTGTGAAG	ACCGGCTACA	600
CCATTGGCTA	CGGCTGTCC	CTCGCCACCC	TTCTGGTCCG	CACAGCTATC	CTGAGCCTGT	660
TCAGGAAGCT	CCAATGCACG	CGGAACATCA	TCCACATGCA	CCTCTTCATA	TCCTTCATCC	720
TGAGGGCTGC	CGCTGTCTTC	ATCAAAGACT	TGGCCCTCTT	CGACAGCGGG	GAGTCGGACC	780
AGTGCTCCGA	GGGCTCGGTG	GGCTGTAAAG	CAGCCATGGT	CTTTTCCCAA	TATTTGTGTA	840
TGGCTAACTT	TTTGGTGGTG	CTGGTGGAGG	GCCTCTACCT	GTACACCCCTG	CTTGCCGCTC	900
CCTTCTCTCT	TGAGCGGAAG	TACTTCTGGG	GGTACATACT	CATCGGCTGG	GGGGTACCCA	960
GCACATTCAC	CATGGTGTGG	ACCATCGCCA	GGATCCATTT	TGAGGATTAT	GGTCTGCTCA	1020
GGTGCTGGGA	CACCATCAAC	TCCTCACTGT	GGTGGATCAT	AAAGGGCCCC	AGCTCACCT	1080
CCATCTTGGT	AAATTCATC	CTGTTTATTT	GCATCATCCG	AATCCTGCTT	CAGAACTGC	1140
GGCCCGCCAG	TATCAGGAAG	AGTGACAGCA	GTCCATATCT	AAGGCTAGCC	AGGTCCACAC	1200
TCCTGTCTGAT	CCCCCTGTTT	GGAGTACACT	ACATCATGTT	CGCCTTCTTT	CCGGACAATT	1260
TTAAGCCTGA	AGTGAAGATG	GTCTTTGAGC	TCGTCTGGGG	GTCTTTCCAG	GGTTTGTGTG	1320
TGGCTATCCT	CTACTGCTTC	CTCAATGGTG	AGGTGCAGCG	GGAGCTGAGG	CGGAAGTGGC	1380
GGCGCTGGCA	CTGTCAGGGC	GTCTCTGGGT	GGAACCCCAA	ATACCGGCAC	CCGTGCGGAG	1440
CGAGCAAGCG	CGCCAGCTGC	AGCACGCAGG	TTTCCATGCT	GACCCGCGTC	AGCCCAGGTG	1500
CCCGCGCTCT	CTCCAGCTTC	CAAGCCGAAG	TTTCCCTGGT	CTGACCACCA	GGATCCACGC	1560
CCAAGCGGCC	CCTCCCGCCC	CTTCCCACTC	GCAGCAGAGC	CCGGGGACAG	AGGCCTGCCC	1620
GGGCGCGCCA	CGCCCGGCCC	TGGGCTCGGA	GGCTGCCCCC	GGCCCCCTGG	TCTTGGTCC	1680
GGACACTCCT	AGAGAAGCCA	GCCCTAGAGC	CTGCCTGGAG	CGTTCTAGAC	AAGTGAGAGA	1740
GATGGGAGCT	CCTCTCTCTG	AGGATGCAGG	TGGAACCTAG	TCATTAGACT	CCTCTCCCAA	1800
AGGCCCCCTA	CGCCAATCAA	GGGCAAAAG	TCTACATACT	TTTATCCTGA	CTCTGCCCCC	1860
TGCTGGCTCT	TCTGCCCAAT	TGGAGGAAAG	CAACCGGTGG	ATCCTCAAAC	AACACTGGTG	1920
TGACCTGAGG	GCAGAAAGGT	TCGTCCCGGG	AAGGTCAACCA	GCACCAACAC	CACGGTAGTG	1980
CCTGAAATTT	CACCATTTGCT	GTCAAGTTCC	TTTGGGTAA	GCATTACCAC	TCAGGCATTT	2040
GACTGAAGAT	GCAGCTCACT	ACCCTATCT	CTCTTTACGC	TTAGTTATCA	GCTTTTAA	2100
GTGGGTATAT	CTGAGGTTTT	TGTTGGAGA	GCACACCTAT	CTTAGTGGTT	CCCCACCGAA	2160
GTGACTGGC	CCCTGGGTCA	GTCTGGTGGG	AGGACGGTGC	AACCAAGGA	CTGAGGGACT	2220
CTGAAGCCTC	TGGGAAATGA	GAAGGCAGCC	ACCAGCGAAT	GCTAGGTCTC	GGACTAAGCC	2280
TACCTGTCT	CCAAGTCTCA	GTGGCTTCAT	CTGTCAAGTG	GGACTCTGTC	ACACCAAGCA	2340
TTCTTATCTC	TCTGTGCTGT	GGAAGCAACA	GGAATCAAGA	GACTGCCCTC	CTTGTCCACC	2400
CACCTATGTG	CCAAGTGTG	TAACTAGGCT	CAGAGATGTG	CACCATGGG	CTCTGACAGA	2460
AAGCAGATCC	TCACCTGTCT	ACACATACAG	GATTTGAAT	CAGATCTGTC	TGATAGGAAT	2520
GTGAAAGCAC	GGACTCTTAC	TGCTAACTTT	TGTGTATCGT	AACCAAGCAG	ATCCTCTTGG	2580
TTATTTGTTT	ACCACCTGTA	TTATTAATGC	CATTATCCCT	GAATCCCCCT	TGCCACCCCA	2640
CCCTCCCTGG	AGTGTGGCTG	AGGAGGCTTC	CATCTCATGT	ATCATCTGGA	TAGGAGCCTG	2700
CTGGTCACAG	CCTCTCTCTG	CTGCCCTTCA	CCCCAGTGGC	CACCTAGCTT	CCTACCCACA	2760
CCTCTGCCAG	AAGATCCCCCT	CAGGACTGCA	ACAGGCTTGT	GCAACAATAA	ATGTTGGCTT	2820
GGAAAAAAA	AAAA					

75

SEQ ID NO:177 PM72 Protein sequence:
Protein Accession #: JC2195

80

1	11	21	31	41	51	
MPPPPLLSLR	RLGGWSAVT	RLVVAAGAR	SRGGRGSRG	AGGGRGGVA	RRRLLELRAA	60
RSLLGSSLOE	ECDDVQMIEV	QHKQCLEEAQ	LENETIGCSK	MWDNLTCWPA	TPRGQVVVLA	120

5 CPLIFKLFSS IQGRNVSRSC TDEGWHLEP GYPPIACGLD DKAASLDEQO TMFYGSVKTG 180
 YTGIVGLSLA TLLVATAILS LPRKLHCTRN YIHMHLFISF ILRAAAVPIK DLALFDSGES 240
 DQCEGSGVGC KAAMVFFQYC VMANFFWLLV EGLYLYTLLA VSFFSERKYF WGYILIGWGV 300
 PSTFTMVWTI ARIHPEDYGL LRCWDTINSS LWMIKGPIL TSILVNFILF ICIIIRILLQK 360
 LRPPDIRKSD SSPYSRLARS TLLLIPLFGV HYIMFAFFPD NFKPEVKMVF ELVVGSFQGF 420
 VVAILYCFLN GEVOAELRRK WRRWHLQGV L GWNPKYRHPG GGSNGATCST QVSHLTRVSP 480
 GARRSSSFQA EVSLV

10 SEQ ID NO:178 BFF8 DNA SEQUENCE
 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCCGAC CCCGGGCTCT 60
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTT TGAGGCCGCA GAGCCCGCAG 120
 CTCAGGCGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCATGAGG AGATCGAGCA TCTGAAGCGG 240
 GAAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCTCCCCA GGCACACTCA 300
 20 ACACTCCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCGCCCTCCAG ACTGTCTCTG CCCACCTGGC TGCACCTGGC 420
 CTGTATGCC AACCCAGTGG GTACAGGTTC TGGGGGACCT GGACAGATGC CGCTACCTCT 480
 AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCAG TGCTGCTCTC GGGAGGCCCA 540
 GGGCCCTGAGG TCATTGACGG GCGGCAGGTG GCCACAGGTT GCTCCCCAGA CCTCCCTCTT 600
 25 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660
 CTCAGATGTC CTGCTGTGGC CAGGCCCAGG ATTTCAGCC CTATGGCTCT GAGTCTCTAC 720
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTCTG TTCTTGCCA CTGTGTCCAG 840
 GCACCTCCCC ATCTTGACAG CGGCCCCAC CCAGCCGAGG ATCCTGGGCT GTGGTCTCAA 900
 30 GTCACTTACC CATTAATCTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGA 960
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCAGGGA 1020
 GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGCCAA CTCAGTAGG 1080
 CTGTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCGAGC CTGTCAGTGC TGGGGACGCT 1140
 GACAGGACAC GGGAGAGGCG CATGCTTTCC CTCGGGACCT GCTGTTCAT GTGTCCCAAG 1200
 35 CCTCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACTTT CCAGGGCCCTC TGCTCCCTTG 1260
 GCGGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320
 AGGCTGAAGG AGGGCTCTCT ACGGACACAC AGGCCAGGAG GCAAGCGTGG CGCTCTTGG 1380
 GCGGCTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
 TCTGTCAAGT CCATCTCTAA TTCAAGCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
 40 TCTTCAACA CCAAGATGTC AAAAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTCTGGG TACAAGGGCA GGCCAGAAAG 1620
 GAGAAAGCAG AGGCTCTTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGCG 1680
 AGGCAGATGG GGGCGGGGCG ACACCCCCCA ATGATCCTGC CCTTCCCTCT GCGAAAGCCC 1740
 ACCACACTTA GGCAGTGGCA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCTGCAG 1800
 45 ACCAAGAGC TGGCGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
 CCGGAGGAG CTAGCTTTCC CAGGACCAA GAAGCCAGCG ATTTCGCCAA GGTCTCCACC 1920
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGCCGG AGCGTGCCAT CCTGCCCGCA 1980
 CTGAAGCAGA CCCCAAGAA CAACCTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040
 AAACGGCGCC TGATCGCTC AGTGCTTGA

SEQ ID NO:179 BFF8 Protein sequence:
 Protein Accession #: T43457

55 1 11 21 31 41 51
 MSGAGVAAGT RPPSSPTPGS RRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
 QQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAH S TLPLPQHRNT AINSSTRLGS 120
 60 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180
 GPEVIAGRQV ATGCSFDLPP PSRAENGRNP WDSPCPARSL PQIAAVARFR ISSPMALSPH 240
 MLGAQGIWTH SIQGSIPAIW AATMGTKGGS RVLFPCHLSK ALPHPDSPGH PAQDPGLWSQ 300
 AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGGP FPSRCGNSSE 360
 LFWAKCGPSR QPQPCSGADA DRTREEMLS LGTCCSMCPK PSCFPDGP SG NHLRSASAPL 420
 GARWVCINGV WVEPGGSPSA RLKEGSSRTH RPKGKRGRLA GGSADTVRSP ADSLSMSSFQ 480
 65 SVKSI SNAN SQKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGOARK 540
 EKAEASNAGA ACMGNSQHQG RQMCAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600
 TQELRHLKSL LEGSORPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILFA 660
 LKQTPKNNFA ERQKRLQAHQ KRRLHRSVL

70 SEQ ID NO:180 BCR4 DNA SEQUENCE
 Nucleic Acid Accession #: NM_012319.2
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 CTCGTGCCGA ATTCGGCAGC AGACCCCGTG TTCGCCCTG GTAGAGATT TCTGAAGACA 60
 CCACTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GCGCGTGGGA CAACGAGGCC 120

	CGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCCTG ACCTTTGCCCC 180
	TCTCTGTAC AAATCCCTTT CATGAACATA AAGCAGCTGC TTTCCCCCAG ACCACTGAGA 240
	AAATTAGTCC GAATTTGGGAA TCTGGCATTAA ATGTTGACTT GGCAATTTCC ACACGGCAAT 300
5	ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT 360
	TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
	ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
	AGCATCACTC AGACCACGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG 540
	CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCATGACTCA GATAGTTTCA 600
10	GTAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
	GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACATG 720
	TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTCTCC 780
	CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACATC AAAGAGCCGG GTGAGCCGGC 840
	TGGCTGGTAG GAAAACAAAT GAATCTGTGA GTGAGCCCCG AAAAGGCTTT ATGATTTCAT 900
	GAAAACAAA TGAATATCCT CAGGAGTGTG TCAATGCATC AAAGCTACTG ACATCTCATG 960
15	GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA TCACTCTGTG CCAGCCATCA 1020
	TCAACCAAT TGAATCTAGA TCTTGTCTGA TTCTACAAAG TGAAGAAGAG GCTGAAATCC 1080
	CTCCAAAGAC CTATTTCATTA CAAATAGCCTT GGGTTGGTGG TTTTATAGCC ATTTCCATCA 1140
	TACGTTCTCT GTCTCTGTCTG GGGGTTATCT TAGTGCTCTT CATGAATCGG GTGTTTTCAT 1200
20	AATTTCTCCT GAGTTTCTCT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTT 1260
	TACACCTTCT TCCATATCTT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320
	CAATGGAAT GAAAGAGGGA CCACTTTTCA GTCATCTGTG TTCTCAAAAC ATAGAAGAAA 1380
	GTGCTATTT TGATTCCACG TTGAAGGGTC TAACAGCTCT AGGAGGCTCT TATTTCATGT 1440
	TTCTTGTGTA ACATGTCCTC ACATTGATCA AACAATTTAA AGATAAGAAG AAAAGAATC 1500
25	AGAAGAAAC GATGATGTGG AGATTAAGAA CAGTGTGTC AAGTATGAAT 1560
	CTCAACTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTAC 1620
	GAGCAGACTC ACAAGAGCCC TCCCCTTTG ATTCTCAGCA GCTGCGATC TTGGAAGAAG 1680
	AAGAGGTCAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
	GGTGCAAGAA TAAATGCCAT TCACATTTC ACAGATACCT CGGCCAGTCA GACGATCTCA 1800
30	TTCAACCACT TCATGACTAC CATCATATTC TCCATCATCA CCACCACCA AACCCATC 1860
	CTCAGAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTGCCACTT 1920
	TGGCTGGTAT GTGATTAATG GGTGATGGCC TGCACAAATT CAGCGATGGC CTAGCAATTG 1980
	GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTGTCT GTGTTCTGTC 2040
	ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTCTTACT AAAGGCTGGC ATGACCGTTA 2100
35	AGCAGGCTGT CTTTATAAT GCATTGTCAG CCATGCTGGC GTATCTTGGA ATGGCAACAG 2160
	GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGTG GATATTTGCA CTTACTGCTG 2220
	GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280
	GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340
	GTTTTGGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTT CGTATAAATT 2400
40	TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGCTAT 2460
	AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATTT 2520
	TTGTATTGAA TTTGCTGTC TGTACAAAAG TCAGTTAAAG GTACGTTTTA ATATTTAAGT 2580
	TATTTATCT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG 2640
	TAAACAAGAG ATTTGGCATG ACATGTTCTG TATGTTTCAG GGAATAATGT CTTTAAATGCT 2700
45	TTTTCAAGAA CTAAACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACTGCTGG 2760
	TGTTTAGGAA TAAGATATGT CATGAAGCCT AAATACCAA GAAAGCTTAT ACTGAATTTA 2820
	AGCAAAGAAA TAAAGGAGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880
	AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAAG TATAAAAAGG 2940
	CAGAATTAGT ATAGAGTACA TTCAATTAAAC ATTTTGTGCA GGATTATTTT CCGTAAAAAC 3000
50	GTAGTGAGCA CTTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060
	AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTTGAA TTTCAAAATG 3120
	TTCTGCGCGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180
	TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGGTTT ACCTGGTTTA 3240
	CAAAATATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAATACT ACATAAGTA 3300
55	TCATTGTATT CGATTACGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATTGT 3360
	GAGCAATGT CTTTATATAC GGTACTGTAG CCATCTAGG CTGTCTGTG GCATCTCTTA 3420
	GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

60 Protein Accession #: SEQ ID NO:181 BCR4 PROTEIN SEQUENCE
NP_036451

	1	11	21	31	41	51	
65	MARKLSVILI	LTFALSVTNP	LHELKAAAFP	QYTEKISPNN	ESGINVDLAI	STROYHLQOL	60
	FYRYGENNSL	SVGEFRKLLQ	NIGIDRIKRI	HIHHDDHHS	DHEHSDHER	HSDHEHSDH	120
	EHHSDHDS	HHNHAASGKN	KRKALCPDHD	SDSSGKPRN	SQKGAHRPE	HASGRNVKD	180
	SVSASEVTST	VYNTVSEGH	FLETIETPRP	GKLPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
	NESVSEPRKG	FMYSRNTNEN	PQECFNASKL	LTSHGMIQV	PLNATEFNYL	CPAILNQIDA	300
70	RSCLHTSEK	KAEIPPKTYS	LQIAWVGFI	AISIIISFLS	LGVILVPLMN	RVFPKPLLSF	360
	LVALAVGTLS	GDALHLLPH	SHASHHSHS	HEEPAMEHMR	GPLFSLSSQ	NIEESAYFDS	420
	TKWGLTALGG	LYFHLVHVH	LTLIKQPKDK	KKNQKKPEN	DDVVEIKQL	SKYESQLSTN	480
	EEKVTDRT	EGYLRADSQE	PSHFDQQPA	VLEEEVIMIA	HAHPQEVYNE	YVPRGCKNKC	540
	HSFEDTLGQ	SDDLHHHHD	YHHILHHHH	QNHHPHSQS	RYSREELKDA	GVATLAWMI	600
75	MGDGLHNSD	GLAIGAAFTF	GLSSGLSTSV	AVFCHLPHE	LGDFAVLLKA	GMTVKQAVLY	660
	NALSAMLAYL	GMATGIFGH	YAEVSNWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDRGCS	720
	RWGYFFLQNA	GMLLFGIHL	LISIFEHKIV	FRINF			

SEQ ID NO:182 BCY2 DNA sequence

Nucleic Acid Accession #:

NM_001203

Coding sequence:

274-1782 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
 CGCGGGGCGG GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTGCGGAGA CCGCGGCGCT 60
 GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTCTTAGAT 120
 GTGAAAGGAA AGGAAGATCA TTTCATGCCCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180
 10 CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAGGTC 360
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
 15 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
 GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGGG ACACCTCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600
 CTGCTCCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGCTTTACTT 660
 ATATCTGTGA CTGCTCTAG TTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCGGG 720
 20 TATAAAAGAC AAGAAACCG AGCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC 780
 ATTCTCTCTG GAGAACTCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAAGTGA 840
 TCAGGCCTCC CTCTGCTGCT CCAAAGGACT ATAGCTAAGC AGATTGAGT GGTGAAACAG 900
 ATTGGAAGAG CTCCTATGG GGAAGTTGG ATGGGAAAGT GCGCTGGCGA AAGGTAGCT 960
 GTGAAAGTGT TCTTACCAC AGAGGAAGCC AGCTGGTTC GAGAGACAGA AATATATCAG 1020
 25 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080
 GGGTCTCTGA CCGAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAGT CCACCACTCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTCTGTC 1200
 AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
 CATCGAGATC TGAAAAAGTA AAACATTCTG GTGAAGAAAA ATGGAAGTTC CTGTATTGCT 1320
 30 GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
 ACTCGAGTTC GCACCAACG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
 GTTGCTAGGA GATGTGATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560
 35 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGAT CAAGAAGTTA 1620
 CGCCCTCAT TCCCAAAACG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAAACTC 1680
 ATGACAGAA GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCTGCG GGTAAAGAAA 1740
 ACACCTGCCA AAATGTCAGA GTCCACGAGC ATTAAGTCTT GATAGGAGAG GAAAAAGTAA 1800
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860
 40 TAAGCATCCA CAGTACAAGC CTGGAACATC GTCTGCTTTC CCAATGGGTT CAGAGCTCAC 1920
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGA GCGGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT

SEQ ID NO:183 BCY2 Protein sequence

Protein Accession #:

NP_001184

45 1 11 21 31 41 51
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCP EDSVNNICSTD GYCFTMIEED 60
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 50 GPIHHRALLI SVTVCSLLL LILFCYFRY KRQETPRYS IGLEQDETYI PPGESLRDLI 180
 EQSQSSGSGS GLPLLVRTI AKQIQMVQKI GKGRYGEVWM GKWRGEKVAV KVFFITEEAS 240
 WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLJTD YHENGSLYDY LKSTTLDAKS 300
 MLKLAYSVSS GLCHLHTEIF STQKPAIAH RDLKSKNIV KKNGTCCIAI LGLAVKFISD 360
 55 TNEVDIPNPT RVGTRKYMPP EVLDESLNRN HFQSYIMADM YSFGLLWEV ARRCVSGGIV 420
 EEYQLPVHDL VPSPSYEDM REIVCIKKLR PSFNRWSSD ECLRQMGKLM TECWAHPAS 480
 RLTLRVKKT LAKMESQDI KL

60 SEQ ID NO:184 CBF9 DNA sequence

Nucleic Acid Accession #:

AC005383

Coding Sequence:

328-2751 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60
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 70 CCTGGCGGTA GTTCTCCGCA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180
 ACAAAACAGT GTCCACAGTG GCAGCCGCGC CCCGGGCGCC CCTCTGTGA TCCCGTAGCG 240
 CCCCCTGGCC CGAGCCGCGC CCGGCTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG 300
 TCGCCGCTCT CTTCCGTTA TATCAACATG CCCCCTTTCC TGTTCCTGGA GGCCGTCTGT 360
 75 GTTTCCTCTG TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA 420
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCACTGGAC 480
 ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCCGGAAAG GGAGCTTTGA AAGGTCCAAG 540
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
 GCATTCCAGT TCAGTTCACG TCCTCATCTG GAATTCCTCT TGGATTCAAT TTCAACCCAA 660

CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
 CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCCC 780
 CAGATCCTCA TCATCGTCACT TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG 840
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGG TCAGGTTTCC CAGGTGGGAG 900
 5 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAG TGCTGTGGG TGAGCAGGTG 960
 GAGGATGCCA CCACAGGCTT CTTCAGCACC CTGAGCAGCT CGGCCATCTG CTCCAGCGCC 1020
 ACGCCAGACT GCAGGGTCCA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG 1080
 GAGTTCGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGG GGACCCCTGC GGTGTGGCTT 1140
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCCTAA CCCACCTGCG CACCTGCTAC 1200
 10 AGGACCACCT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
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 TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCCAGCTCC TCTTCTTGCT GGACAGCTCT 1380
 GCGGGCACCA CTCTGGACGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
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 15 CTGGTGGCGG TGCCGTGTGGG GGAGTACCAG GATGTGCTTG ACCTGGTCTG GAGCCTCGAT 1560
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 20 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAAAATCCCT 1860
 GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG CGGCCAGGGT GCCGGACACA AGCCCTGGAC 1920
 CTCGTCTTCA TGTGGAACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
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 25 GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTTACCTAG GTGGGGTGGG CTCAGCCGGC 2160
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 GTCCCAAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT 2280
 GCCCAGAAAG TGAGGAACAA TGGCATCTCT GTCTTGGTCG TGGGCGTGGG GCCTGTCTTA 2340
 30 AGTGAGGCTC TGCGGAGGCT TGCAGGTCCC CGGGATTCCC TGATCCACGT GCAGCCTTAC 2400
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 CCAGTCAACC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAAAT 2520
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 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATTC TTGAGACGCC CCTGAGGCAC 2640
 35 ATGSGTCCCG TGCAGGAGCG CAGCAGCCGT ACCCTCCCA GCAACTACAG AGAAGGCGTG 2700
 GGCACGTGAA TGGTGCCTAC CTCTGGAAT GTCTGTGCCC CAGGTCTCTA GAATGTCTGC 2760
 TTCCCGCCGT GCCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTACCCACA AACGATGTTG TTGAAAAGTT 2880
 TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGTCTGT CCTTGTGAG GCTATGTCAT 2940
 40 CTGCCACCTT TCCCTTGAGG ATGAACAAGG GCTCCTGAAG ACTTAAATTT AGCGGCTGA 3000
 CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060
 AGGCCCTTTC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAAGCA 3120
 GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAAGGGGG 3180
 CTTGAGGGAC GTTGTGACT TCTTGGCGAC TGCCCTTTGT GTGTGGAAGA GACTTGGAAA 3240
 45 GGTCTCAGAC GAAATTAACA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300
 TGTGCATGGG CCCAGGTCTG GAGGGCCACG TAAATCTGTT CTGAGTCTGT AGCAGTGTCC 3360
 ACCTTGAAGG TCTTC

SEQ ID NO:185 CBF9 Protein sequence
 Protein Accession #: none found

50

1 11 21 31 41 51
 MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETICKISAA SQMWCSAAV DIMFLLDGSN 60
 55 SVKGKSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
 MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIITDG KSQGDVALPS KQLKERGVTV 180
 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHC PFYSWK RVFLTHPATC YRTTCFPGPCD 300
 50 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTFLDGFL 360
 RAKVFKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIFPRGGPT 420
 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLETSHSEDE VAGPARHARA RBLLLGVGS 480
 EAVRAELEEI TGSFKHVMVY SDFQDLFNQI PELQKLCRSR QRPGRCTQAL DLVFLDTS 540
 65 SVGPENFAQM QSFVRSALQ FEVNPDTVOV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVSGA GTALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQKLRNNGI 660
 SVLVVGVGPV LSEGLRLLAG PRDSLIHVAA YADLRYHQDV LIEMLCGEAK QPVNLCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAFGP

70

SEQ ID NO:186 PAV1 DNA sequence

Nucleic Acid Accession #:

AF272890

Coding Sequence:

87-1520 (underlined sequences correspond to start and stop codons)

75

1 11 21 31 41 51
 TGCTACCCCG GCCCGGGCTT CTGGGGTGTG CCCCACACAC GGCCAGCCCC TGCCACACCC 60
 CCCGCCCCCG GCTTCCGCAG CTGGCATGG GCGCGGGGCT GCTGCTCTTG GCGGCTCCCG 120
 AGCCCGGTAA CCTGTCTGTC GCCGCACCCG TCCCGCAGCG CCGGCCACCC GCGGCGCGGC 180

5 TGCTGGTGCC CGCGTCGCCG CCCGCTCGT TGCTGCCTCC CGCCAGCGAA AGCCCCGAGC 240
 CGCTGTCTCA GCACTGGACA GCGGGCATGG GTCTGCTCAT GCGCTCATC GTGCTGCTCA 300
 TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCCGCGG CTGCAGACGC 360
 TCACCAACCT CTTCATCATG TCCCTGGCCA GCGCCGACCT GGTCTATGGG CTGCTGGTGG 420
 TGCCGPTCGG GGGCACCATC GTGGTGTGGG GCGCTGGGA GTACGGCTCC TTCTTCTGCG 480
 AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
 TTGCCCTTGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCAGAGC CTGCTGACGC 600
 GCGCGCGGGG GCGGGGCTTC GTGTGCACCG TGTGGGCCAT CTCGGCCCTG GTGTCTCTCC 660
 10 TGCCCATCTT CATGCACTGG TGCGGGGCGG AGAGCGACGA GCGCGCGCGG TGCTACAACG 720
 ACCCAAGTG CTGCGACTTC GTACCAACCC GGGCTACGCG CATCGCCTCG TCCGTAGTCT 780
 CCTTCTACGT GCCCTGTGCG ATCATGGCCT TCGTGTACCT GCGGGTGTTC CGCGAGGCCG 840
 AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCCGTTT CCTCGGCGGC CCAGCGCGGC 900
 CGCCCTCGCC CTCGCCCTCG CCCGTCCCGG CGCCCGCGCC GCGCGCCGGA CCCCGCGGCC 960
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 15 CGCGCCCTCGT GGGCTTACGC GAGCAGAAGG CGCTCAAGAC GCTGGGCAAT ATCATGGGCG 1080
 TCTTCAAGCT CTGCTGGCTG CCGTCTTCTC TGGCCAACGT GGTGAAGGCC TTCCACCGCG 1140
 AGCTGGTGCC CGACCGCCTC TTCGTCTTCT TCAACTGGCT GGGCTACGCC AACTCGGCCT 1200
 TCAACCCCAT CATCTACTGC CGCAGCCCGG ACTTCCGCAA GGCTTCCAG GGACTGCTCT 1260
 20 GCTGCGCGCG CAGGGCTGCG CGCGCGCGCC ACGCGACCCA CGGAGACCGG CGCGCGCCT 1320
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 ACGACGATGT CGTGGGCGCG ACGCGCGCGG CGCGCTGCTT GGAGCCCTGG GCGCGCTGCA 1440
 ACGCGGGGCG GCGCGCGGAC AGCGACTCGA GCCTGGACGA GCCGTGCGCG CCCGGCTTCG 1500
 CCTCGGAATC CAAGGTGTAG GGGCCGCGCG GGGCGCGGGA CTCGCGGCAC GGCTTCCCG 1560
 25 GGGAAAGGAG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAACCTCA AGCCCAACA 1620
 CCTGCTCTGA ATCATCCGAG GCAAAGAGAA AAGCCACGGA CCGTTCACCA AAAAGGAAAG 1680
 TTTGGGAAGG GATGGGAGAG TGGCTTGTCT ATGTTCCTTG TTG

SEQ ID NO:187 PAV1 Protein sequence

Protein Accession #:

AA011176

30

1 11 21 31 41 51
 35 MGAGVLVLGA SEFPGNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQQWTAG 60
 MGLLHALIVL LIVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVMGLL VVPGATIVV 120
 WGRWETGSGF CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSLI TRARARGLVC 180
 TVWAISALVS FLFILMHWNR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCLM 240
 40 AFVYLRFVRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAAAAATAP 300
 LANGRAGKRR PSRILVALRQ KALKTLGIIM GVFTLCWLFP FLANVVKAFH RELVFDRLFV 360
 FFMWLYANS AFNPFIYCRS PDFRKAFOGL LCCARRAARR RHATHGDRPR ASGCLARPGP 420
 PPSPGAASDD DDDDVVGATP PARLLEPWAG CNGGAAADSD SSLDEPCRPG FASESKV

45

SEQ ID NO:188 BC02 DNA sequence

Nucleic Acid Accession #: AJ400877

Coding sequence:

81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 50 GGCGTCCGCG CACACCTCCC CGCGCCGCGG CCGCCACCGC CCGCACTCCG CCGCCTCTGC 60
 CCGCAACCGC TGAGCCATCC ATGGGGGTCG CGGGCCGCAA CCGTCCCGGG GCGGCCTGGG 120
 CGGTGCTGCT GCTGCTGCTG CTGTGCGCGC CACTGTGCTG GCTGGCGGGG GCGGTCCCGC 180
 55 CGGTGCGGGG CCGTGGCGCG GGGCCGCGAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA 300
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAATGAGC 360
 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT 420
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480
 60 AGAACAATGG CGGCTGCCAG CATACTGTG TCAACGTCAT GGGGAGCTAT GAGTGTCTGCT 540
 GCAAGGAGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTACCCGC TCGGAAGAGG 600
 GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660
 GCAGCGTGC CTGTGAGTGC AGGCCCTGGT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780
 65 GCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
 AGCGAGAGGA CACTGTCTCT GAGGTGACAG AGAGCAACAC CACATCAGT GTGGATGGGG 900
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG 960
 ACCGCACTGT TAAGGATACT TCGACAGGTG TCCACTGCAG TTGCTCTGTT GGATTCACTC 1020
 TCCAGTTGGA TGGGAAGACA TGTAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080
 GTGATCATTT CTGCAAAAAA ATCGTGGGCA GTTTTGACTG CCGCTGCAAG AAAGGATTTA 1140
 70 AATTATTAAC AGATGAGAAG TCTTGCCAAAG ATGTGGATGA GTGCTCTTGT GATAGGACCT 1200
 GTGACCACAG CTGCATCAAC CACCTTGCCA CATTGCTTGT TGCTTGAAC CGAGGGTACA 1260
 CCCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCTGGGTACA 1380
 75 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCCC ACAAGTGTGT 1440
 CACCCCGTGT GTCCCTGCAAC TGCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500
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 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680
 80 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT 1740
 TTATCACTGT TGAGTTTGG CTGAAACTA ACCAAAGGA GGTGACAGCT TCTGTGACG 1800

5 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCGTAA AGCCATCCGC ACGCTCAGAA 1860
 AGGCCGTCCA CAGGGAGCAG TTTCACCTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCTG TGGAGTGGGC CAGGGTCATG 1980
 CAGAAAACCA ATGTGTCACT GTCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT 2040
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT 2100
 GCGCAAGACC AGGAAATTTCT GGGGCCCTGA AGACCCCAAG AGCTTGAAT ATGTCTGAAT 2160
 GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGCACCT TGCCAGCTCT 2220
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 10 GCCTTGGCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340
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 ACTTGTATGG CTCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGA GGGGAGCTGG 2520
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 15 AGTGTACGTG GACCATCAAC CCACCCCCA AGCGCCGAT CCTGATCGTG GTCCTTGAGA 2640
 TCTTCTGCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTTTCAT 2700
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 CCAGGTCAAA GAAGCTGTGG ATTCAGTTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT 2820
 TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCAGGA ACTCATTGAA GACATAGTTC 2880
 GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAAT ACTTAAGGAT AAGAAACTTA 2940
 20 TCAAGGCTCT GTTGATGTC CTGCCCCATC CCCAGAACTA TTCAAGTAC ACAGCCAGG 3000
 AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCAAA GTGTCCAGGT 3060
 TTTTGAGACC TTACAAATGA CTCAGCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120
 GGTGTGGTGG ACAGAGCTGT CTTCCTCTG CATGTACGCA CAGTCGGGTA TTGCTGCCTC 3180
 CGGTATCAGT GACTCTATAG AGTTCAATTT TTATAGATA TACAGATATT TTGTTAAAT 3240
 25 GAACTTGGTT TTTCTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
 CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGGCTGGCT GAGCTGGACT 3360
 TTGTCAGACC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTAECTCTCC TCAAGGAGTC 3420
 TGTAGTGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCTCTAGC 3480
 CCGGCCCTCT CTAAGGGAGC CCTCTGACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG 3540
 30 CAAGAGGGGA GGAAGAGAGA CCCCTGCAGG CTCCTCCAC CCACCTTGA ACCTGGGAGG 3600
 ACTCAGTTTC TCACAGCCT TCTCCAGCCT GTGTGATACA AGTTGATCC CAGGAACITG 3660
 AGTTCTAAGC AGTGCTCTG AAAAAAAGAA GCAGAAAGAA TTAGAAATAA ATAAAACTA 3720
 AGCACTTCTG GAGACAT

35 SEQ ID NO:189 BC02 Protein sequence
 Protein Accession #: CAB92285

40 1 11 21 31 41 51
 | | | | |
 MGVAGRNRPG AAWAVLLLL LLPLLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60
 LCQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNYR CTCFDGFMFA 120
 HDGHNCLDVD ECLNNNGGCQ HTCNVNMGSY ECCCKEGFFL SDNQHTCIHR SEEGLSMKNK 180
 45 DHGCSHICKE APRGSVACEC RPFELAKNQ RDCILTCNHG NGGCQHSDD TADGPECSCH 240
 PQYKMHITDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCRTCKDT 300
 STGVHCSPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK 360
 SCQDVDECSL DRTCDHSCIN HPGTAFACN RGYTLYGFTH CGDINECSIN NGGCQVCVN 420
 TVGSYECQCH PGYKLHWNNK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
 SSDVTITRTS VITKLNKGC SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSGQKV 540
 50 PGAPGRPSTP KEMFTVVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAQTYDGA RERCILCPNG 660
 TFQNEEGQMT CEPFPRPNS GALKTPEAWN MSECGLCQF GEYSADGFAP CQLCALGTFQ 720
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHYF NTTTHRCIRC PVGTYPQEPF 780
 55 KNNVCSPGN TTTDFDGSN ITQCKNRRCG GELGDFTYI ESPNYPGNYP ANTECTWTIN 840
 PPPKRLIV VPEIFLPIED DCGDYLVMRK TSSNSVTY ETCQTYERPI AFTSRSKLW 900
 IQFKSNEGNS ARGQVPYVT YDEDYQELIE DIVRDGRLYA SENHQELKD KKLKALFDV 960
 LAHPQNYFKY TAQESREMF RSRFLLRSK VSRFLRPYK

60 SEQ ID NO:190 BFG1 DNA sequence
 Nucleic Acid Accession #: AF007170
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

65 1 11 21 31 41 51
 | | | | |
 AAGGAGGCGG CCTCCGGGAA AAGCGACCG AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60
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 AGCTACCTCA AGCCAGAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
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 70 ATGAAGGAGG CACAGATGCT GTGTACAGAG CACCGAGGA AGTCTTCTGT AACAGATTCC 300
 TTCAGCAGCC TGGTGAACCG CCCCACGCTG GGCCAATTCA CTGAAGAAGA AATCCACGCT 360
 GAGGTCTGCT ATGCAGAGTG CTGCTGCAG CGAGCAGCCC TGACCTTCTC GCAGGACGAG 420
 AACATGGTGA GCTTCATCAA AGGCGGCATC AAAGTTTCGAA ACAGCTACCA GACCTACAG 480
 GAGCTGGACA GCTCTGTICA GTCTCACA TACTGCAAGG GTGAGAACCA CCGCACTTT 540
 75 GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTACT 600
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 CAGCTGGAGG AGGGAGCGTC AGGOCACAGC TTCCGCTCTG TGCTCTGTGT CATGCTCCTG 720
 CTGTGCTACC ACACCTTCTC CACCTTCGTG CTCGGTACTG GGAACGTC AA CATCGAGGAG 780
 CGCGAGAAGC TCTTGAAGCC CTACCTGAAC CGGTACCCTA AGGGTGCCAT CTTCTGTTTC 840
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5 GAGTGTGTG AGGCCACGA GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
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 AGCAAGGAGA ACTGCTGGTC CAAGGCCACC TACATTTACA TGAAGGCCGC CTACCTCAGC 1080
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 10 TCAGTGGATG ACGAGTGCTT GGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440
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 TCCATGGAGT CAAGGACACA CTTTCGAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680
 15 CTAGAGAACG CGACGACATC CATGGTCTCA TCAGTGTCTT GTAGCTTTG TGCAGCAGTT 1740
 CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCT 1800
 CCCCTGCCC TGCCCTGCTT TTGGGGTCCA CCGGCACCTC AGTTGGATGG CACAACATAG 1860
 TGTATCCGTG CAGAAGCCGA GCTGGCATT TACACAGTGT AGCCAAGGCC CTTTGCCAAG 1920
 GGCAGAGCAG GTGGAGCCCT CTGCTGCCC TATCACACAT ACGGGTACTT GCTTTTCACT 1980
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 20 CACAGTTGGC TTTAAAAACC AACAAACATC AACCACTGT AAGTCTTTGT CTCACCTAT 2100
 TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAAATT CTTTCAAAT 2160
 TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCTTCAGA GGACCTGAGG AATGCTGGG 2220
 AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTGGGC ATGAGGATGT ACACAGACAC 2280
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 25 AAGCAGCTGT TTTAGTGAG ATAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400
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 30 CATTTGCTTA CTGACAGCAT TTTTGTAAA ACTGTATTTC TTGAAAAAAA AAAAAAAAAA 2640
 AA

SEQ ID NO:191 BFG1 Protein sequence

Protein Accession #: AAC39582

35 1 11 21 31 41 51
 | | | | |
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 40 QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEEIHAECYV AECLLQRAAL TFLQDENMVS 120
 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEQGV KLGVGAFNLT LMLPTRLR 180
 LLEFVGFSNG KDGGLLLEE GASGHSFRSV LCVMLLLCYH TFLTFVLGT NVNIEEAEL 240
 LKPYLNRYPK GAIFLFFAG IEVIKGNIDA AIRFECECE AQQHWKQFHH MCYWELMWCF 300
 TYKQWKMYSY FYADLLSKEN CWSKATYIYM KAAVLSMFGK EDHKPFGDDE VELFRAVPL 360
 45 KLKIAKSLP TEKFAIRKSR RYFSSNPISL PVPALMMYI WNGYAVIGKQ PKLTDGILEI 420
 ITKAEEMLEK GPENEYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480
 LIPNALLELA LLLMEQDRNE EAIKILLES AK QNYKNYSMES RTHFRIQAAT LQAKSSLENS 540
 SRSMVSSVSL

SEQ ID NO:192 BFG6 DNA sequence

Nucleic Acid Accession #: NM_032583

Coding sequence: 1-404 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
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 GGCCCTGGGA GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCACCG 180
 TGGGGGAAGT ATGATGCTGC CTTGAGAACC ATGATTCCCT TCCGTCCAA GCCGAGGTTT 240
 60 CCTGCCCCCC AGCCCTGGA CAAATGCTGC CTGTTCTCTT ACCTACCGT GTCATGGCTC 300
 ACCCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCTCCACTG 360
 TCAGTCCATG ATGCTCAGA CAAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA 420
 GTCTCAAGGC GAGGGATTGA AAAAGCTTCA GTGCTTCTG TGATGCTGAG GTTCCAGAGA 480
 65 ACAAGGTGA TTTTCGATG ACTTCTGGG ATCTGCTTCT GCATTGCCAG TGTACTCGG 540
 CCAATATTGA TTATACAAA GATCCTGGA TATTGAGAAG AGCAGTTGGG GAATGTTGTC 600
 CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC 660
 TCCTCCAGTT GGATCACTAA CCAACGCACA GCCATCAGGT TCCGAGCAGC TGTTTCTCTC 720
 TTTGCTTTG AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC 780
 70 ATCAGCTTCT TCACCGGTGA TGTAACCTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840
 GTACTGATCA CTGCGCATC GCTGGTATC TGCAGCATTT CTCTCTACTT CATTATTGGA 900
 TACACTGCTT TATGCTCAT CTTATGCTAT CTCTGCTT TCCCACTGGC GGTATTTCATG 960
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 TTTGCAAAAA TCATTGAAGG TATGGAAGT CTGACTTTCT GCTCCAAACC TGGTGATGGC 1140
 75 ATGGCCTTCA GCATGCTGGC CTCTTGAAT CTCTTGGC TGTAGTGT CTTTGTGCTT 1200
 ATTGCAATGA AAGTCTCAC GAATTCGAAG TCTGAGTGA TGAGGTTCAA GAAGTTTTC 1260
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 TTTGAGGAGG CCACTTGTG ATGGCAACAG ACCTGTCCCG GGATCGTCAA TGGGGCACTG 1380
 GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCTTAGAGA TGCCCTCGGG 1440

5 CCAGAGGAAG AAGGGAACAG CCTGGGCCCA GAGTTGCACA AGATCAACCT GGTGGTGTCC 1500
 AAGGGGATGA TGTTAGGGGT CTGCGGCAAC ACGGGGAGTG GTAAGAGCAG CCTGTTGTCA 1560
 GCCATCCTGG AGGAGATGCA CTGCTCGAG GGCTCGGTGG GGTGTCAGGG AAGCCTGGCC 1620
 TATGTCCCCC AGCAGGCCCTG GATCGTCAGC GGGAAACATCA GGGAGAACAT CCTCATGGGA 1680
 10 GGCGCATATG ACAAGGCCCG ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC 1740
 CTGGAACCTC TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCCCT CAACCTCTCT 1800
 GGGGGGCAGA AACAGAGGAT CAGCCTGGCC CGCGCCGTCT ATTCCGACCG TCAGATCTAC 1860
 CTGCTGGACG ACCCCTGTCT TGCTGTGGAC GCCACCGTGG GGAAGCAGAT TTTTAGGGAG 1920
 TGCATTAAGA AGACACTCAG GGGGAAGACG GTGCTCTGG TGACCCACCA GCTGCAGTAC 1980
 15 TTAGAATTTT GTGGCCAGAT CATTTTGTG GAAAAATGGGA AAATCTGTGA AAATGGAAC 2040
 CACAGTGAGT TAATGCAGAA AAAGGGGAAA TATGCCAAC TTATCCAGAA GATGCACAAG 2100
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SEQ ID NO:193 BFO6 Protein sequence

Protein Accession #:

NP_115972.1

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 60 SVHDASDKNV QRLHRLWEEE VSRRGIEKAS VLLVMLRFQR TRLJFDALLG ICFCIASVLG 180
 PILJPKILE YSEEQLGNVY HGVGLCFALF LSECVKLSF SSSWINQRT AIRFRAAVSS 240
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 YTAFAILCY LLVFLVAFM TRMAVKAQHH TSEVSDQIR VTSEVLTCIK LIKMYTWEKP 360
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 PEEBNSLGP ELHKINLVVS KGMMLGVCGN TSGKSSLLS AILEEMHLE GSVGVQGSIA 540
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 GGQKQRISLA RAVYSDRQIY LLDDPLSAVD AHVGKHIFE CIKTLRGT VVLVTHQLQY 660
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 70 SQALATSLER SLNGNAVEH QLTQEEEMEE GSLSWRVYH YIAAGGYMV SCIFFFVVL 780
 IVFLTIFSW WLSYWLEQGS GTNSSRESNG TMADLGNAD NPQLSFYQLV YGLNALLIC 840
 VGVCCSGIFT KVTFRKASTAL HNKLFNKVFR CPMSFFDPT IGRLLNCFAG DLEQLDQLP 900
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 KMCVSEAPLH MEGTSCPGQW PQHGEIIFQD YHMKYRDNTF TVLHGINLTI RGHEVVGIVG 1140
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SEQ ID NO:194 BH88 DNA sequence

Nucleic Acid Accession #:

AA983251

Coding sequence:

1-1749 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51

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GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180

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TTTTTTAATA ACCAAAGGCA GGGAAAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660

TGAAAAAAA AAAAAAAA AAAAAAAA

SEQ ID NO:195 BHR8 Protein sequence

Protein Accession #: none found

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SGRQPRGSPD	CIPRFPSSASA	THKAVPKGTG	PPAEDGDGLG	APGPRARRRR	LLGVAAEGSG	180
PRGKRRGTVS	DEARSGSPGPR	LLGDRPALSG	DALSAPRVVP	CGALAAPRSP	HPGTPLRSCS	240
CCWLRCWRRG	RGPSGEYCHG	WLDAGQVWRI	GFQCPERFDG	GDATICCGSC	ALRYCCSSAE	300
ARLDQGGCDN	DRQQGAGEPG	RADKDGPRRL	GRASCLRGTQ	GDGEGAPFV	RAWQRCSPG	360
SPKGRQLLRA	FPGLLPARRR	RGFPSSPRGG	PSPLQRPALP	IYVPFLIVGS	VFVAFIILGS	420
LVAACCCRCL	RPKQDPQQR	APGGRNLMET	IPMIPASSTS	RGSSSRQSS	AASSSSSANS	480
GARAPFTRSQ	TNCCLEPGTM	NNVYVNMPTN	FSVLNCQQAT	QIVPHGQQL	HPPYVGYTVQ	540
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SEQ ID NO:196 CQA5 DNA SEQUENCE

Nucleic Acid Accession #: AA088458

Coding sequence:

862-1995 (underlined sequences correspond to start and stop codons)

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CTGGGCCAGA	GCAGAGCCAG	CGCCGACTTT	GGGGCTGCAG	GGAGCCCCCG	CCCACTGGGG	240
CGGCTACTGC	CCAAGGTACA	AGAGGTGGCC	CGGTGCTGG	GGGAGCTGCT	GGCTGCAGCC	300
TGTGCCAGCC	GGGCCCTGCC	CCCGTCTTCC	TCCGGGCCCC	CCTGCCCTGC	CCTGACGTCC	360
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CTCACCCAGG	AGGTGACCGA	GAAGAGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAAGTCG	480
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GATTCCACCT	TCATCTAGTC	CTTGTGGGCC	CGGTGGGCC	CCAGGGCCAG	CCTGGCACTC	600
AGCCCTTCGA	GGGTGGGGCC	CCCATCGCAC	CCACCCTCTC	TGGCTGGAGA	CCCCGGGACG	660
GGCCAGGCAC	AGTCCCGGAG	TGGGCGCCTT	CCTGCCCGCC	TGCCAGATG	GGCTCCCCAG	720
GGCTGCCCCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTPTKGCCTC	CTGGTGTGTYG	780
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TGGACAGTGG	GGTACCCCTC	CATGAGTTAG	CGTCCCCCGG	TTTCCAGCGG	TGCCCGCCCTG	900
GGTCCCATCT	TCCAGGAAAG	GCATGCCCA	CGCCAGGCTG	CACCTTCCAC	AACGGGCGAG	960
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CAGGACGAGG	TGGCTGTAGC	TCGGACGGAC	GGAAAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
GTAAGCGGGG	GGTGCCTGCC	TGGCTGGGGA	GGCCAGGGA	TAGCGGTCCG	ACTTCAGGTT	1140
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GAGACAGGCT	GGCACCCTCC	GAAAAACTGC	CTTTCAGCCT	TGGTGTTCGG	TGCAAGGTGA	2340
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CACGAGGGGA	GAATTTAAAG	GGCCCGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGACATG	2460
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GGTGCACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2640
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SEQ ID NO:197 LBG2 DNA SEQUENCE

Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

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 ACCATGCCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAAGC CTTGTGCGCC 1740
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 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
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 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGGTAA CACAGACCCC ACAGCCCGCG CTAACGACAC CCTCTGGTG TTCGACTATG 2400
 AGGGCAGCGG TCCGACGCC CGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGGTGGCGG GGAGGACGAC TAGCGGCGCT GCCTGCAGGG CTGGGGACCA AACGTACAGC 2580
 CACAGAGCAT CTGCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GCGCGAGACA GGCTATGAGT CTGACGTTAG AGTGGTGTCT 2700
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGC TTAGCACTG AAAACCTCTC 2760
 CACCTGGGCC AGGTTGGCT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820
 TGCTCAACCC TGTGTCTG GCGTGGGCTC GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAAATGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTITTTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTCAAAAGT GCAGCCAGA GCTGCTGGC CCACTGGCCG 3000
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATC GGATGGATCT CTGCGTTTTT 3060
 ATACTGAGT TGCTAGGTT GCCCCTTATT TTTTATTTT CCTGTTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAAGTTTTT TATTAAAGAA A

SEQ ID NO:198 LBG2 Protein sequence:

Protein Accession #: CAA54177

65 1 11 21 31 41 51
 | | | | |
 MGLPRGLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 70 KGFPPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWILLN KPLDREEIAK 180
 YELFGHAVSE NGASVEDPMN ISHIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSISQ EPKDPHDLMF THIRSTGTIS VISSGLDREK VPEYTLTQA 300
 TDMDGDSGTT TAVAVVEILD ANDNAPMFD P QKYEAHVPE AVGHEVQRLT VTDLDAPNSP 360
 AWRATYILMG GDDGDHFTT THIESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 75 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGITGPEVC VYTAEDPDK NQKISYRILR 480
 DPAGWLAMPD DSGQVTA VGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLD 540
 VNDHGPVPEP RQITCNQSP VRHVLNITDK DLSPHSTPFQ AQLTDDSDI WTAEVNEEGD 600
 TVVLSLKKFL QDQTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPG WKGGFLPVL 660
 GAVLALLFL LVLLLLVRKK RKIKEPLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720

GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAAANTDPT APPYDTLLVF 780
 DYEYSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

5 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

SEQ ID NO:199 OBIS DNA SEQUENCE

10	1	11	21	31	41	51	
	CTTCTTTAAA	TTTCTTTCTA	GGATGTTTAC	TTCTTCTCCA	CAATGAATGA	GTGTCACAT	60
	GACAAGCACA	TGGACTTTT	TTATAATAGG	AGCAACACTG	ATACTGTGCA	TGACTGGACA	120
	GGAAACAAAC	TGTGATTTGT	TTTGTGTGTT	GGGACGTTTT	TCTGCCTGTT	TATTTTTTTT	180
	TCTAATCTCT	TGGTCATCGC	GGCAGTGATC	AAAAACAGAA	AATTTCATTT	CCCCTTCTAC	240
15	TACCTGTG	CTAATTTAGC	TGCTGCCGAT	TTCTTCGCTG	GAATTCGCTA	TGTATTCCTG	300
	ATGTTTAAAC	CAGGCCAGT	TTCAAAACT	TTGACTGTCA	ACCGCTGGTT	TCTCCGTCAG	360
	GGGCTTCTGG	ACAGTAGCTT	GACTGCTTCC	CTCACCACCT	TGCTGGTTAT	CGCCGTGGAG	420
	AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
	CTGCTCATTT	TGCTTGTCTG	GGCCATCGCC	ATTTTATGG	GGCGGTCCC	CACACTGGGC	540
20	TGGAATGCC	TCTGCAACAT	CTCTGCCCTG	TCTTCCCTGG	CCCCCATTTA	CAGCAGGAGT	600
	TACCTTGT	TCTGGACAGT	GTCCAACTCT	ATGGCCTTCC	TCATCATGGT	TGTGGTGTAC	660
	CTCGGATCT	ACGTGTACGT	CAAGAGGAAA	ACCAACGTCT	TGCTCCCGCA	TACAAGTGGG	720
	TCCATCAGCC	CCCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	TGTCTTAGGG	780
	CGGTTTGTGG	PATGCTGGAC	CCCGGGCCTG	GTGGTTCTGC	TCCTCGACGG	CCTCAACTGC	840
25	AGGCAGTGTG	CGCTGCAGCA	TGTGAAAAGG	TGGTTCTCTG	TGCTGGCGCT	GCTCAACTCC	900
	GTCTGTAACC	CCATCATCTA	CTCTTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
	ATGATCTGCT	GCTTCTCTCA	GGAGAACCCA	GAGAGGCGTC	CCTCTCGCAT	CCCCCTCAC	1020
	GTCTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CCAAGGTGCA	1080
30	GTCTGCAATA	AAAGCACTTC	<u>CTAAACTCTG</u>	<u>GATGCTCTC</u>	<u>GGCCACCCA</u>	<u>GGTGATGACT</u>	1140
	GTCTTAGG						

SEQ ID NO:200 OBIS Protein sequence:

Protein Accession #: NP_036284

35	1	11	21	31	41	51	
	MNECHYDKHM	DEFFYNRSNTD	TVDDWTGFKL	VIVLCVGTFF	CLFIFFSNLS	VIAAVIKNRK	60
	FHPFFYYLLA	NLAADPFAG	IAYVELMNT	GPVSKLTIVN	RWFLRQGLLD	SSLTASLTNL	120
40	LVIIVERHMS	IMRMRVHSNL	TKKRVTLIL	LVWAIAPFM	AVPTLGNCL	CNISACSSLA	180
	PIYSRSLVF	WTVSNLMAFL	IMVVYLRIY	VYVKKRTNVL	SPHTSGSISR	RRTPHKLMKT	240
	VMTVLGAFVV	CWTPLVLL	LDGLNCRQCG	VQHVWRWFL	LALLNSVNP	IISYKDEDM	300
	YGTMKMKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

SEQ ID NO:201 PAA6 DNA SEQUENCE

Nucleic Acid Accession #: AA569531
 Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

50	1	11	21	31	41	51	
	ATGACCTACA	GTTACTCATT	TTTCAGGCCT	GAGTTGATCG	TTAATCATCT	TAATTATGTT	60
	CATCTGAAG	CCAACAGGAG	AACCAAGACC	AAAACCTTAT	TGCTCTGCT	TTCAATTCTT	120
	GATGAACCT	CTGACTAAG	CACACATCTT	CCTTGTATT	CTCTCTCAA	GGAGTGTGGA	180
	GTGCTTCATC	TGGACATCCA	CGGGAAGAAG	GAAGACATGA	GAATCACCCA	ACAGTCTTCC	240
55	CAGCTATACC	TGTGGACAT	GGGTGGTTT	ACAATATTTA	AGAACCTGTG	GATGAGCCTC	300
	ATACCCAGAG	GAAGCAAAAC	CTCCCCAAA	AGAGTTACAG	AAACCATCCT	GAGAGATTTT	360
	AAGCAGAAGC	AAAGTTCAAA	GATCCAAGAG	GAGAGACGAA	GAGAGTCTGC	AGGACCAAAC	420
	CTCTCTTCAT	TCTGGTTTGT	GGGGAATGCT	GGAAGAGGAG	ACAGGCCCCA	GATTGAGGCA	480
	GGAAAGTAAAC	AGTTTTCAGG	CTGAGGCCAA	CTGAGCAGG	AACATTCCAA	TATTTCTTCA	540
60	GCTACGTTGT	CCCAGCACTT	CACCTGGTTAA	CCTTTTATGT	CCACCATTTG	TGGATTTTAC	600
	AGCTACTTGT	CAATGGTGAA	TATTGATCAT	CATCATTATC	TACTGAGCTG	CTACCATATC	660
	CCAGTACTCT	CTTGCAATGT	GTTTCAATTT	TTCTCAACAC	TCAGCATATT	TGCAATATGT	720
	TATGTAATAT	CACAGACAAG	GAACTGAAC	GCAGAAATGT	TTTATTTCTT	GCCAAACATC	780
65	ACATGAGGAT	GAACAATGAA	ACCGATTGGA	AACCAAGGAT	GTCTGATTCC	AACATCTCTG	840
	GGTCTTTT	CACTCTGATA	TGCTGCAATT	AAAAAGCCAT	TTCTAAGACT	GT	

SEQ ID NO:202 PAA6 Protein sequence:

Protein Accession #: none found

70	1	11	21	31	41	51	
	MTYSYSFFRP	ELIVNHLNV	HSEANRRTKT	KTLLSLLSFL	DETSGLSTHL	PCLSLSKECG	60
75	VLHLDIHGKK	EDMRITQQSS	QLYLWDMGGF	TIFKNLWMSL	IPRGNKRSKP	RVTETILRDF	120
	KQKQSSKIQE	ERRRESAGPN	LSSFVWVGNA	GRGDRPQIWA	GSKQFSQ		

SEQ ID NO:203 PAB2 DNA SEQUENCE

Nucleic Acid Accession #: XM_050197
Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCCCTGGC TCCGGGTGAC 60
      AGCCGGGGCG CTCGGCCAGG ATCTGAGTGA TGAGACGTGT CCCACTGAG GTGCCCCACA 120
      GCAGCAGGTG TTGACCATGG GCTGAGAAGC TGGACCGGCA CCAAAGGGCT GGCAGAAATG 180
      GGGCCTGGC TGATTCTTAG GCAGTTGGCG GCAGCAAGGA GGAGAGGCCG CAGCTTCTGG 240
      AGCAGAGCCG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCCTGAGC CTAACCCGCC 300
      TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCCCGCTGC TGGCGCACCG GAAAGCCACG 360
      CTCTTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTGGCGCG AGGCATCACC 420
      TATGTCCCGC CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTTCATGAC CATGGTGTCTG 480
      GGCATGTGTC CAGTGTCTGG CTGTGCTGTG GTCCCGCTCC TAGGCTCAGC CAGTGACCAC 540
      TGGCGTGGAC GTATGTGGCG CCGCCGGGCC TTCACTGGG CACTGTCTCT GGGCATCTCTG 600
      CTGAGCCTCT TCTCATCTCC AAGGGCCGGC TGGCTAGCAG GGCTGCTGTG CCGGATCTCC 660
      AGGCCCTGG AGCTGGCACT GCTCATCTCG GCGTGGGGC TGCTGGACTT CTGTGGCCAG 720
      GTGTGCTTCA CTCCACTGGA GGCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780
      CGCCAGGGCT ACTCTGTCTA TGCTTCTATG ATCAGTCTTG GGGGTGCTT GGGCTACCTC 840
      CTGCTGGCCA TTGATGTGGA CACCACTGCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG 900
      TGCTCTTTTG GCTCTCTCAC CCTCATCTTC CTCACCTGCG TAGCAGCCAC ACTGTCTGGT 960
      GCTGAGAGGG CAGCGCTGGA CCCCACCGAG CCAGCAGAAG GGCTGTCTGG CCCCCTCTTG 1020
      TCGCCCCACT GCTGTCCATG CCGGGCCCGC TTGGCTTTCC GGAACCTGGG CGCCCTGCTT 1080
      CCCCCTGTC ACCAGCTGTG CTGCGCATG CCCCACCC TGCGCCGGCT CTTCGTGGCT 1140
      GAGCTGTGCA CAGTGTGTC ACTCATGACC TTCAGCTGT TTTACACGGA TTTCGTGGGC 1200
      GAGGGGCTGT ACCAGGGCGT GCGCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT 1260
      GATGAAGCGT TCGGATGGG CAGCGTGGGG CTGTCTCTGC AGTGCCTCAT CTCCCTGGTC 1320
      TTCTCTCTGG TCATGGACCG GCTGTGTCAG CGATTCCGCA CTCGAGCAGT CTATTTTGGCC 1380
      AGTGTGGCAG CTTCCTCTGT GGCTGCCGGT GCCACATGCC TGTCCACAG TGTGGCCGTG 1440
      GTGACAGCTT CAGCGCGCTT CACCGGGTTC ACCTTCTCAG CCTGCGCAT CCGTCCCTAC 1500
      ACACTGGCTT CCTCTACCA CCGGAGAAAG CAGGTGTTC TGCCCAAATA CCGAGGGGAC 1560
      ACTGAGAGTG TCTGATGGA GGACAGCCTG ATGACCAGCT TCCTGCCAGG CCTAAGCCT 1620
      GGAGCTCCCT TCCCTAATGG ACACGTGGGT GCTGGAGGCA GTGGCTGCT CCCACCTCCA 1680
      CCGCGCTCT GCGGGGCTCT TGCTGTGAT GTCTCCGTAC GTGTGGTGGT GGGTGAGCCC 1740
      ACCGAGGCCA GGGGTGGTTC GGGCCGGGGC ATCTGCTTGG ACCTCGCCAT CCGTATAGT 1800
      GCGTCTCTGC TGTCCAGGT GCGCCCATCC CTGTTTATGG GCTCCATTGT CCGACTCAGC 1860
      CAGTCTGTCA CTGCTATPAT GGTGTCTGCC GCAGGCTTGG GTCTGGTGGC CATTTACTTT 1920
      GCTACACAGG TAGTATTGA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAACTTCC 1980
      AGCACATTGG GGTGGAGGGC CTGCTCACT GGGTCCAGC TCCCGCTCC TGTAGCCCC 2040
      ATGGGCTGCT CAGGCTGGCC GCCAGTTTCT GTTGTGCTCA AGTAATGTG GCTCTCTGCT 2100
      GCCACCTGCT GCTGTGAGG TCGTAGCTG CACAGCTGGG GGCTGGGGCG TCCCTCTCCT 2160
      CTCTCCCGAG TCTCTAGGCG TGCTGACTG GAGGCTTCC AAGGGGTTT CAGTCTGAC 2220
      TTATACAGGG AGGCCAAGG GGCTCCATGC ACTGGAATGC GGGGACTCTG CAGGTGGATT 2280
      ACCCAGGCTC AGGGTTAACA GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTTCT 2340
      GGGAGCTGAA TAACTCAGT CACCTGGTTT CCCATCTCTA AGCCCCCTAA CCGTCAAGCT 2400
      CGTTTAAATG AGCTCTGCA TGGGAGTTTC TAGGATGAAA CACTCTCCA TGGGATTTGA 2460
      ACATATGAAA GTTATTTGTA GGGGAAGAGT CTTGAGGGGC AACACACAAG AACAGGTCC 2520
      CCTCAGCCCC ACAGGCACTG GTCTTTTTTG CTNGANTCCA CCCCCCCTT CTTTACCCTT 2580
      TT
  
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SEQ ID NO:204 PAB2 Protein sequence:

Protein Accession #: XP_050197

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55      1      11      21      31      41      51
      |      |      |      |      |      |
      MVQRLWVSR LHRKAQLLL VMLLTFGLEV CLAAGITYVP PLLLEVGVEE KFMTHVLGIG 60
      PVLGLVCPVL LGSADHWRG RYRRRRPFIW ALSLGILSL FLIPRAGWLA GLLCPPDRPL 120
      ELALLILGVG LDFCGQVCF TPLEALLSDL FRDPDHCROA YSVYAFMISL GGCLGYLLPA 180
      IDWDTALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH 240
      CCPCTRARLAP RNLGALLPRL HQLCRMRPT LRRLFVLELC SNMMLTFTL FTTDFVGEGL 300
      YQGVPRAEFG TEARRHYDEG VRHGSGLGLFL QCAISLVFSL VMDRLVQRFG TRAVYLASVA 360
      APFVAAGATC LSHSVAVVTA SAALTGPTFS ALQILPYTLA SLYHREKQVP LPKYRGDTGG 420
      ASSEDSLMTS FLPGPKPGAP FPNHGVGAGG SGLPPPPAL CGASACDVSF RVVVEPTEA 480
      RVVFGRGICL DLALDSAFI LSQVAPSLFM GSTIVQLSQSV TAYMVAAGL GLVAIYPATQ 540
      VVFDKSLAK YSA
  
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SEQ ID NO:205 PAJ3 DNA SEQUENCE

Nucleic Acid Accession #: AK002126
Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

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75      1      11      21      31      41      51
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      ATGGTTCGCC GGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60
      TGCTGTGCTA TCTCTGTCT GTACATGTTT GCCTGCACCC CAAAGGTGA CGAGGAGCAG 120
      CTGGCACTGC CCAGGGCCAA CAGCCCCACG GGAAGGAGG GGTACCAGGC CGTCTTCAG 180
      GAGTGGGAGG AGCAGCACCG CAACTACGTG AGCAGCTGA AGCGGCAGAT CGCACAGCTC 240
  
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5	AAGGAGGAGC	TGCAGGAGAG	GAGTGAGCAG	CTCAGGAATG	GGCAGTACCA	AGCCAGCGAT	300
	GCTGCTGGCC	TGGGTCTGGA	CAGGAGCCCC	CCAGAGAAAA	CCCAGGCCGA	CCTCCTGGCC	360
	TTCTGCTACT	CGCAGGTGGA	CAAGGCAGAG	GTGAATGCTG	GGCTCAAGCT	GGCCACAGAG	420
	TATGCAGCAG	TGCCCTTCGA	TAGCTTTACT	CTACAGAAGG	TGTACCAGCT	GGAGACTGGC	480
	CTTACCCGCC	ACCCCGAGGA	GAAAGCTGTG	AGGAAGGACA	AGCGGGATGA	GTTGGTGGAA	540
	GCCATTGAAT	CAGCCTTGGA	GACCCGTGAAC	AATCCTGCAG	AGAACAGCCC	CAATCACCGT	600
	CCTTACACGG	CCTCTGATTT	CATAGAAGGG	ATCTACCGAA	CAGAAAAGGA	CAAAGGGACA	660
	TTGTATGAGC	TCACCTTCAA	AGGGGACCAC	AAACACGAAT	TCAAACGGCT	CATCTTATTT	720
10	CGACCATTCG	GGCCCATCAT	GAAAGTGAAA	AATGAAAAGC	TCAACATGGC	CAACACGCTT	780
	ATCAATGTGA	TGCTGCTCT	AGCAAAAAGG	GTGGACAAGT	TCCGGCAGTT	CATGCAGAA	840
	TTACAGGAGA	TGTGCAATTGA	GCAGGATGGG	AGAGTCCATC	TCACCTGTGT	TTACTTTGGG	900
	AAAGAAGAAA	TAAATGAAGT	CAAAGGAATA	CTTGAAAAA	CTTCCAAAGC	TGCCAACTTC	960
	AGGAACTTTA	CCTTCATCCA	GCTGAATGGA	GAATTTTCTC	GGGGAAAGGG	ACTTGATGTT	1020
15	GGAGCCCGCT	TCTGGGAAGG	AAGCAACGTC	CTTCTCTTTT	TCTGTGATGT	GGACATCTAC	1080
	TTACATCTGT	AATTCCTCAA	TACGTGTAGG	CTGAATACAC	AGCCAGGGAA	GAAGGTATTT	1140
	TATCCAGTTC	TTTTCACTCA	GTACAAATCCT	GGCATAATAT	ACGGCCACCA	TGATGCAGTC	1200
	CCTCCCTTGG	AACAGCAGCT	GGTCATAAAG	AAGGAAACTG	GATTTTGGAG	AGACTTTGGA	1260
	TTTGGGATGA	CGTGTCACTA	TGCGTCAGAC	TTCATCAATA	TAGGTGGGTT	TGATCTGGAC	1320
20	ATCAAAGGCT	GGGGCGGAGA	GGATGTGCAC	CTTTATCGCA	AGTATCTCCA	CAGCAACCTC	1380
	ATAGTGGTAC	GGCGCCTCT	GCGAGGACTC	TTCCACCTCT	GGCATGAGAA	GCGCTGCATG	1440
	GACGAGCTAC	CCCCGAGACA	GTACAAGATG	TGCATGCAGT	CCAAGGCCAT	GAACGAGGCA	1500
	TCCCACGGCC	AGCTGGGCAT	GCTGGTGTTC	AGGCACGAGA	TAGAGGCTCA	CCTTCGCAAA	1560
	CAGAAACAGA	AGACAAGTAG	CAAAAAACA	<u>TGA</u>			

25

SEQ ID NO:206 PAJ3 Protein sequence:

Protein Accession #: NP_060841

30	1	11	21	31	41	51	
	MVRRGLLAWI	SRVVVLLVLL	CCAISVLYML	ACTPKGDDEQ	LALPRANSPT	GKEGYQAVLQ	60
	EWEEQHRYNY	SSLKRQIAQL	KEELQERSEQ	LRNGQYQASD	AAGLGLDRSP	PEKTQADLLA	120
	FLHSQVDRKE	VNAGVKLATE	YAAVPPDSPT	LQKVYQLETG	LTRHPEEKPV	RKDKRDELVE	180
35	AIESALETLN	NPAENSPNHR	PYASDFIEG	IYRTERDKGT	LYELTFKGDH	KHEFKRLILF	240
	RFFGPIIMKVK	NEKLNMANLT	INVIVPLAKR	VDKPRQFMQN	FREMCIEQDG	RVHLTVVVYFG	300
	KEEINEVKGI	LEWTSKAANF	RNFTPIQLNG	EP SRGKGLDV	GARFWKGSNV	LLFFCDVDYI	360
	PTSEFLMYCR	LNTQPGKKVF	YPVLF SQYNP	GIYGHHDVA	PPLEQQLVIK	KETGFWDFG	420
	FGMTCQYRSD	FINIGGFDLD	IKGWGGEDVH	LYRYLHNSLN	IVVRTPVRLG	FHLWHEKRCM	480
40	DELTPQYKYM	CMQSKAMNEA	SHGQLGMLVF	RHEIEAHLRK	QKQKTSSTKT		

SEQ ID NO:207 PAJ5 DNA SEQUENCE

Nucleic Acid Accession #: AF189723.

Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

45

50	1	11	21	31	41	51	
	ATGATTCCCTG	TATTGACATC	AAAAAAGCA	AGTGAATTAC	CAGTCAGTGA	AGTTGCAAGC	60
	ATTCTCCAAG	CTGATCTTCA	GAATGGTCTA	AACAAATGTG	AAGTTAGTCA	TAGGCCAGCC	120
	TTTCATGGCT	GGAAATGAGT	TGATATTAGT	GAAGATGAGC	CACGTGTGAA	GAAGTATATT	180
	TCTCATGTTA	AAAATCCCTC	TATTATGCTG	CTTCTGGCTT	CTGCAGTCA	CAGTGTPTTA	240
	ATGCATCACT	TTGATGATGC	CGTCAGTATC	ACTGTGGCAA	TACTTATCGT	TGTTACAGTT	300
55	GCCTTTGTTT	AGGAATATGC	TTCAGAAAAA	TCTCTGAAG	AATTGAGTAA	ACTTGTGCCA	360
	CCAGAATGCC	ATTGTGTGCG	TGAAGGAAAA	TTGGAGCATA	CACITGCCCG	AGACTTGGTT	420
	CCAGGTGATA	CAGTTTGCCT	TTCTGTTGGG	GATAGAGTTC	CTGCTGACTT	ACGCTTGTPT	480
	GAGGCTGTGG	ATCTTTCCAT	TGATGAGTCC	AGCTTGACAG	GTGAGACAAC	GCCTTGTCTT	540
	AAGGCTGACG	CTCCTCAGCG	AGCTGCAACT	AATGGAGATC	TTGCATCGAG	AAGTAACATT	600
60	GCCTTTATGG	GAACACTGGT	CAGATGTGGC	AAAGCAAAAG	GTGTTGTTCAT	TGGAACAGGA	660
	GAATAATCTG	AATTITGGGA	GGTTTTTAAA	ATGATGCAAG	CAGAAGAGGC	ACCAAAACC	720
	CCTCTGCAGA	AGAGCATGGA	CCTCTTAGGA	AAACAACCTT	CCTTTTACTC	CTTTGGTAPA	780
	ATAGGAATCA	TCATGTTGGT	TGGCTGGTTA	CTGGGAAAAG	ATATCCTGGA	AATGTTTACT	840
	ATTAGTGTAA	GTTTGGCTGT	AGCAGCAATT	CCTGAAGGTC	TCCCATTTGT	GGTCACAGTG	900
65	ACGCTAGCTC	TTGGTGTATT	GAGAAATGGT	AAGAAAAGGG	CCATTGTGAA	AAAGCTGCCT	960
	ATTGTTGAAA	CTCTGGGCTG	CTGTAATGTG	ATTGTTTCTG	ATAAAACTGG	AACACTGACG	1020
	AAGAATGAAA	TGACTGTTAC	TCACATATTT	ACTTCAGATG	GTCTGCATGC	TGAGGTTACT	1080
	GGAGTTGGCT	ATAATCAATT	TGGGGAAGTG	ATTGTTGATG	GTGATGTTGT	TCATGGATTTC	1140
	TATAACCCAG	CTGTTAGCAG	AATTTGTTAG	GCGGGCTGTG	TGTGCAATGA	TGCTGTAATT	1200
70	AGAAACAATA	CTCTAATGGG	GAAGCCAACA	GAAGGGGCTC	TAATTTGCTCT	TGCAATGAAG	1260
	ATGGGTCTTG	ATGGACTTCA	ACAAGACTAC	ATCAGAAAAG	CTGAATACCC	TTTTAGCTCT	1320
	GAGCAAAAGT	GGATGGCTGT	TAAGTGTGTA	CACCGAACAC	AGCAGGACAG	ACCAGAGATT	1380
	TGTTTATATGA	AAGTGTCTTA	CGAACAAAGTA	ATTAAGTACT	GTACTACATA	CCAGAGCAAA	1440
	GGGCAGACCT	TGACACTTAC	TCAGCAGCAG	AGAGATGTGT	ACCAACAAGA	GAAGGCACGC	1500
75	ATGGGCTCAG	CGGGACTCAG	AGTTCTTGCT	TTGGCTTCTG	GTCTGTAAGT	GGGACAGCTG	1560
	ACATTCTCTG	GCTTGGTGGG	AATCATGTAT	CCACCTAGAA	CTGCTGTGAA	AGAAGCTGTT	1620
	ACAACACTCA	TTGCCCTCAG	AGTATCAATA	AAAATGATTA	CTGGAGATTTC	ACAGGAGACT	1680
	GCAAGTGGCA	TCGCCAGTCG	CTCGGATTTG	TATTCCAAAA	CTTCCCAAGT	AGTCTCAGGA	1740
	GAAGAAATAG	ATGCAATGGA	TGTTTACGAG	CTTTCACAAA	TAGTACCAAA	GGTTGCAGTA	1800
80	TTTTATCAGT	CTAGCCCAAG	GCACAAGATG	AAAATATATTA	AGTCGCTACA	GAAGAACGGT	1860
	TCAGTTGTAG	CCATGACAGG	AGATGGAGTA	AATGATGCAG	TTGCTCTGAA	GGCTGCAGAC	1920

5
 10
 15

ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
 CTAGTGGATG ATGATTTTCA AACCATATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040
 AATAACATTA AAAATTTCTG TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACTTTA 2100
 ATCTCATTTG CTACATTAAT GAATTTCTCT AATCTCTCA ATGCCATGCA GATTTTGTGG 2160
 ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
 GATGTCATTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280
 CTTAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTTTGT CTTCTGGCGT 2340
 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
 TTTTTCGACA TGTCAATGC ACTAAGTTCC AGATCCAGA CCAAGTCTGT GTTTGAGATT 2460
 GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520
 CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
 GATCTGTGTT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
 CTTGAAGTAT GA

SEQ ID NO:208 PAJ5 Protein sequence:

Protein Accession #: AAF27813

20
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1' 11 21 31 41 51
 MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNEFDIS EDEPLWKYI 60
 SQFKNPLML LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQYRSEK SLEELSKLVP 120
 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180
 KVTAPQPAAT NGDLASRSNI AFMGTLVRCG KAKGVVIGTG ENSEFGEVFK MMQAEAPKT 240
 PLQKSMIDLK KQLSFYSFGI IGIIMLVGWL LGKDILEMPT ISVSLAVAAI PEGLPVVTV 300
 TLALGVRRMV KKRATVKKLP IVETLGCCNV ICSDRTGTLT KNEMTVTHIF TSDGLHAEVT 360
 GVGYNQFGEV IVDGVVHGF YNPAVSRIE AGCVNCDAVI RNTLMGKPT EGALIALAMK 420
 MGLDGLQDY IRKAEYFFSS EQKMAVKCV HRTQDRPEI CFMKGAYEQV IKYCTTYQSK 480
 GQTLTLTQQQ RDVYQEKAR MGSAGLRVLA LASGPELGQL TPLGLVGIID PPRTGVKEAV 540
 TTLIASGVSI KMITDSDQET AVAIA SRLGL YSKTSQSVSG EEDAMDVQQ LSQIVPKVAV 600
 FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEADMI 660
 LVDDDFQFIM SAIEEGKGIY NNINKFVRFO LSTSLAALT ISLATLMNFP NPLNAMQILW 720
 INIIMDGPFA QSLGVEFPDK DVIRKPPRNW KDSILTQNL LKILVSSIII VCGTLFVFW 780
 ELRDNVITPR DTHMTFTCFV FFDMPNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840
 LVITYPPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSREKIQ KHVSSSTSSP 900
 LEV

SEQ ID NO:209 PAV4 VARIANT 1 DNA SEQUENCE

Nucleic Acid Accession #: N62096

Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

45
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 65

1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGA GAGGATTGCC TTATTCAATG 60
 AAGCAAGCTG GGTTCCTTTT GGGAAATATTG CPTTTATTCT GGGTTTCATA TGTACAGAC 120
 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCGCTCTCTG GAACAGATAC CTACCACTCT 180
 TTGGTCAATA AAATTTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTC TCAGTTTGTG 240
 TATCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATAGTCT GAGCAAAAGTT 300
 TTTCAAGAA TCCAGGAGT TGATCTGAA AACGTGTTTA TTGGTCGCCA CTTCATTATT 360
 GGACTTTCCA CAGTTACCTT TACTCTGCTT TTATCTTGT ACCGAAATAT AGCAAAAGCTT 420
 GGAAAGGTCT CCTCATCTC TACAGTTTGA ACAACTCTGA TTCTTGAAT TGTAATGGCA 480
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAA AGCCTTGGGT ATTTGCAAG 540
 CCAATGCGCA TTCAAGCGGT CGGGGTATG TCTTTTGAT TTATTGCGCA CCATAACTCC 600
 TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
 ATGTCCATCG TGATTCTCTG ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA 720
 TTTACTGGCT TCACCCCAAG GGAATTATT GAAATTAAT GCAGAAATGA TGACCTGGTA 780
 ACATTGGAA GATTTTGTGA TGGTGTCACT GTCAATTTGA CATACCCCTAT GGAATGCTTT 840
 GTGACAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTTCATC GGTTTTCCAC 900
 ATTGTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC 960
 CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCTCTCAT TTTTATCATT 1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTAAT 1080
 TCTGTGTCA TGCCTTCCAT TGGTGTCTGT GTGATGGTTT TTGATTCGT CATGGCTATT 1140
 ACAAAATCTC AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTCC TGACAATTTT 1200
 TCTCTCAAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
 ATTAGTATCT TTCAACTCGA GTAA

SEQ ID NO:210 PAV4 Variant 1 Protein sequence:

Protein Accession #: none found

75
 80

1 11 21 31 41 51
 MGQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWSVYTD FSLVLLIKGG ALSGTDYQS 60
 LVNKTFFGPG YLLLSVLQFL YPFIAMISYN IAGDLSKV FQRI PGVDPE NVFIGHFPII 120
 GLSTVFTFLP LSLYRNIAKL GKVSISTGL TTLILGIVHA RAISLGPPIH KTEDAWVFAK 180
 PNAIQAVGVN SPFAICTHNS FLVYSSLEEP TVAKWSRLIH MSIVISVPIC IFFATCGVLT 240
 FTGFTQGLDF ENYCNRDLDV TFGRFCYGVV VILTYPMECF VTREVIANVF FGGNLSVPH 300
 IVTVHVITV ATVLVSLDLC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360
 SCVMLPIGAV VMVFGFVMAI TMTQDCTHQ EMFYCFPNDF SLTNTSESHV QQTQLSTLN 420

ISIPQLE

SEQ ID NO:211 PAV4 VARIANT 2 DNA SEQUENCE

5 Nucleic Acid Accession #: N62096
Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
| | | | | |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGT TTTCCCTTGT TTTATTGATA 60
AAAGGAGGGG CCCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCGGC 120
TTTCCAGGGT ATCTGCTCCT CTCGTGTCCT CAGTTTGTGT ATCCTTTTAT AGCAATGATA 180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT 240
15 GATCCTGAAA ACGTGTTTAT TGGTCGCCAC TTCAATTATT GACTTTCAC AGTTACCTTT 300
ACTCTGCCCT TATCCTTTGC CCGAAATATA GCAAAGCTTG GAAAGGCTC CCTCATCTCT 360
ACAGGTTTAA CAACTCTGAT TCTTGAATT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420
CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC 480
GGGGTTATGT CTTTGCATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540
20 GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCATCGT GATTCTCTGA 600
TTTATCTGTA TATCTTTTGC TACATGTGGA TACTTGACAT TTAAGGCTT CACCAAGGG 660
GACTTATTTC AAAATTACTG CAGAAATGAT GACCTGGTAA CATTTGGAAG ATTTTGTAT 720
GGTGTCACTG TCATTTTGAC ATACCTATG GAATGCTTTG TGACAAGAGA GGTAAATGCC 780
25 AATGTGTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGAATGTC 840
ATCACTGTAG CCACGCTTGT GTCATGTCTG ATTGATGACC TCGGGATAGT TCTAGAACTC 900
AATGGTGTGC TCTGTGCAAC TCCCTTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960
CTGTCTGAAG AACCAAGGAC ACACTCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020
GGTGTCTGGG TGATGTTTAT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080
30 CATGGGCAAG AAATGTTCTA CTGCTTTCCT GACAATTTC CTCTCAGAAA TACCTCAGAG 1140
TCTCATGTC AGCAGACAAC ACAACTTCT ACTTTAAATA TTAGTATCTT TCAACTCAGAG 1200
TAA

SEQ ID NO:212 PAV4 Variant 2 Protein sequence:

35 Protein Accession #: none found

40 1 11 21 31 41 51
| | | | | |
MGYQREQEVI PPOFSLVLLI KGGALSGTDT YOSLVNKTFG PPGYLLLSVL QFLYPFIAMI 60
SYNIIAGDTL SKVFRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLLS 120
TGLTTLILGI VMARAILSGP HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180
EETPVAKWSR LIHMSIVISV FICIFFATCG YLFTTGFTQG DLFENYCRND DLVTFGRFCY 240
45 GVTVILTYFM ECTVPREVIA NVFFGGNLSS VFHIVTVMV ITVATLVSLI IDCLGIVLEL 300
NGULCATPLI FIIPSACVLYK LSEEPRTSD KIMSCVHLPI GAVVMVFGFV MAITNTQDCT 360
HGQEMFYCFP DNFSLTNTSE SHVQQTQLS TLNISIFQLE

SEQ ID NO:213 PAV4 VARIANT 3 DNA SEQUENCE

50 Nucleic Acid Accession #: N62096
Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
| | | | | |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCCGCTTT 60
CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTGATC CTTTATAGC AATGATAAGT 120
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAACAG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT 240
60 CTGCTTTTAT CCTGTGACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300
GGTTTAACAA CTCTGATCTT TGGAAATGTA ATGGCAAGGG CAATTTCAC TGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTCCGG 420
GTTATGTCTT TTGCAATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCAATCGTAT TTCTGTATTT 540
ATCTGTATAT TCTTTGCTAC ATGTGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
65 TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAGAGAT TTGTTATGGT 660
GTCACGTGCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTTG GTGGGAATCT TTCAATCGGT TTCCACATG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
70 GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTCAT CAGCCTGTTA TCTGAAACTG 900
TCTGAAGAAC CAAGGACACA CTCCGATAAG ATTATGCTT GTGTCATGCT TCCCATTTGT 960
GCTGTGGTGA TGGTTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
GGGCAGGAAA TGTTCTACTG CTTTCTGAC AATTTCCTC TCACAAATAC CTCAGAGTCT 1080
CATGTTACAG AGACAACACA ACTTCTACT TTAATATTA GTATCTTTCA ACTCAGATAA

SEQ ID NO:214 PAV4 Variant 3 Protein sequence:

75 Protein Accession #: none found

80 1 11 21 31 41 51
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MGYQRQEPVI PPQVNKTFGF PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRI PGVD 60
PENVPFGRHF IIGLSTVTFE LPLSLYRNIA KLKVSLSIST GLTTLILGIV MARAISLGPB 120
IPKTEDAMVF AKPNAIQAVG VMSFAFICHH NSFLVYSLE EPTVAKWSRL IHMSIVISVF 180
ICIFPATCGY LFTGFTQGD LFENYCRNDD LVTGGRFCYQ VTILTYPM ECPVTREVLN 240
VFPFGLSSV PHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300
SEEPRTSHDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH QQEMFYCFPD NPSLTNTSES 360
HVQQTQLST LNTSIFQLE
  
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10
 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

15
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1 11 21 31 41 51
| | | | |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGATTAGA TGACAGAGAA 60
ACCTTGTGTT CTGAACATGA GTATAAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
GTGTGCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180
GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTATACAGA CTTTTCCTT 240
GTTTATATGA TAAAGGAGG GGCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT 300
AAAACCTTCG GCTTCCAGG GTATCTGCTC CTCTCTGTTT TTCAGTTTTT GTATCCTTTT 360
ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAAGT TTTTCAAGA 420
ATCCAGGAGG TTGATCTGTA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC 480
ACAGTTACCT TTACTCTGCC TTTATCCTTG TACCGAAATA TAGCAAGCTC TGGAAAGGTC 540
TCCCTCATCT CTACAGGTTT AACAACTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT 600
TCACTGGGTC CACACATACC AAAACAGAA GACGCTTGGG TATTTCGAAA GCCCAATGCC 660
ATTCAAGCGG TCGGGGTTAT GTCTTTTGCA TTTATTGGCC ACCATAACTC CTCTTAGTAT 720
TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
GTGATTCTCG TATTTATCTG TATATTCTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840
TTCAACCCAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTGGA 900
AGATTGTTGT ATGGTGTGAC TGTCAATTTG ACATACCTTA TGGAAATGCTT TGTGACAAGA 960
GAGGTAAATG CCAATGTGTT TTTTGGTGGG AATCTTTTCAT CGGTTTTCCTA CATTTGTTGA 1020
ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATTG CCTCGGGATA 1080
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATTCAT TCCATCAGCC 1140
TGTATATGTA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
ATGCTTCCCA TTGGTGTGTT GGTGATGGTT TTTGGATTGC TCATGGCTAT TACAAATACT 1260
CAAGACTGCA CCCATGGGCA GGAATGTGTC TACTGCTTTC CTGACAATTT CTCTCTCACA 1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC 1380
TTTCAATGA
  
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SEQ ID NO:216 PAV4 Variant 4 Protein sequence:

45
 Protein Accession #: none found

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1 11 21 31 41 51
| | | | |
MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60
GFPLGILLLF WVSYYTDFSL VLLIKGGALS GTDTYQSLVN KTFGFPYLL LSLQLPLYPF 120
IAMISYNIIA GDSYKVFQR IPGVDPENVF IGRHPIIGLS TVTFTLPLSL YRNIA RLKGV 180
SLISTGLTTL ILGIVMHARI SLGPHIPKTE DAWVPAKPNA IQAVGVMSFA FICHNSFLV 240
YSSLEBPVVA KWSRLIHMSI VISVPICIFF ATCGVLTFTG FTQGDLFENY CRNDDLVTFG 300
RFCYGVTVIL TYPMECFVTR EVLANVFFGG NLSSVFHIVV TVMVTIVATL VSLIIDCLGI 360
VLELNGVLCA TPLIFIPISA CYLKLSEEP THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420
QDCTHQQEMF YCFPDNFSLT NTSSEHVQQT TQLSTLNI SI FQ
  
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60
 Nucleic Acid Accession #: NM_017636
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCAG 60
GAGAAGCCCA CCGATGCCTA CGGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACAGC 120
AATTTCCTCC GGCTCTCTGA CCGAACGGAT CCAGCTGCAG TTTATAGTCT GGTACACAGC 180
ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCAATGC TGGGGGGATC GGGGGGGCCC 240
GTCTCCAGA CTTGGCTGCA GGACCTGCTG CGTCTGGGCG TGGTGGGGGC TGCCAGAGC 300
ACAGGAGCCT GGATGTGAC TGGGGGTCTG CACACGGGCA TCGGCCGCCA TGTGGTGTG 360
GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGGCACCA AGGTGGTGGC CATGGGTGTG 420
GCCCTTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCAAGGG CTCGTTCCCT 480
GCGAGGTACC GGTGGCGCGG TGACCGGAG GACGGGGTCC AGTTTCCCTT GGACTACAAC 540
TACTCGGCTT TCTTCTGGT GGACGACGGC ACACACGGCT GCCTGGGGGC CGAGAACCGC 600
TTCCGCTTGC GCCTGGAGTC CTACATCTCA CAGCAGAAGA CGGGCGTGGG AGGACTCGGA 660
ATTGACATCC CTCTCTGCT CTCTCTGATT GATGGTGATG AGAAGATGTT GACCGGAATA 720
GAGAAGCCCA CCCAGCTCAT GCTCCCATGT CTCTCTGTTG CTGGCTCAGG GGGAGCTCGG 780
GACTGCCTGG CCGAGACCTT GGAAGACACT CTGGCCCAAG GGAGTGGGGG AGCCAGGCAA 840
GGCGAAGCCC GAGATCGAAT CAGGCGTTTC TTTCCCAAG GGGACCTTGA GTCTCTGAGC 900
GCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCTGTA CAGTCTATTC TTCTGAGGAT 960
  
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GGGTCTGAGG AATTCGAGAC CATAGTTTTC AAGGCCCTTG TGAAGGCCTG TGGGAGCTCG 1020
 GAGGCTCTAG CCTACCTGGA TGAGCTGCGT TTGGCTGTGG CTGGAAACCG CGTGGACATT 1080
 GCCCAGAGTG AACTCTTTTC GGGGACATC CAATGGCGGT CCTTCCATCT CGAAGCTTCC 1140
 CTCATGGACG CCTGCTGAA TGACCGGCTT GAGTTCGTGC GCTTGCCTAT TTCCACGGC 1200
 CTCAGCCTGG GCCACTTCCT GACCCGATG GCCTTGGCCC AACTCTACAG CGCGGCGCCC 1260
 TCCAACCTGC TCATCCGCAA CCTTTTGGAC CAGGCGTCCC ACAGCGCAGG CACCAAAGCC 1320
 CCAGCCTTAA AAGGGGAGC TGGCGAGCTC CGGCCCTCTG ACGTGGGCA TGTGCTGAGG 1380
 ATGCTGCTGG GGAAGATGTG CGCGCCGAGG TACCCCTCCG GGGCGCCTG GGACCCCTAC 1440
 CCAGGCCAGG GGTTCGGGGA GAGCATGTAT CTGCTCTCGG ACAAGGCCAC CTCGCCGCTC 1500
 TCGCTGGATG CTGGCTTCGG CGAGGCCCCC TGGAGCGACC TGCTCTTTTG GGCACGTGTT 1560
 CTGAACAGGG CACAGATGGC CATGTACTTC TGGAGATGG GTTCCAATGC AGTTTCCCTCA 1620
 GCTCTTGGGG CCTTTTGTCT GCTCCGGGTG ATGGACGCCG TGGAGCCTGA CGCTGAGGAG 1680
 GCAGCAGGA GGAAGAACCT GGCCTTCAAG TTTGAGGGGA TGGCGTGA CCTCTTTGGC 1740
 GAGTGCTATC GCAGCAGTGA GGTGAGGGCT GCCCGCTCC TCCTCCGTG CTGCCGCTC 1800
 TGGGGGATG CCACTTGCCT CCAGCTGGCC ATGCAAGCTG ACGCCGTGC CTCTTTTGGC 1860
 CAGGATGGG TACAGTCTCT GCTGACACAG AAGTGGTGGG GAGATATGG CAGCACTACA 1920
 CCCATCTGGG CCTTGTCTCT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CGCCTTCTAC 1980
 ACCTTCAGGA AATCAGAAGA GGAGCCACAC CGGAGGAGC TAGAGTTTGA CATGGATAGT 2040
 GTCATTAAAG GGAAGGGGCC TGTGCGGACG GCGGACCCAG CCGAGAAGAC GCCGCTGGGG 2100
 GTCCCGCGCC AGTCGGGCGG TCCGGGTTCG TCCGGGGGCC GCTCGGGGG GCGCCGCTGC 2160
 CTAGCGCGCT GGTTCACCTT CTGGGGCGCG CCGGTGACCA TCTTCATGGG CAACGTGGTC 2220
 AGCTACCTGC TGTTCCTGCT GCTTTTCTCG CGGGTGTGTC TCGTGGATTG CCAGCCGGCG 2280
 CCGCCCGGCT CCTTGGAGCT GCTGCTCTAT TTCTGGGCTT TCACGCTGCT GTGCGAGGAA 2340
 CTGCGGACG GCTGAGCGG AGCGGGGGG AGCCTCGCCA GCGGGGGGCC CGGCCCTGGC 2400
 CATGCCCTAC TGAGCCAGCG CCTGCGCTC TACCTCGCCG ACAGCTGGA CCAGTGCAGC 2460
 CTAGTGGCTC TCACCTGCTT CCTCTTGGG GTGGGCTGCC GGCTGACCCC GGGTTTGTAC 2520
 CACCTTGGGC GCATCTGCTT CTGCATCGAC TCTATGTTT TCACGGTGGC GCTGCTTAC 2580
 ATCTTCACGG TCAACAAACA GCTGGGGCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG 2640
 GACGTGTCTT TCTTCTCTT CTTCCTCGG GTGTGGCTGG TAGCCTATGG CGTGCCACG 2700
 GAGGGGCTCC TGAGGCCAGG GCACAGTGAC TTCCCAAAGTA TCTTCGCGCG CGTCTTCTAC 2760
 CGTCCCTACC TGCAGATCTT CGGGCAGATT CCCCAGGAG ACATGGACGT GGCCCTCATG 2820
 GAGCAGCACT ACTGCTGCTG GGAGCCCGGC TTCTGGGCAC ACCCTCTCTG GCGCCAGCGC 2880
 GGCACCTGCG TCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTCTGT CATCTTCTG 2940
 CTCGTGGCCA ACATCTGCTT GGTCAACTTG CTCATTGCCA TGTTCAGTTA CACATTCGGC 3000
 AAGTACAGG GCAACAGCGA TCTCTACTGG AAGCGCAGC GTTACCGCT CATCCGGGA 3060
 TTCCACTCTC GGGCCCGCTT GGGCCCGCCC TTTATCTGTA TCTCCACTT GCGCCTCTG 3120
 CTCAGGCAAT TGTGAGGCG ACCCCGAGC CCCCAGCGT CCTCCCGGC CCTCGAGCAT 3180
 TTCCGGGTTT ACCTTTCTAA GGAAGCCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGCAT 3240
 AAGAGAACT TCTGCTGGC ACGCGCTAGG GACAAGCGG AGAGCGACT CGAGCGTCTG 3300
 AAGCGCAGT CCCAGAAGT GGACTTGGCA CTGAAACAGC TGGGACAT CCGCGAGTAC 3360
 GAACAGCGCC TGAAGATGCT GGAGCGGAG GTCCAGCAGT GTAGCCCGT CCTGGGGTGG 3420
 GTGGCCGAGG CCTTGAGCG CTCTGCCCTG CTGCCCCAG GTGGGCCGCC ACCCCCTGAC 3480
 CTGCTGGGT CCAAAGACTG A

SEQ ID NO:218 PAV9 Protein sequence:

Protein Accession #: none found

50
 55
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1 11 21 31 41 51
 MEDAFGAADV TVWDSDAHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
 TWGRAPFNLV VSVLGGSGGP VLQTLWQDLL RRLVRAAQS TGAWIVTGL HTGIGRHVGV 120
 AVRDRHQMST GGTQVAMGV APWGVVRNRD TLINPKGSFP ARYRWGRDPE DGVQFPLDYN 180
 YSAFFLVDDG THGCLGGENR FRLRLESYIS QOKTGVGGTG IDIPLVLLLI DGDEKMLTRI 240
 ENATQAQLPC LLVAGSGGAA DCLAETLEDT LAPGSGGARQ GEARDRIIRF FPKGDLEVLQ 300
 AQVERIMTRK ELLTVYSSED GSEEFETIVL KALVKACGSS EASAYLDEL R LAVAMNRVDI 360
 AQSELFRGDI QWRSFHLEAS LMDALLNDRP EFRVLLISHG LSLGHFLTPM RLAQLYSAAP 420
 SNSLIRNLID QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
 PQQGFSGESMY LLSDKATSPL SLDAGLGQAP WSDLLHALL LARAQMAHYF WEMGSNAVSS 540
 ALGACLLLRV MARLEPDAEE AARRKDLAFK FEGMGVDLFG ECYRSSEVRA ARLLLRRCPL 600
 WGDATCLQLA MQADARAFFA QDGVQSLLTQ KWWGDMASTT PIWALVLAP CPPLIYTRLI 660
 TFRKSEEEPT REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGRCCGRRR 720
 LRRWFHFWGA PVTIFPMNVV SYLLFLLLF S RVLLVDFOPA PPSLELLLY FWAFTLLCEE 780
 LRQGLSGGGG SLASGGFGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
 HLGRTVLCID FHVFTVRLH IFTVNKQLGP KIVIVSIOHK DVFFFLFPLG VWLVAYGVAT 900
 EGLLRPRDS FFSILRRVFY RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPPGAQA 960
 GTCVSQYANM LVVLLVIFL LVANILLVNL LIAMFSYTFG KVQGNSDLYN KAQRYLIRE 1020
 FHSRPAAPP FIVISHLRL LRLQCRPRPS POPSSPALEH FRVYLSKEAE RKLLTWESVH 1080
 KENFLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY BQRLKVLERE VQCSRVLGW 1140
 VAEALSRSAL LPPGGPPPPD LPSKSD

SEQ ID NO:219 PBF1 DNA SEQUENCE

Nucleic Acid Accession #: AA054237

Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
 ATGGAGCCCG GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCTTGGGG 60
 CTGCTGCTCA CGGCCATCTT CACCGACCAC TGGTACGAGA CCGACCCCGC GCGCCACAAG 120
 GAGAGCTGCG AGCGCAGCGG CGCGGGCGCC GACCCCCCGG ACCAGAAGAA CCGCCTGATG 180

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CCGCTGTCGC ACCTGCCGCT GCGGGACTCG CCCCCGCTGG GCGGCCGGCT GCTCCCGGGC 240
GGCCCCGGGC GCGCCGACCC CGAGTCCTGG CGTCGCTCC TGGGGCTCGG CCGGCTGGAC 300
GCCGAGTGGC GCCGGGCCCC CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGGCATCG ACCGGGACAT CGACACCCCTC ATCTGAAAG GTATTGCGCA GCGATGCACG 420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCGAA ACATTCTTTT TAATTTAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTAA GAAGAATCAC TGCTGGCTTC 540
CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT 660
TGCAACATTT CCCCTCTGTAC TTATGCCGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCCTGGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA

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SEQ ID NO:220 PBF1 Protein sequence:
Protein Accession #: none found

1 11 21 31 41 51
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM 60
PLSHLPLRDS PPLGRRLLP GPGRADPEW RSLGLGLD AECGRPLFAT YSGLWRKCYF 120
LGIDRDIIDL ILKGIAQRCT AIKYHFSQPI RLRLNIPNLT KTIQDDEWHL LHLRRITAGF 180
LGHAVAVLLC GCIVATVSFF WEESLTQHVLA GLLFLMTGIF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

SEQ ID NO:221 PCM DNA SEQUENCE

Nucleic Acid Accession #: NM_016570
Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGAGGCGAC TGAATCGGAA AAAAAGCTTAA AGTTTGGTAA AAGAGTTGGA TGCTTTCCG 60
AAGGTTCCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
TTTACAACFA TGCGTTTATT AACCATAAATG GAATTCCTCAG TATATCAAGA TACATGGATG 180
AAGTATGAAT ACCAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
ACTGTGCGCA TGAAGTGCTA ATATGTTGGA CGGATGTATG TGGAATTAGC AGAAACAATG 300
GTTGCATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACAT 420
CAAGATGTGA TATTTAAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCATAAAA 540
GTAGCAGGGA ATTTTACATC AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600
CATTTGGCAG CACTTGTCAA CCAATGAATCT TACAATTTT CTATAGAAT AGATCATTG 660
TCTTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAAGTGA AAAAATTGCT 720
ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
TATAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAA 840
CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTTCTCTT 900
ATGCTGACAG TTAATGAGGA GCACATGCCA TTCTGGCAGT TTTTGTGAAG ACTCTGTGGT 960
ATTGTTGGAG GAATCTTTTC AACACAGGC ATGTTACATG GAATTGGAAT ATTTATAGTT 1020
GAAATAATTT GCTGCTGTTT CAGACTTGA TCCATATAAC CTGTCAATTC TGTTCCTTTT 1080
GAGGATGGCC ACACAGACAA CCACCTACCT CTTTTAGAAA ATAATACACA TTGA

SEQ ID NO:222 PC14 Protein sequence:
Protein Accession #: NP_057654

1 11 21 31 41 51
MRRLNRKKT SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
KYEYEDKDF SSKLRINIDI TVAMKCQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQ 120
KEWQRLQLI QSRLQEEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180
VAGNFHITVG KAI FHPRGHA HLAALVNHE S YNFSHRIDHL SFGLVPAII NPLDGTEDIA 240
IDHNQMFQYF ITVVPKTLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
MVTVTTEHMP FWQPFVRLCG IVGGIFSTTG MLHGIGKFIV EIICCRFRIG SYKPVNSVFP 360
EDGHTDNHLP LLENNTN

SEQ ID NO:223 PEZ3 DNA SEQUENCE

Nucleic Acid Accession #: NM_001935.1
Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CGCGCGTCTC CGCGCGCCGC GTGACTTCTG CCTCGGCTCC TTCTCTGAAC GCTCACTTCC 60
GAGGAGACGC CGACGATGAA GACACCGTGG AAGATTCTTC TGGGACTGCT GGGTGCTGCT 120
GCGCTGTGCA CCAATCATCAG CGTGGCCGTG GTTCTGCTCA ACAAAGGCAC AGATGATGCT 180
ACAGCTGACA GTCCGAAAAC TTACACTCTA ACTGATTACT TAAAAAATAC TTATAGACTG 240
AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAAACA AGAAAAAAT 300

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ATCTTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT 360
 GATGAGTTTG GACATTCTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTTCTC 420
 TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCCTACA CAGCTTCATA TGACATTTAT 480
 GATTTAAATA AAAGCCAGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC 540
 ACATGGTCAC CAGTGGGTCA TAAATGGCA TATGTTTGA ACAATGACAT TTATGTTAAA 600
 ATTGAACCAA ATTTACCAAG TTACAGAATC ACATGGACGG GGAAGAAGA TATAATATAT 660
 AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTCCCTACTC TGCTCTGTGG 720
 TGGTCTCAA ACGGCACATT TTAGCATAT GCCCAATTA ACACACAGA AGTCCACATT 780
 ATTGAATACT CCTTCTACTC TGATGAGTCA CTGCAGTACC CAAAGACTGT ACGGGTTCCA 840
 TATCCAAAGG CAGGAGCTGT GAATCCAAC TAAAGTTCT TTGTTGTAAA TACAGACTCT 900
 CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCTGTCTC TATGTTGATA 960
 GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAAGAATTTC TTGCACTGG 1020
 CTCAGGAGGA TTCAAGAACTA TTCGGTCATG GATATTTGTG ACTATGATGA ATCCAGTGA 1080
 AGATGGAAC ATATAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA 1140
 AGATTTAGGC CTTCAGAAC TCATTTTACC CTGATGGTA ATAGCTTCTA CAAGATCATC 1200
 AGCAATGAAG AAGGTTACAG ACACATTTCG TATTTCCAAA TAGATAAAAA AGACTGCACA 1260
 TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAA CTCTAACAG TGATTTATCTA 1320
 TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAAAATCAA 1380
 CTTATTGACT ATACAAAAGT GACATGCCTC AGTTGTGAGC TGAATCCGGA AAGGTGTGAG 1440
 TACTATTCTG TGTCATTCTG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500
 GGTCTGCCCC TCTTACTCTC ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCTTGGAA 1560
 GACAATTCAG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAAACTGGAC 1620
 TCAATATTTT TGAATGAAC AAAATTTTGG TATCAGATGA TCTTGCTTCC TCAATTTGAT 1680
 AAATCCAAAG ATATCTCTCT ACTATTAGAT GTGTATGCA GCGCATGTAG TCAAAAAGCA 1740
 GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTTATAGTA 1800
 GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860
 AGAAGACTGG GAACATTTGA AGTTGAAGAT CAAATTGAAG CAGCCAGACA ATTTTCAAAA 1920
 ATGGGATTTG TGGACAAACA ACGAATTGCA ATTTGGGGCT GGTCAATGAG AGGGTACGTA 1980
 ACCTCAATGG TCCTGGGATC GGAAGTGGC GTGTTCAAGT GTGGAATAGC CGTGGCGCCT 2040
 GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100
 CCAGAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAATAATTT 2160
 AAACAAGTTG AGTACCTCCT TATTCTGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG 2220
 TCAGCTCAGA TCTTCAAAG CCTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280
 ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340
 AGCCACTTCA TAAAAAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400
 AAGCTTATTA AAATCACTTT TTGTTTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
 TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAAGT TACCTTTGTT CCAAAATTTT 2520
 ATACCTATCA TCTTAAGTAG GGAATCTGT CTTCACAACA GATTATTACC TTACAGAAAT 2580
 TTGAATATC CGGTGGGGTT TTATTGTTTA AAATCATTTT TGCATCAGCT GCTGAAACAA 2640
 CAAATAGGAA TTGTTTTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700
 TTCTTAACCT GACTGGTTCA AATGTGTTTC TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760
 AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA 2820
 TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTGAG CTCCCTCGG 2880
 AGAAGAGCTG TTCACCAGA GACTGGCACA GTTTTCTGAG AAAGACTATT CAAACAGTCT 2940
 CAGGAAATCA AATATCGAAA GCACGACTTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000
 AAAGAAATGT AAGGGAATC GCCAGCAACG CAGCCCCAG GTGCCAGTTA TGGCTATAGG 3060
 TGCTACAAA ACACAGCAAG GGTGATGGGA AAGCATTGTA AATGTGCTTT TAAAAAATA 3120
 TACTGATGTT CCTAGTGAAG GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180
 CTGTTAAAG ATGAAATAT TTGTATCACA AATCTTAAC TGAAGGAGTC CTGCAATCAA 3240
 TTTTCTTAT TTCAATTTCT TGAGTGTCTT AATTAAGAAG ATATTTTAACT TTCCTTGGAC 3300
 TCATTTTAAA AAATGGAACA TAAATACAAA TGTTATGTAT TATTATTCCC ATTCTACATA 3360
 CTATGGAATT TCTCCCAATC ATTTAATAAA TGTGCCTTCA TTTTTC

55
 SEQ ID NO:224 PFZ3 Protein sequence:
 Protein Accession #: NP_001926.1

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1 11 21 31 41 51
 MKTPWKILLG LLGAAALVTI ITVPVLLLNK GTDDATADSR KTYTLTDYLK NTYRLKLYSL 60
 RWISDHEYLY KQENNLVFN AEYGNSSVFL ENSTFDEFH SINDYSISPD GQFILLENYN 120
 VKQMRHSYTA SYDIYDLNKR QLITEERIPN NTQVTVSPV GHKLAYVWNN DIYVKIEPNL 180
 PSYRITWTGK EDIINYGITD WYEEVFPFA YSALWNSPFG TFLAYAQFND TEVPLIEYSF 240
 YSDESLOYPK TVRVPPKAG AVNPTVKPFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
 CDVTWATQER ISLQWLRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360
 EPHFTLDGNS FYKIISNEEG YRHICYFQID KDCCTFITKG TWEVIGIEAL TSDYLYYISN 420
 EYKMPGGRN LYKIQIDYT KVTCLSCBLN PERCQYYSVS FSKEAKYYQL RCGSPGLPLY 480
 TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDPIILN ETKFWYQML PPHFDKSKKY 540
 PLLLDVYAGP CSOKADTVFR LNWTYLAST ENIIVASFDG RSGGYOGDKI MHAINRRLGT 600
 FEVEDQIEAA RQFSKMGFVD NKRIAIWGS YGGVYVSMVL GSGSGVFKCG IAVAPVSRWE 660
 YYDSVYTERY MGLPFPEDNL DRYRNSTVMS RAENFKQVEY LLIHGTADDN VHFQQAQIS 720
 KALVDVGVPD QAMWYDDEHD GIASSTAHQH IYTHMSHFIK QCFSLP

75
 Nucleic Acid Accession #: none found
 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

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 1 11 21 31 41 51

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ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAAATGACA ATGCCATCAG AGTTGACAAC 60
 AGAAGTGTGA TTAAGTGGC TGCTAACCAAG TGTTCCTGTC ATGAGGCAGA AAGTGAATCC 120
 AGAAACCTTC AGGAGCTCTG GATGGGCCCTG CTCCTCTTGA TGGGGGTCTT AGAAGCATGT 180
 GTGGAATGA GGCTCTGTCT AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC 240
 CAGCCACAC TGGATGTCTA A

SEQ ID NO:226 PB12 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
 MALAKVREPN ANDNAIRVDN RSVIKVRANQ CSLHEAESES RNPQELWMGL LLLMGVLEAC 60
 VEMRPLSVWS LRDDKEQSPH QPTLDV

SEQ ID NO:227 PBM2 DNA SEQUENCE

Nucleic Acid Accession #: none found
 Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTGGAAGCA GTAAATGTTT AAAAAGTCTGCT 60
 CTGATCTCTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT 120
 ATTGATGTAT CTCTCAAGA TCTGGACAGA CGCCAGAGA GTATGCTGTT TCTAGTCATC 180
 ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
 TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTGATGTGGG ATTCCAGAA 300
 AACCTGACTA ATGGTGGCGC TGCTGGCAAT GGTGATGATG GATTAAATCC TCCAAGGAAG 360
 AGCAGAACAC CTGAAGCCA GCAATTCTCT GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
 GTCAAAGATC AGATAGTTGT AGATATGCGG CGTTATTCTT GA

SEQ ID NO:228 PBM2 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
 MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPLEQN IDVSSQDLDR RPESMLFLVI 60
 DMVTSFVEDN LSMGWGKLED FMAIEEMKK HGSTHVGFE NLTNAGAAAGN GDDGLIPPRK 120
 SRTPEQQFP DTENEYHFR VKDQIVVDMR RYF

SEQ ID NO:229 PEZ2 DNA SEQUENCE

Nucleic Acid Accession #: NM_014253
 Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GACTGCTTGC ATTAAGGAC TTCTCATCC TTTTTCAT GAAACTGAGC TTGCTTAATC 60
 AGAGATGGAG CAAACTGACT GCAAACCTTA CCAGCCTCTA CCAAAAGTCA AGCATGAAAT 120
 GGATCTAGCT TACACAGTT CTCTGATGA GAGTGAAGAT GGAAGAAAC CAAGACAGTC 180
 ATACAACCTC AGGAGAGACC TGCAAGAGTA TAAACAGGAG CTGAGGATGA ATTACAATAG 240
 CCAGAGTAGA AAGAGGAAAG AAGTAGAAAA ATCTACTCAA GAGATGGAAT TCTGTGAAC 300
 CTCTCACTCT CTGTGCTCTG GCTACCAAAC AGACATGCAC AGCGTTTCTC GGCATGGCTA 360
 CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGCCT CACCTGACCA 420
 TGCACTAAGA ATGTGGATAA GGGGAATGAA ATCAGAGCAT AGTTCCTGTT TGTCCAGCCG 480
 GGCCAACCTC GCATTATCCT TGACTGACAC TGACCATGAA AGGAAGTCTG ATGGGGAAAA 540
 TGGTTTCAAA TTCTCTCCTG TTTGTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA 600
 TGTGCAGAGC AGCCACACA ACCAGTTCAC CTTACAGACC CTCCCACGC CACTCCGCC 660
 TCCTCATGCC TGACCTGTG CCAGGAAGCC ACCCCCTGCA GCGGACTCTC TTCAGAGGAG 720
 ATCAATGACT ACCCGCAGCC AGCCAGGCC AGCTGCTCCA GCTCCCCAA CCAGACGCA 780
 GGATTCAGCT CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCAG 840
 GCATTCCCTG TTCAACATG GATCTGGTTC CTCTGCATC TTCAGTGCAG CCAGTCAGAA 900
 CTACCTCTCT ACATCCAATA CCGTGTACTC GCCCCCTCCC AGGCTCTCTC CTCGAAGCAC 960
 CTTTCCCGA CCTGCTTTA CCTTTAACA ACCTTACAGG TGCTGCAACT GGAAGTGCAC 1020
 AGCATTGAGC GCCACTGCAA TCACAGTGAC TTTGGCCTTG TTACTAGCCT ATGTGATTGC 1080
 AGTGCAATTT TCTGGCCTGA CTTGGCAGTT GCAACCAAGT GAAGGAGAGC TGTATGCAAA 1140
 TGGAGTTAGC AAAGGGAACA GGGGGACCGA GTCCATGGAC ACTACTTACT CTCCAATTGG 1200
 AGGAAAAGTT TCTGATAAAT CAGAGAAAAA AGTGTTCAG AAGGAGACGG CGATAGACAC 1260
 TGGAGAAGTT GACATTGGTG CACAGGTCAT GCAGACCATT CCACCTGGTT TATTCTGGCG 1320
 TTTCCAGATT ACTATCCACC ATCCAATATA TCTGAAGTTC AATATTTCCT TAGCCAAGGA 1380
 CTCTCTAGCT GGAATTATAG GCAGAAGAAA CATTCCACCT ACACATACTC AGTTTGATT 1440
 TGTAAAACCT ATGATGGGCA AACAGCTGGT CAAGCAGGAC TCCAAGGGCT CTGATGATAC 1500
 ACAGCACTCC CCTCGAACCT TGATCTTAAC TTGCTTCAG GAGACAGGTT TCATAGAGTA 1560
 TATGGATCAA GGACCTTGGT ATCTGGCGTT TTACAATGAT GGAAGAAAGA TGGAGCAAGT 1620
 ATTCTGTGTA ACTACAGCAA TTGAATAAT GGATGACTGT TCAACCAAT GCARTGAAA 1680
 TGGAGAGTGT ATCTCTGGCC ATTGTCAATT TTTCCAGGA TTCTTGGAC CTGACTGTGC 1740
 TAGAGATTCC TGCCCTGTGC TGTGTGGTGG GAATGGAGAA TACGAGAAAG GACACTGTGT 1800
 CTGCGCGCAT GCTTGAAGG GGCAGAGTG TGACGTTCCG GAAGAACAAT GCATTGATCC 1860
 AACATGCTTT GGCCACGCA CCTGCATCAT GGGAGTCTGC ATCTGTGTGC CAGGATACAA 1920

	AGGAGAAATA	TGCGAGGAAG	AGGACTGCCT	AGACCCAAATG	TGTTCCAACC	ATGGCATCTG	1980
	TGTAAGGA	GAATGTCACT	GTCTACTGG	CTGGGGAGGA	GTAACTGTG	AAACACCACT	2040
	TCCTGTATGT	CAAGAGCAGT	GCTCAGGACA	CGGAACCTTT	CTTCTGGAGC	CTGGAGTATG	2100
5	CAGCTGTGAT	CCCAAGTGA	CAGGATCTGA	CTGCTCAACA	GAGCTGTGTA	CCATGGAGTG	2160
	TGCTAGCCAT	GGAGTCTGCT	CAAGAGGAAT	TTGCCAGTGT	GAAGAAGGCT	GGGTAGGACC	2220
	AAACATGTGAG	GAACGCTCCT	GTCAATCTCA	TTGTACTGAG	CATGGCCAAT	GCAAAGATGG	2280
	AAAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACCTG	ACAATTGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGACGATGTA	CCCTGGATCA	2400
10	AAATGGTTGG	CACTGTGTGT	GTCAAGTGGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTCAT	2460
	GGAAATGCTT	TGTGGAGATA	ACTTGGACAA	TGATGGAGAT	GGTTAAACCG	ACTGTGTGGA	2520
	TCCTGACAT	TGTCAACAAA	GCAACTGTTA	TATAAGTCTC	CTCTGCCAGG	GCTCACCAGA	2580
	TCCTCTTGAC	CTCATTCAGC	AAAGCCAAAC	TCTCTTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	GATCAATTC	TCATTTGGCAA	GGACAGTACT	CATGTCATTC	CTCCTGAGGT	2700
15	GTCAATTTGAC	AGCAGGCGTG	CCTGTGTGAT	TCGAGGCCAA	GTGGTGGCCA	TAGATGGAA	2760
	TCCTCTAGTG	GGAGTGAATG	TCAGTTTCTT	GCACACAGT	GATTTATGGT	TTACCATCAG	2820
	CCGGCAAGAT	GGAGCTTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCGATCC	CTTTCTCTGC	CTGAGAAGAG	AACACTCTGG	TTGCCCTTGA	ATCAGTTTAT	2940
	TGTGTAGAG	AAAGTACCA	TGCAGAGAGT	TGTATCAGAC	CCGCCATCTT	CGGATATCTC	3000
20	CAACTTTATC	AGCCCCAAAC	CTATTGTGCT	TCCTTCACCG	CTCACATCAT	TTGGAGGGTC	3060
	CTGTCCAGAG	AGGGGAACATA	TGTTCTCTGA	GCTGCAGGTT	GTACAGGAGG	AAATTTCCCAT	3120
	TCCTTCAGC	TGTTGAGAGT	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAACCTT	3180
	GCTACGGATC	CTTCTGACAC	ATTCAACGAT	TCCCGTAGGC	ATGATAAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCGAG	TCACACAGAA	GTGGTTTCCC	GCCGCAATTA	ATCTTGTCTA	3300
25	CACATTTGCT	TGGAACAAGA	CCGATATCTA	TGGACAGAAG	GTTTGGGGCC	TGGCAGAGGC	3360
	TTTGGTATCT	GTGGGATATG	AATATGAAAC	GTGCCCTGAC	TTTATTTCTT	GGGAGCAAG	3420
	GACAGTCTGT	TTACAAGGTT	TTGAGATGGA	TGCTTCTAAC	CTAGGAGACT	GGTCTTTGAA	3480
	TAAGCATCAC	ATTTTGAATC	CTCAAGTGG	AATCATACAT	AAAGGGAATG	GAGAAAATAT	3540
	GTTCATTTCC	CAGCAGCCCC	CAGTCATATC	AACCATATG	GGTAATGAC	ACCAAAGGAG	3600
30	TGTAGCTTGC	ATCAACTGCA	ATGGCCAGC	CCACAACAC	AAACTCTTTG	CTCTCTGCG	3660
	CTTAGCTTCT	GGCCCTGATG	GCAGTGTGTA	TGTTGGCGAC	TTCAATTTTG	TAAGGAGAAT	3720
	ATTTCCCTCG	GGAACTCCG	TTAGTATTTT	GGAATTAAGC	ACAAGTCTGT	CTCACAAATA	3780
	CTATCTGCT	ATGGACCTTG	TGCTGAATC	ACTCTATCTA	TCAGACACCA	ATACTCGCAA	3840
	AGTCTACAAG	TTGAAATCTC	TTGTGGAGAC	GAAAGATCTG	TCCAAGAAAT	TTGAAGTGGT	3900
35	GGCAGGAATC	GGTATCTAGT	GCCTTCCCTT	TGACCAGAGT	CATTTGGAG	ATGGTGGGAG	3960
	AGCATCGGAA	GCTTCACTGA	ATAGCCCTCG	AGGCATCACA	GTGTAGAGC	ATGGATTTAT	4020
	TTACTTTGTG	GATGGAGCTA	TGATTCGCAA	AATTGATGAG	AATGCTGTGA	TCACAACCTG	4080
	AATCGGCTCA	AATGGTCTGA	CTTCCACACA	ACCACTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CACCTCAGGT	CGATTAGAGT	GGCCAACAGA	CCTTGCAGTA	AATCCTATGG	ACAATTCATT	4200
40	GTATGCTTTG	GATACAACAA	TTGTGCTGCA	AATTTCTGAG	AACAGGCGTG	TTCCGGATCAT	4260
	CCGAGGAGCG	CCCATCTCAT	GCCAGTGGC	AGGCATCGAT	CATTTCCTGG	TCAGCAAGGT	4320
	AGCAATTCAC	TCCACTCTAG	AGTCAGCGAG	GGCCATCAGT	GTCTCCACCA	CGCGGCTGCT	4380
	CTTCATAGCT	GAACACAGCG	AGAGGAAAGT	AAACCGCAT	CAGCAAGTAA	CCACCAATGG	4440
	GGAGATCTAT	ATCATCTGCT	GTGCCCCAC	TGACTGTGAC	TGCAAAATG	ATCCAAACTG	4500
45	TGACTTTTAT	TCAAGTGTATG	GTGGCTATGC	CAAGATGCA	AAGATGAAAG	CCCCCTCCTC	4560
	CTTAGCAGTG	TGCGCTGATG	GAACCTCTA	TGTGGCAGAC	CTCGGAAATG	TTGGAATTCG	4620
	TACCATTCAG	TCCGACCAAG	CCCACTGAA	TGACATGAAC	ATTATGAGA	TTGCTTCACC	4680
	CGCTGATCAG	GAACGTATCC	AGTTCACTGT	AAATGGAAAC	CACCTACACA	CCCTGAACCT	4740
	GATAACAAGG	GACTATGTTT	ATAACTTCAC	CTACAATTCT	GAAGGTGACT	TGGGCGCGAT	4800
50	TACCAAGCAG	GAAGTCAAT	CAGTGACAT	TGCGCTGAT	GCAGGCGGAA	TGCCGCTATG	4860
	GCTTGTGTG	CCTGGCGGAC	AAGTATACCT	GCTGACTATA	AGCAGCAATG	GAGTCTTGAA	4920
	AAGATGCTAC	GCCCAAGGCT	ATAATCCGGC	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCTGGCTACC	AAAAGTAAAG	AAAATGGATG	GACAACCGTT	TATGAGTATG	ACCCGAGGG	5040
	ACACCTGACC	AAATGCAAGT	TTCCCACTGG	AGAGGTACAG	AGCTTCCACA	GTACCTGGA	5100
55	GAAGCTGACA	AAAGTGGAGC	TAGATACTTC	CAACCGTGAA	AATGTCTCTA	TGTCAACCAA	5160
	CTTGACGGCA	ACTAGTACCA	TATATATTTT	AAAACAAGAA	AATACTCAAA	GTACCTATCG	5220
	GGTGAATCCA	GATGGTTCCC	TGCGTGTAC	TTTTGGCAGC	GGGATGGAGA	TCGGCCTCAG	5280
	CTCAGAGCCC	CACATCTTGG	CAGGGGAGT	CAACCTTACC	CTGGGCAAT	GCAACATCTC	5340
	ATTGCCCGGA	GAGCACAATG	CAACCTCAT	CGAGTGGCGG	CAGAGGAAGG	AGCAAAACAA	5400
60	AGGCAATGTT	TCGGCTTTTG	AAAGGAGGCT	GAGGGCCAC	AACAGAAACC	TACTCTCCAT	5460
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SEQ ID NO:231 PFD4 DNA SEQUENCE:

Coding sequence:

225-2567 (underlined sequences correspond to start and stop codons)

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      TCTAGGCTTT ATTTATAAAA TAAACACCTT ATCCCTAACA TGGGCAAAAT GGCTAGAATT 2760
      ATTCAGACGA TTTCGACGCG TCCAGGGTAA GCTGGTGTTA TAATACGCTG CTGATCTACA 2820
      TCACAGATTG GCTAATAATG TTCACGTGGG CCCTGGCATA TCTCTGTTCG GTTAGAGTGA 2880
      GTGCTGACCC AACAGCCTCT GTGGTCAAGC GAGTCACGAA TGATTAAATCA TAAAGAAAAA 2940
55     TCAGTTTTTG ACTGACCTGG ATATCCATGA GCTGCACATG TCACCATGTA AGGTCACTAT 3000
      TAGTAAATGC TGAAATAAAA TGATTAATGC ATTTATCAAT AAAAGCCTTT GAAATACTT 3060
      TGGATAATAA ATTCGAGTTT TAAAAATGCA AATTTGCTTA GTATCTAATA ATGAAGTGT 3120
      ATTACATATA CCGCGAAATG AGGATCTCTT TGATCCTGGA AATGTTTAC CTAAAAGCTA 3180
      CAGAACCAGG CCAATATATT TTGAAATATT GATGCAGACA AATGAAATAA TAAAGAGATT 3240
60     TTCAATGTTT ATAAAAATCT TTTTGTATAT GATAATAATC ATGATCACAA CTGAGATCAA 3300
      AAAAAATATC GACAGATTAT TTTGTTTAAA AATGCAGTTT TAATTATCTT AGTCTATAGA 3360
      AATGATCAAT GCATGGAGGC ATGTATAGGT ATGATCTGTG TAAATCTGA CATAAAAAA 3420
      GTGCTATCTT GAGTGAAAAA TTTTGTGATG TGCTTACATA ACCATGGTGA TTAATAATGAG 3480
      TTTATATTTT TTCTCAAAAA TTTTAGCAGT GTGTAAAGTA AGTAATCTTT AACTGAACCTC 3540
65     TGACCACTTA AAAAAAATCT TAAAAATGTA ACTACCTATA GTAGTCTGTG TTTAAAGTGA 3600
      ATTTTAAAG ACAAGCATTT CTAAATGAAC TCAATATAAA AACATTCAAT TGGAAATGAC 3660
      ATACTGAAAA ATACAGGTTT TTTTGACCAA AAGTTTTAT ATCTTTTCTT TTTATTTTAT 3720
      TTTTCTCTAA GTGCCAACAA TTTTCTAGAT ATTATATACA ACACAGGCTT TGATCTTGGG 3780
      GACTTTTCCC ATATATTTCA CACTGGAGTG AATGAAGTTG TACTTCATTT CTAGAGAAAA 3840
70     GTTATACCCA GGTCCCAATT TGAGAAATGC TTGCTTGATG GAAAACGACA TCATCCCTTG 3900
      GTATACTCTA GGGATTGGTT TCAGGACCCC TGCAATTACC AAAATTGTGT CACACTCAAG 3960
      TCCTGCAATC ACCCTCGCTT AAAGATAGAA TGGCTTCTCT GTTTTCTTTC TGAATAACAA 4020
      CCAGAAACAA TGTGTCTATT TCTGAAAGAA TAGGATTAAT GATCATACAA ATGGGTTAAT 4080
      CCTGAATCTT GGTGTGTAAT CTGGTTACAG CATAACTAGG ATTATAATGC TGCTCATTTT 4140
75     TCACAGCACT ACTTGCTTAT ATTGACAACA AATCATCTCG CTAAAGAGTG AATGTAGGCC 4200
      AGGCGCGGTG GCTCATCCCT GTAATCCAG CACTTTGGGA GCGCGAGGCG GGTGGATCAC 4260
      GAGGTGAGGA GATCGAGACC ATCTGGCTA ACATGGTAAA ACCCGCTCTC TACTAAAAAT 4320
      AGAAAAAAG AAATTAGCCT AGCGTGGTGG CTGGCGGGCG CCTGTAGTCT CAGCTATTTG 4380
      GGAGGCTAAG GCAGGAGAAAT GCGGTGAACC CCGGAGGCGG AGCTTGCACT GAGCCGAGGT 4440
80     CGTGCCACTG CACTCCAGCC TGGGCGACAG AGCAAGACTC CGTCTCAAAA AAAAAAATAA 4500

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AAAAAAAA AGAGTGAATG TAATAGTCTT GCAGAAAATG AATGAATACC TTTGTTCAAT 4560
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GGCTAGAGTT TGTAAATCTT GGGTTCATTG GTGATGACAT AAGTCAGCAA ACTGCGGGAA 4680
TACTGTCTCT TCTATGTATT TTGTGAATAG TAAGCATAAT TTTAGITTTG TATTATCAAT 4740
GAAAATTTC A CTTGAAATTA AAGCTGCCCT TTGTTATATT TTTAACCTAT AGGATAAGAT 4800
TCCAGTATTG TATATGAGTT TTAACAAAT AAAAAATCAA ATCATGTACA TTTGAAAATA 4860
TTTGCACACA TTTAAAAATA AATGTAAAGT TGTCTTTTAA ACTACTCGGA TGTGTCCTTT 4920
CTGAACAAAA

SEQ ID NO:232 PFD4 Protein sequence:
Protein Accession #: O43511

1 11 21 31 41 51
MAAPGGRSEP POLPEYSCSY MVSRLPYSEL AFQQQHERRL QERKTLRESL AKCCSCSRKR 60
APGVLTLPV ILEWLKPYRV KEWLLSDVIS GVSTGLVATL QGMAYALLAA VPVGGLYLA 120
RFPILPYFIF GTSRHSVSGP FPVSLMVGSL VVLSMAPDEH FLVSSSNGTV LNTTMDTAA 180
RDTARVLIA ALTLVLGIIQ LIPGGLQIGF IVRYLADPLV GGFTTAAAFQ VLVSLQKIVL 240
NVSTKKNYGV LSIITYLVEI FQNIQDTNLA DFTAGLLTIV VCMAYKELND RFRHKIPVPI 300
PIEVIVTIIA TAISYGANLE KNYNAGIVKS IPRGFLPPEL PFVSLPSEML AASFSIAVVA 360
YAIASVSGKV YATKYDYTTID GNQEFIAFGI SNIFSGFFSC FVATTALSRT AVQESTGGKT 420
QVAGIISAAI VMIAILALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LWRQNKIDAV 480
IWVFTCIISI ILGLDLGLLA GLIFGLLTIV LRVQPPSWNG LGSIPSTDYI KSTKNYKNIE 540
EPQGVKILRF SSPIFYGNVD GFKKCIKSTV GFDAIRVYNK RLKALRKIQK LIKSGQLRAT 600
KNGIISDAVS TNNAFEPDED IEDLEELDIP TKEIEIQVDW NSELPVKVVV PKVPIHSLVL 660
DCGAISFLDV VGVRSRLRVIV KEFQRIDVNV YFASLQDYVI EKLEQCGFFD DNIRKDTFFL 720
TVHDAILYLQ NQVKSQEGQG SILETITLIQ DCKDTLELIE TELTEEELD V QDEAMRTLAS 780
QDEAMRTLAS

SEQ ID NO:233 PFH2 DNA SEQUENCE:

Nucleic Acid Accession #: NM_016029
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CTGCGATCCC GCAGGGCAGC GACGCGACTC TGGTGCGGGC CGTCTTCTTC CCCCCGAGCT 60
GGGCGTGCAC GGGCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGCGC 120
TGCTCTCTGT CTGTGGTGAG CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC 180
TATGGGCCCA TGGGAGGAGA CGACGCCAGC AATGGGAGCT GACTGATATG GTGGTGTTGG 240
TGACTGGAGC CTGAGTGGA ATTGGTGAGG AGCTGGCTTA CCACTGTGCT AACTAGGAG 300
TTTCTCTTGT CCTGTGAGC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360
TAGAGAAATG CAATTTAAAA GAAAAAGATA TACTTGTITT GCCCCTTGAC CTGACCGACA 420
CTGTGTTCCA TGAAGCGGCT ACCAAGCTGT TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480
TGGTCAACAA TGGTGGAATG TCCCAGCGTT CTCTGTGCAT GGATACCAGC TTGGATGTCT 540
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC 600
CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660
TATCTGTACC TCTTTCATTT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTTTTTTTA 720
ATGGCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCCAG 780
GACCTGTGCA ATCAATATT GTGGAGAAAT CCCTAGCTGG AGAAGTCACA AAGACTATAG 840
GCAATATGG AGACCACTCC CACAAGATGA CAACCACTCG TTGTGTGCGG CTGATGTTAA 900
TCAGCATGCC CAATGATTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960
CATATTTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCACCAAG ATGGGGAAGA 1020
AAAGGATTGA GAATCTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080
AGACAAAACA TGAAGTAAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140
AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200
ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AATAATAAAA 1260
AGATTGCCAT GAATCTTGCA AA

SEQ ID NO:234 PFH2 Protein sequence:
Protein Accession #: NP_057113

1 11 21 31 41 51
MNWELLWLVL VLCAALLLVV QLLRFLRADG DLTLWAEWQ GRRPEWELTD MVVWVTGASS 60
GIGEEAYQL SKLGVSLVLS ARRVELERV KRRCLENGSL KEKDILVPL DLDTGSHSEA 120
ATKAVLQEPG RIDILVNNGG MSQRSLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHMER 180
KQKIVTVNS ILGII SVPLS IGYCASKHAL RGFNGLRTE LATYPGIIVS NICPGPVQSN 240
IVENS LAGEV TKPTGNGDQ SHKMTTSRCV RLMLISMAND LKEVWIEQF PLLVTYLVQY 300
MPTWAWITN KMGKKRIENF KSGVDADSSY FKIFKTRHD

SEQ ID NO:235 ACCS DNA SEQUENCE

Nucleic Acid Accession #: NM_000450

Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

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5  ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGG 60
   GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
   CAGCAAAAGT ACACACACCT GGTTCGAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
   TCCATATTGA GCTATTTCACC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
10  TGGGCTCGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
   GAACCCACCA ATAGGCAAAA AGATGAGGAC TCGTGGAGA TCTACATCAA GAGAGAAAAA 360
   GATGTGGGCA TGTGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCTT ATGCTACACA 420
   GCTGCCTGTA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
   TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAT TGTGAACGTG 540
   ACAGCCCTGG AATCCCTCGA GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAACTTC 600
15  AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
   ACCATGCAGT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
   GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGG 780
   AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTTGA ACTAATGGGA 840
   GCGCAGAGCC TTCAGTGTAC CTCACTCTGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
20  GCTGTGACAT GCAGGCGCGT CCGCCAGCCT CAGAAATGGT CTGTGAGGTG CAGCCATTCC 960
   CCTGTGGAG AGTTTCACTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
   TTGCAGGGAC CAGCCAGGTG TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCCA 1080
   GTTGTGAAG CTTTCACAGT CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
   CTTCCTAGTG TTCTCTGGAG TTTCCTTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
25  GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
   GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCG GAAGGGTTTG 1320
   GTGAGGTGTG CTCAATCCCC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCCTTCAGC 1380
   TGTGAGGAGG GATTGTGAAT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
   TGGACAGAAG AGGTTCTCTT CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCGGGA 1500
30  AAGATCAACA TGAGCTGACG TGGGGAGCCC GTGTTTGCCA CTGTGTCAA GTTCGCCTGT 1560
   CCTGAAGAT GGACGCTCAA TGGCTCTGCA GCTCGGACAT GTGAGGCCAC AGGACACTGG 1620
   TCTGGCCTGC TACCTACCTG TGAAGCTGCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
   CTTCCTGCTG CTGGACTCTC CCTCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
35  TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGT GCCAAAGCCT TGAATCAGAC 1800
   GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

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SEQ ID NO:236 ACC5 Protein sequence:

Protein Accession #: NP_000441

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1      11      21      31      41      51
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   SILSYDSPSY WIGIRKVVNV WVVVGTQKPL TEEAKNWAPG EPNRQKDED CVEIYIKREK 120
   DVGWMDERC SKKILALCYT AACTNTSCSG HGECVETINN YTCKDPPGFS GLKCEQIVNC 180
   TALESPERGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
   ECDAVINPAN GPVECFQNPQ SPFWNTCTCF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300
50  AVTCRAVRQP QNGSVRCSHS PAGEFTPKSS CNFTCEEFGM LQGPQVQECT TQGWTOQIIP 360
   VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEMDN 420
   EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAFS CEEGPELYGS TQLECTSQGQ 480
   WTEEVPSQVQ VKCSSLAVPG KINMSCSGEP VFGTVCKPAC PEGWTLNGSA ARTCGATGHW 540
55  SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRL CLRKAKKVP ASSCQSLESD 600
   GSYQKPSYIL

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SEQ ID NO:237 PM28 DNA SEQUENCE

Nucleic Acid Accession #: N51002

Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

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65  ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGGTCC 60
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   GAAAGGGATC GTCTCTAGA CACCTTCGG GAGACCCAGG AAAGCCTCTC ACTTGCCAG 180
   CAAAGACTTC AGGATGTCTA CTATGACCGA GACTCACTCC AGAGACAGCT CAATTACAGC 240
   CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GCGTGATCCA 300
   CCGGAATTTC CTGCACTGAC AAAAGAAATTA AATGCCTGCA GGGAAACAAC TCTAGAAAAG 360
70  GAAGAAGAAA TCTCTGAAC TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT 420
   TTGGAGTGCC TTGTGTACG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480
   GCCCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCACT GAAATCTTTG 540
   TTTGAGCACC ACAAGGCCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGCT TTCTTTAGAA 600
   AGAGTCTCTG CACTGGAAGA AGAAGTAGCT GCTGCTAATC AGGAGATTGT TGCCCTGCGT 660
75  GAACAAAATG TTCAATACA AAGAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720
   CATCTTGAAG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTGTC CAATGGTTCT 780
   ATAGACTCAA CCGATGAAAC TAGTCAATA GTTGAAC TAC AAGAATTGCT TGAAGAAGCAA 840
   AACTATGAAA TGGCCAGAGT GAAAGAACGT TTAGCAGCCC TTTCTTCCCG AGTGGGAGAG 900
   GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATTA AAACAGAAGA AATGAACACC 960
80  AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAAGAATT 1020
   ACAACCCCTT AAAAGCGTTA CCTCAGTGCT CAGAGAGAA TACCTCCAT ACATGACATG 1080

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	AATGATAAAC	TAGAAAATGA	GTTAGCAAAT	AAAGAAGCTA	TCCTACGGCA	GATGGAAGAG	1140
	AAAAACAGAC	AGTTACARGA	ACGTCTTGAG	CTAGCTGAAC	AAAAGTTGCA	GCAGACCATG	1200
	AGAAAGGCTG	AAACCTTGCC	TGAAGTAGAG	GCTGAAGTGG	CTCAGAGAAT	TGCAGCCCTA	1260
5	ACCAAGGCTG	AAGAGAGACA	TGGAAATATT	GAAGAACGTA	TGAGACATTT	AGAGGGTCAA	1320
	CTTGAAGAGA	AGAAATCAAGA	ACTTCAAGA	GCTAGGCCAA	GAGAGAAAAT	GAATGAGGAG	1380
	CATAACAAGA	GATTATCCGA	TACGGTTGAT	AGACTTCTGT	CTGAATCCAA	TGAACGCCCTA	1440
	CAACTACACT	TAAAGGAAAG	AATGGCTGCT	CTAGAAGAAA	AGAATGTTTT	AATTCAAGAA	1500
	TCAGAAACTT	TCAGAAAGAA	TCTTGAAGAA	TCTTTACATG	ATAAGGAAAG	ATTAGCAGAA	1560
10	GAAATTGAAA	AGCTGAGATC	TGAACCTGAC	CAATTGAAAA	TGAGAACTGG	CTCTTTAATT	1620
	GAACCCACAA	TACCAAGAAC	TCATCTAGAC	ACCTCAGCTG	AGTTGCGGTA	CTCAGTGGGA	1680
	TCCCTAGTGG	ACAGCCAGCT	TGATTACAGA	ACAACATAAG	TAATAAGAAG	ACCAAGGAGA	1740
	GGCCGCATGG	GTGTCGGAAG	AGATGAGCCA	AAGGTGAAAT	CTCTTGGGGA	TCACGAGTGG	1800
	AATAGAACTC	AACAGATTGG	AGTACTAAGC	AGCCACCCCT	TGAAAAGTGA	CACTGAAATG	1860
	TCTGATATTG	ATGATGATGA	CAGAGAAACA	ATTTTATAGT	CAATGGATCT	TCTCTCTCCA	1920
15	AGTGTGCTATT	CCGATGCCCA	GACGCTAGCC	ATGATGCTTC	AGGAACAATT	GGATGCCATC	1980
	AACAAAGAAA	TCAGGCTAAT	TCAGGAAGAA	AAAGAATCTA	CAGAGTTGCG	TGCTGAAGAA	2040
	ATPGAAAATA	GAGTGGCTAG	TGTGAGCCTC	GAAGGCTCGA	ATTTGGCAAG	GGTCCACCCA	2100
	GGTACTCTCA	TACTGCTCTC	TGTTACAGCT	TCATCGCTGG	CCAGTTTATC	TCCCCCAGT	2160
	GGACACTCAA	CCCCAAAGCT	CACCCCTCGA	AGCCCTGCCA	GGGAAATGGA	TGGATGGGA	2220
20	GTCATGACAC	TGCCAAGTGA	TCTGAGGAAA	CATCGGAGAA	AGATTGCACT	TGTGGAAGAA	2280
	GATGCTCAG	AGGACAAAGC	AACAATTAAA	TGTGAAACTT	CTCTCTCTCC	TACCCCTAGA	2340
	GCCTTCAGAA	TGACTCACAC	TCTCCCTTCT	TCCTACCACA	ATGATGCTCG	AAGTAGTTTA	2400
	TCTGTCTCTC	TTGAGCCAGA	AAGCCTCGGG	CTTGGTAGTG	CCAACAGCAG	CCAAGACTCT	2460
	CTTCACTAAG	CCCCAAGAA	GAAAGGAATC	AAGTCTTCAA	TAGGACGTTT	GTTTGGTAAA	2520
25	AAAGAAAAAG	CTCGACTTGG	GCAGCTCCGA	GGCTTTATGG	AGACTGAAGC	TGCAGCTCAG	2580
	GAGTCCCTGG	GGTTAGGCAA	ACTCGGAAGT	CAAGCTGAGA	AGGATCGAAG	ACTAAGAGAA	2640
	AAGCATGAAC	TCTTTGAAGA	AGCTCGGAGA	AAGGGATTAC	CTTTTGCCCA	GTGGGATGGG	2700
	CCAACGTGGG	TCGCATGGCT	AGAGCTTTGG	TTGGGAATGC	CTGCGTGGTA	CGTGGCAGCC	2760
30	TGCCGAGGAA	AGCTGAAGAG	TGGTGCCATC	ATGCTGCTTT	TATCTGACAC	TGAGATCCAG	2820
	AGAGAAATGG	GAATCAGCAA	TCCACTGCAT	CGCTTAAATC	TTGATTTAGC	AATCCAGGAG	2880
	ATGGTTTCCC	TAAACAGTCC	TTTCACTCTC	CCAACATCTC	GAACTCTCTC	AGGCAACGTT	2940
	TGGGTGACTC	ATGAAGAAAT	GGAAATCTTT	GCAGCTCCAG	CAAAAACGAA	AGAACTGTAG	3000
	GAAGGAAGCT	GGGCCAGGTG	TCCGGTTTTT	CTACAGACCC	TGGCTTATGG	AGATATGAAT	3060
35	CATGATGGA	TTGGAATGA	ATGGCTTCCC	AGCTTGGGGT	TACCTCAGTA	CAGAAGTTPAC	3120
	TTTATGGAAT	GCTTGGTAGA	TGCAAGAAATG	TTAGATCACC	TAACAAAAAA	AGATCTCCGT	3180
	GTCCATTATA	AAATGGTGGG	TAGTTTCCAT	CGAACAAAGT	TACAATATGG	AATTATGTGC	3240
	TTAAAGAGGT	TGAATTATGA	CAGAAAAGAA	CTAGAAAAGAA	GACGGGAAGC	AAGCCAAAT	3300
	GAAATAAAG	ACGTGTTGGT	GTGGAGCAAT	GACCGAAATTA	TTGCTGGAT	ACAAGCAATT	3360
40	GCAGTTCCAG	AATATGCAAA	TAAATACTTT	GAGAGCGGTG	TGCATGGCTC	ACTTATAGCC	3420
	CTGGATGAAA	ACTTTGACTA	CAGCAGCTTA	ACTTTATTAT	TACAGATTCC	AACACAGAAC	3480
	ACCCAGGCAA	GGCAGATTCT	TGAAAGAGAA	TACAATAACC	TCTTGGCCCT	GGGAAGTCAA	3540
	AGGCGACTGG	ATGAAAGTGA	TGACAAAGAA	TTAGAGCTGG	GATCAACCTG	GAGAAGGCAAG	3600
	TTTCTCTCTC	GTGAAGTACA	TGGAATCAGC	ATGATGCTTG	GGTCTCTAGA	AGCATTTACCA	3660
45	GCTGGATTTA	GTTTAAACAC	AACCTCTGGG	CAATCAAGAA	AAATGACAA	AGATGTTGCT	3720
	TCATCAAGAC	TGCAGAGGTT	AGACAACCTC	ACTGTTTCGA	CATACTCATG	TCTCGAGTAA	3780
	GGGGCCGCTT	<u>TAA</u>					

SEQ ID NO:238 PM28 Protein sequence:

Protein Accession #: none found

	1	11	21	31	41	51	
55	HMCEVHPTIN	EDTPMSQRGS	QSSGSDSDSH	FEQLMVNMLD	ERDRLLDTLR	ETQESLSLAQ	60
	QRLQDVYDR	DSLQRLNSA	LPQDIESLTG	GLAGSKGADP	PEFAALTKEK	NACREQLLEK	120
	EEEISELKAE	RNNTRLLLEH	LECLVSRHER	SLRMTVVKRQ	AQSPSGVSSE	VEVLKALKSL	180
	FEHHKALDEK	VRELRVLSLE	RVSALAEELA	AANQEIVALR	EQNVHIQRKM	ASSEGSTESE	240
	HLEGMFGQK	VHEKRLSNGS	IDSTDETSQI	VELQELLEKQ	NYEMAQMKER	LAALSSRVGE	300
60	VEQEAETARK	DLIKTEEMNT	KYQRDIREAM	AQKEDHEERI	TTLEKRYLSA	QRETSIHDM	360
	NDKLENELAN	KEAILRQMEE	KNRQLQERLE	LAEQKLQQT	RKAETLPEVE	AELAQRILAA	420
	TKAERHGNII	EERMRHLEGQ	LEEKNQELQR	ARQREKMNZE	HNKRLSDTV	RLLTESNERL	480
	QLHLKERMAL	LEEKVNLQIE	SETFRKNLEE	SLHDKERLAE	EIEKLRLSEL	QLKMTGSLI	540
	EPTIPTHLD	TSAELRYSVG	SLVDSQSDYR	TTKRVIRRRR	GRMGVRRDEF	KVKSIGDHEW	600
65	NRTQIGVLS	SHPFESDTEM	SDIDDDRET	IFSSMDLLSP	SGHSDAQTLA	HMLQEQLDAI	660
	NKEIRLIQEE	KESTELRAEE	IENRVASVSL	EGLNLARVHP	GTSITASVTA	SSLASSPPPS	720
	GHSTPKLTPR	SPAREMDRMG	VMTLPDDLRL	HRKIAVVEE	DGREDKATIK	CETSPPTPTP	780
	ALRMTHLTPS	SYHNDARSSL	SVSLEPEPSL	LGSANSQSDS	LHKAPKKKGI	KSSIGRLFGK	840
70	KEKARLGLR	GFMEFEAAAQ	ESLGLGKLTG	QAEKDRRLKX	KHELLEEAR	KGLPQAQWDG	900
	PTVVAWLELW	LGMFAWYVAA	CRANVKSAGI	MSALSDTEIQ	REIGISNPLH	RLKLRLAIQE	960
	MVSLTSPSAP	PTSRTPSGNV	WVTHEEMENL	AAPAKTKESE	EGSWAQCPVP	LQTLAYGDMN	1020
	HEWIGNEWLP	SLGLPQVRSY	FMECLVDARM	LDHLTKKDLR	VHLKQVDSFH	RTSLQYQIMC	1080
	LRRLNYDRKE	LERRREASQH	EIKDVLVWSN	DRIIRWIAQI	GLREYANNIL	ESGVHGSLLA	1140
75	LDENFDYSSL	TLLLIQIPQN	TQARQILERE	YNNLLALGTE	RRLDESDDKN	PRRGSTMRQ	1200
	PPPPEVHGIS	MMPGSETLTP	AGFRLTTTSG	QSRKMTTDDA	SSRLQRLDNS	TVRTYSCL	

SEQ ID NO:239 PC4 DNA SEQUENCE

Nucleic Acid Accession #: NM_016570

Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

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5	ATGAGCGCAC	TGAATCGGAA	AAAAACTTTA	AGTTTGGTAA	AAGAGTTGGA	TGCCTTTCCG	60
	AAGGTTCTCT	AGAGCTATGT	AGAGACTTCA	GCCAGTGGAG	GTACAGTTTC	TCTAATAGCA	120
	TTTACAACATA	TGGCTTTATT	AACCATAATG	GAATCTCTAG	TATATCAAGA	TACATGGATG	180
	AAGTATGAAT	ACGAAGTAGA	CAAGGATTTT	TCTAGCAAAT	TAAGAATTAA	TATAGATATT	240
	ACTGTTGCCA	TGAAGTGTCA	ATATGTTGGA	GCGGATGTAT	TGGATTTAGC	AGAAACAATG	300
10	GTTGCATCTG	CAGATGGTTT	AGTTTATGAA	CCAACAGTAT	TTGATCTTTC	ACCACAGCAG	360
	AAAGAGTGGC	AGAGGATGCT	GCAGCTGATT	CAGAGTAGGC	TACAGAAGA	GCATTCACCT	420
	CAAGATGTGA	TATTTAAAG	TGCTTTTAA	AGTACATCAA	CAGCTCTTCC	ACCAAGAGAA	480
	GATGATTCAT	CACAGTCTCC	AAATGCATGC	AGAATTCTAT	GCCATCTATA	TGTCATAAAA	540
	GTAGCAGGGA	ATTTTCACAT	AACAGTGGGC	AAGGCAATTC	CACATCTCTG	TGGTCATGCA	600
	CATTGTGGCAG	CACCTGTCAA	CCATGAATCT	TACAATTTTT	CTCATAGAAT	AGATCATTTG	660
15	TCTTTTGGAG	AGCTTGTTCC	AGCAATTATT	AATCCTTTAG	ATGGAAGTGA	AAAAATGCT	720
	ATAGATCACA	CACAGATGTT	CCAATATTTT	ATTACAGTTG	TGCCAACAAA	ACTACATACA	780
	TATAAAATAT	CAGCAGACAC	CCATCAGTTT	TCTGTGACAG	AAAGGGAACG	TATCATTAAC	840
	CATGCTGCAG	GCAGCCATGG	AGTCTCTGGG	ATATTTATGA	AATATGATCT	CAGTCTCTTT	900
20	ATGGTGACAG	TACTGTAGGA	GCACATGCCA	TTCTGGCAGT	TTTTTGTAA	ACTCTGTGGT	960
	ATTGTTGGAG	GAATCTTTTC	AACAACAGGC	ATGTTACATG	GAATTTGAAA	ATTTATAGTT	1020
	GAATAATTTT	GCTGTGTTT	CAGACTTGGG	TCCTATAAAC	CTGTCAATTC	TGTTCTTTT	1080
	GAGGATGGCC	ACACAGACAA	CCACTTACCT	CTTTTAGAAA	ATAATACACA	<u>TGTA</u>	

25 SEQ ID NO:240 PC14 Protein sequence:
 Protein Accession #: NP_057654

	1	11	21	31	41	51	
30	MRRLNRKKTLL	SLVKELDAFP	KVPESYVETS	ASGGTVSLIA	FTTMALLTIM	EFVYQDTWM	60
	KYEYEVKDFP	SSKLRLNIDI	TVAMKCQYVG	ADVLDLAETH	VASADGLVVE	PTVFDLSFPQ	120
	KEMQRMQLLI	QSRLEEHSL	QDVIFKSAFK	STSTALPPRE	DDSSQSPNAC	RIHGHLYVVK	180
	VAGNFHITVG	KAIHPHPRGA	HLAALVNHEH	YNFSHRIDHL	SFGELVPAII	NPLDGTEDIA	240
35	IDHNQMFQYF	ITVVPKLTHT	YKISADTHQF	SVTERERIIN	HAAGSHGVSG	IFMKYDLSSL	300
	MVTUTEHHP	FWQFFVRLCG	IVGGIFSTTG	MLHGIGKFIV	EIIICRFRLG	SYKPVNSVPF	360
	EDGHTDNHLP	LLENNTHT					

SEQ ID NO:241 PBA7 DNA SEQUENCE

40 Nucleic Acid Accession#: AA219134

Coding sequence: 24-1815 (underlined sequences correspond to start and stop codons)

	AATTCGCCCT	TGCTTAATTA	AGCATGTTTA	CCTTCCTGTC	ATCTGTCACT	GCTGCTGTCA	60
	GTGGCCTCTC	GGTGGGTAT	GAACCTGGGA	TCATCTCTGG	GGCTCTCTT	CAGATCAAAA	120
45	CCTTATTAGC	CCTGAGCTGC	CATGAGCAGG	AAATGGTGTG	GAGCTCCCTC	GTCAATTGGAG	180
	CCCTCCTTGC	CTCACTCACC	GGAGGGGTCC	TGATAGACAG	ATATGGAAGA	AGGACAGCAA	240
	TCATCTGTCT	ATCCTGCTCT	CTGGACTCG	GAAGCTTAGT	CTTGATCCTC	AGTTTATCCT	300
	ACACGGTCTT	TATAGTGGGA	CGCATTGCCA	TAGGGGTTTC	CATCTCCCTC	TCTTCCATTG	360
50	CCACTGTGTG	TTACATCGCA	GAGATTGCTC	CTCAACACAG	AAGAGGCCCT	CTTGTGTAC	420
	TGAATGAGCT	GATGATTGTC	ATCGGCAATC	TTCTGCGCTA	TATTTCAAAT	TACGCATTTG	480
	CCAAATGTTT	CCATGGCTGG	AAGTACATGT	TGGTCTTGT	GATTCCTTGT	GGAGTTTTC	540
	AAGCAATTGC	AATGTATTTT	CTTCTCCAA	GCCCTCGGTT	TCTGGTGATG	AAAGGACAAG	600
	AGGGAGCTGC	TAGCAAGGTT	CTTGGAAAGT	TAAGAGCACT	CTCAGATACA	ACTGAGGAAC	660
55	TCAGTGAT	CAATCTCTC	CTGAAAGATG	AATATCAGTA	CAGTTTTTGG	GATCTGTTTC	720
	GTTCAAAAGA	CAACATCGCG	ACCCGAATAA	TGATAGGACT	AACACTAGTA	TTTTTTGTAC	780
	AAATCACTGG	CCAACCAAA	ATATTGTCT	ATGCATCAAC	TGTTTTGAAG	TCAGTTGGAT	840
	TTCAAAGCAA	TGAGGACAGT	AGCCTCGCCT	CCACTGGGGT	TGGAGTCGTG	AAGGTCAATTA	900
	GCACCATCCC	TGCCACTCTT	CTTGTAGACC	ATGTGCGGCA	CAAAACATTC	CTCTGCATTG	960
60	GCTCCTCTGT	GATGGCAGCT	TCGTTGGTGA	CCATGGGCAT	CGTAAATCTC	AACATCCACA	1020
	TGAACCTTAC	CCATATCTGC	AGAAGCCACA	ATTCTATCAA	CCAGTCTTGT	GATGAGTCTG	1080
	TGATTTATGG	ACCAGGAAAC	CTGTCAACCA	ACAACAATAC	TCTCAGAGAC	CACCTCAAA	1140
	GGATTCTCTC	CCATAGCAGA	AGCTCACTCA	TGCCCTGAG	AAATGATGTG	GATAAGAGAG	1200
	GGGAGACGAC	CTAGCATCTC	TTGCTAAATG	CTGGATTAAG	CCACACTGAA	TACCAGATAG	1260
65	TCACAGACCC	TGGGACGTC	CCAGCTTTT	TGAAATGGCT	GTCTTAGCC	AGCTTGGTTG	1320
	TTTATGTGTC	TGCTTTTICA	ATTGGTCTAG	GACCAATGCC	CTGGCTGGTG	CTCAGCGAGA	1380
	TCCTTCTCTG	TGGGATCAGA	GGACGAGCCA	TGGCTTTAAC	TTCTAGCATG	AACTGCGGCA	1440
	TCAATCTCCT	CATCTCGCTG	CAATTTTGA	CTGTAACTGA	TCTTATTGGC	CTGCCATGGG	1500
	TGTGCTTAT	ATATACAATC	ATGAGTCTAG	ATCTTATTGG	CCTGCCATGG	GTGTGCTTTA	1560
70	TATATACAAT	CATGAGTCTA	GCATCCCTGC	TTTTTGTGT	TATGTTTATA	CCTGAGACAA	1620
	AGGGATGCTC	TTTGGAAACA	ATATCAATGG	AGCTAGCAAA	AGTGAACAT	GTGAAAAACA	1680
	ACATTTGTTT	TATGAGTCAT	CACCAAGAAG	AATTAGTGCC	AAAAACAGCT	CAAAAAAGAA	1740
	AACCCGACGA	GCAGCTCTTG	GAGTGTAACA	AGCTGTGTGG	TAGGGGCCAA	TCCAGGCAAG	1800
	TTTCTCCAGA	GACCTAATGG	CCTCAACACC	TTCTGAACGT	GGATAGTGCC	AGAACAACCTA	1860
75	GGAGGGGTGC	TTTGGACCAA	TGCATAGTTG	CGACTCTCTG	GCTCTCTTTT	CACTGTCTATG	1920
	GAACCTGGTT	TGAAGAGACA	CTCTGAAATG	ATAAAGACAG	CCTTTAATCC	CCCTCCTCMC	1980
	CAGAAGGAAC	CTCAAAAGGT	AGATGAGGTA	CAAGTCCCTA	AGTGATCTCT	TTTTCTGAGC	2040
	AGGATATCAG	TGTAATAAGAC	TATGTCCTAG	TGAAGACATC	AACCTCCGCC	TTAAGCTATG	2100
	AGAGCAGCCT	TGAATAGAC	TATGTCCTAG	TGAAGACATC	AACCTCCGCC	TTAAGCTATG	2160
80	TATGTATGGA	GGCCAGTCCG	AGCTTTATTA	TGCAGACACA	CAAGTGGTCT	GGACATGAGG	2220
	GTACAGTTTC	TGCTTACCAA	GACACTACTT	GCACTGGATC	TTACGCAAAA	AAGAACCAGA	2280

ACACACAGTG TGGACAACCTG CCCATATATT CTATCTAGAT TAGGAGAGGG TCCTGGCTAG 2340
 GATTTTAGTG GTAATTCCTA GTTACATTCA ACAAGTATAA AGATTATAGA GCTTATTITA 2400
 TGAACATAAA ACTATAATTT AATGCAAAAT ATCCTTTTAT GAATTTTCATG TTAATATTGT 2460
 GAAATATTAA AATAATTCCR CAATAGTTGA GAAAAATGAG CATTITTTTC CATTITTTAAA 2520
 5 AAATGTCATAG AAAAGACAAT TTTAAATCC TGGGACCATA TTTATTTAGA AGTAGCTGTT 2580
 AGTAAACAT TAGAAAAGGA GTCAGGCCAT TAGGTTATTT ATCCAAATCT CTAAGCAATT 2640
 AGGTTGAAGT TATTAAGTCA AGCCTAGAAA AGCTGCCTCC TTGTAAGGCT TTCATGACAA 2700
 TGTATAGTAA TCCACAGTGT CCAATTCTTC ACACCTCCTCA GGAATATCAC TACCTCAGGT 2760
 10 TACGGTACAC AGGCTATAAT TGATGATGAT GTTCAGATAA CTGAAGACAC AATAAATGAC 2820
 ATTACAGACAT CAGGAMAAWW CCCTCATGTT CTTTCTATG ATGGCCACCT GTACCAGCAA 2880
 CGTGGGTTTC ACCACACAA CGATGAACTG TTTCTTACT TCTCCAGTTG ATTTTAAAGA 2940
 CTGTGTAAGA GGTCTTACTA ATAAAAATTG GGTATGATAG AAAAWCCACA ATCAAAWCIT 3000
 GAACCAATAA ACATATTAAA TTAATAAT TTAAGTGATG GAAGACACAC AAAAAACTTA 3060
 15 AAAGCACGAA CAACCTAAT TGAAAAAGAA TTTTAAATA TGATTAACCT GAAGAAAAAGA 3120
 GAATCCTAAG AGCCAAAGCT CCTTTTATT TAGCTTGGA TTTTCTATT GGTTCCTAAC 3180
 AAAGTGTCCC AATGTCATAT AAGGAAACAT GATCTATTAC ATTCCTTTAT AACATGTGG 3240
 AGAGACTATA AACTATGTA AGTAGTAAAA CTATATYAGA GACTCAGGAG ACTGACTAAA 3300
 AGGCCTGGAT CTGCACTGTA TTATCTGTAT AAAAAATGGC AGGGGGAAGC TAAAGGAAA 3360
 20 GGAGATTGGA GATCTGAA CTATCATGTT GTATTTCATA CGCAATCAG AGCATGCATT 3420
 GTTTTGTGTT TTTGGAAGA GAAGGGAAGT GTGTCTGCC CCATGTTTCC TTCCGTTGTT 3480
 ATAGTCAAAA CTCTATATAT ACTTCAGGTA TTTTGTGTT AGCCCTTCAT TATAAATGGG 3540
 CAGGAAATTT TTTATCAACC TAGCCAGTTT ATTACTAGTG ACCTTGACTT CAGTATCTTG 3600
 AGCATTCITT TATATTTTTC TTTTATTATC CTGAGTCTGT AACTAAACAA TTTGTCTTTC 3660
 25 AAATTTTAT CCAATATCCA TTGCACCACA CCAATCAAG CTCTTGATT TCAAAAAATA 3720
 AAAAGGGGGA AATACCTACA ACTTGACAT ATATATTCAC AGTTTATTAT TATAAAAAAA 3780
 ATTTACAGTA CTTATGGAGA GCCAGCAGAA GACATCAGAG CACTCACTTC TTCCCATCTT 3840
 TGTTAAGGTT AGCGAATTAC CCATGGACAC TGTTAGGTGA GGCTCATTTC GCAGCCCTGA 3900
 AAACAAACCT GGTACACTG TCTTACCCT CTCCCTTCAG ATAAAGCACT TCGATTATCT 3960
 30 ATTGATCTGC CCAGTTTICA AGTCATGCGA ATACTAAAAA GGTACATCA TCTGGATCTG 4020
 TACCTTGGCT ATATAAGCAT GTTTCCTCCC TATCTATGTT TTTTGTGTT GGTGAACATT 4080
 GAAAAACAGG AGGTGACTTA TTAAGTTTAA TTAATACTAA ATGAAAAATG TCAAGTCTTT 4140
 AAAACACTGA GCTTGTAAGT CTTTCATGTA ATTTTATTCT CTATGAATTT GGCTATCTTA 4200
 CTGAATCTTA AATAAAGGA AATAAACACT TTTTITTTWAA AAAAAAGGAA AAATAMAARW 4260
 35 MWAAAAATCT CAATGAAATA TTTCACAAGA AGGAAAAA

SEQ ID NO:242 PBA7 Protein sequence:

Protein Accession #: AAF91431
 40 MFTFLSSVTA AVSGLLVGYE LGIISGALLQ IKTLALSCH EQEMVVSSLV IGALLASLTG 60
 GVLDTRYGRR TAILSSCLL GLGSLVLILS LSYTVLIVGR IAIGVSISLS SIATCVYIAE 120
 IAPQHRRLGL VSLNELMIVI GILSAYISNY AFANVFHWK YMFGLVPLG VLQAIAMYFL 180
 PPSRFLVMK QGEGAASKVL GRRLALSDTT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
 45 RIMIGLTLVF FVQITGQPNL LFYASTVLKS VGFQSNAAAS LASTGVGVVK VISTIPATLL 300
 VDHYGSKTFL CIGSSVMAAS LVTMGIVNLN IHMNFTHICR SHNSINQSLD ESVYDGPGLN 360
 STNNNTLRDH FKGISHSRSL SLMPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420
 AFLKWLASL LLVYVAAFSI GLGPMPLVL SEIFPGGIRG RAMALTSSMN WGINLLISLT 480
 50 FLTVTDLIGL PWVCFYTIM SLDLIGLPWV CFYTIMSLA SLLFVVMFIP ETKGCSLEQI 540
 SMELAKVNYV KNNICFMSHH QEELVPKQPQ KRKPQEQLLE CNKLCGRGQS RQLSPET 580

SEQ ID NO:243 PBA4 DNA sequence:

Nucleic Acid Accession#: AA172056

Coding sequence: 121-339 (underlined sequences correspond to start and stop codons)

55 TTTAGCCACC AGAGGANTTC TCTTGAAATA CCAAAATCC ATCAGTATCT TGAATCATGC 60
 TGGATTTTGA AGAATTCCTA AGAAGCCATG TAAAGGGGGC TCTCTGGCCT TGAAATAGTG 120
 60 ATGTTTITTTA TACAGAAAGG AGAATGCAGA ATGGTCAGAC TATCATGCAC TGTTAAATTT 180
 GATTTCAGAA AATTACAGGA AAACTTTCCA AAGTTCCATC TCACAGAANN TTATTTTNCC 240
 AAGAATTCCTA AGATAAGTTT AGTTTATGGA AAGACTTTTA TGTGGTTTTT ACTCACTCTT 300
 CATCTCAGAC ATCGACAGAT GATTACATCA CTTATAGTTC TAGTAAATTT ATTAATATAA 360
 AACTCAGAGA CATTCGAATA TCCACATTGC TTACACCATT AGGCATAGAT TCAGTGTGAG 420
 65 CTATGACAAAT TGAAGATGAG CTGTTTGTG ATTTAAAGGT TTAATTTTCT CTAACCAAC 480
 TGCTTGATCC AGATGCAGGA CTGCAAAATGT TAATATTGTT TCTGGAAGAA CAATCAATA 540
 AGACTTAAGA GGAAGGGGAA TGGCCACAAT CCACCTGAAA TTTTITCTTA AAAAGTGTGC 600
 AGCCTACTAA ATCAGAATGA AAATAGAAGT ACAAGATTAT AAACAAAATG CAATCAAACT 660
 70 TTTCTTAAGC TTACTTAAAG TTATTTTATC TGAATAATTC AAGCACTTT GTTCAACATT 720
 AAATTGACAA TCTAAACTAA CAAGTCTTTT GAATTTATGC ATGGTAGTAA ACATTCTCTC 780
 TATTAATCTT ATTACCTAAG GCTAAACCTA AAATTTTAA GCAAAATTAG AAAAAATAGT 840
 TTCACTCATC AAAAAATAAA GTTTGTGACA TTAGTATTTT TCCCAATAAA ATTGGTCGTT 900
 75 CTTGGTTTTT TATTGGAGA GTCTGTGCAA AATGTCATA AAAATAAATT AGCACTAGAA 960
 ATTATTCTTA AATACCAAA

SEQ ID NO:244 PBQ8 DNA SEQUENCE

Nucleic Acid Accession#: X51405

Coding sequence: 3-1721 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51

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| AAATGGCGTG | CCCGTCTCTC | GCGCGGCCCC | CTGCCTGGCA | GTGGTTTCTC | CTGCAGCTCC | 60
| CCTGGGCTCC | GCGGCCAGTA | GTGCAGCCCG | TGGAGCCGCG | GCTTTGCCCG | TCTCTCTCGG | 120
| GTGGCCCCAG | TGGCGGGGCT | GACACTCATT | CAGCCGGGGA | AGGTGAGGCG | AGTAGAGGCT | 180
| GGTGCGGAAC | TTGCGGCCCC | CAGCAGCGCC | GCGCGGCTAA | GCCCAGGGCG | GGGCAGACAA | 240
| AAGAGGCCCG | CCGCGTAGGA | AGGCACGGCC | GCGCGCGGCG | GAGCGCAGCG | ATGGCCGGGC | 300
| GAGGGGGCAG | CCGCGTGCTG | GCTCTGTGCG | GGGCACTGGC | TGCTTGGCGG | TGCTCTCTGG | 360
| GCGCGGAACG | CCAGGAGCCC | GGGGCGCCCG | CCGCGGGCAT | GAGCGGCGCG | CCGCGGCTGC | 420
| AGCAAGAGGA | CGGCATCTCC | TTCCAGTACC | ACCGCTACCC | CGAGCTGGCG | GAGGCGCTCG | 480
| TGTCCGTGTG | GCTGCAGTGC | ACCGCCATCA | CGAGGATTTA | CACGGTGGGG | CGCAGCTTCG | 540
| AGGCGCGGGA | GCTCCTGGTC | ATCGAGCTGT | CCGACAACCC | TGGCGTCCAT | GAGCCTGGTG | 600
| AGCCTGAATT | TAAATACATT | GGGAAATATG | ATGGGAATGA | GGCTGTGGGA | CGAGAAGTGC | 660
| TCATTTTCTT | GGCCCACTAC | CTATGCAACG | AATACCAGAA | GGGGAACGAG | ACAATTGTCA | 720
| ACCTGATCCA | CAGTACCCGC | ATTCACATCA | TGCTTCCCTT | GAACCCAGAT | GGCTTTGAGA | 780
| AGGCAGCGTC | TCAGCCTGCT | GAACCTCAAG | ACTGGTTTGT | GGGTCGAAGC | AATGCCCAGG | 840
| GAATAGATCT | TTCCAGGACC | TGGATAGGAT | AGTGACGCTG | AATGAGAAAG | 900
| AAGTGGTCC | AAATAATCAT | CTGTTGAAAA | ATATGAAGAA | AATGTGGAT | CAAAACACAA | 960
| AGCTTGCTCT | TGAGACCAAG | GCTGTCAATC | ATTGGATTAT | GGATATTCTT | TTTGTGCTTT | 1020
| CTGCCAATCT | CCATGGAGGA | GACCTTGTGG | CCAATTATCC | ATATGATGAG | ACGCGGAGTG | 1080
| GTAGTGCTCA | CGAATACAGC | TCCTCCCCAG | ATGACGCCAT | TTTCCAAGCG | TTGGCCCGGG | 1140
| CATACTCTTC | TTTCAACCCG | GCCATGTCTG | ACCCCAATCG | GCCACCATGT | CGCAAGAAATG | 1200
| ATGATGACAG | CAGCTTTGTA | GATGGAACCA | CCAACGGTGG | TGCTTGGTAC | AGCGTACCTG | 1260
| GAGGGATGCA | AGCCTTGAAT | TACCTTAGCA | GCAACTGTTT | TGAGATCACC | GTGGAGCTTA | 1320
| GCTGTGAGAA | GTTCCCACTT | GAAGAGACTC | TGAAGACCTA | CTGGGAGGAT | AACAAAAACT | 1380
| CCCTCATTTG | CTACCTTTAG | CAGATACACC | GAGGAGTTAA | AGGATTGTGC | CGAGACCTTC | 1440
| AAGGTAAACC | AATTGCGAAT | GCCACCATCT | CCGTGGAAAG | AATAGACCAC | GATGTTACAT | 1500
| CCGCAAGGA | TGGTGATTAC | TGGAGATTGC | TTATACCTGG | AAATAATAAA | CTACAGCCTT | 1560
| CAGCTCCAGG | CTATCTGGCA | ATAACAAAGA | AAGTGGCAGT | TCCTTACAGC | CCGCTGCTGG | 1620
| GGGTTGATTT | TGAACCTGGG | TCATTTTCTG | AAAGGAAAGA | AGAGGAGAAG | GAAGAATTGA | 1680
| TGGAAATGGT | GAAATGATG | TCAGAAACTT | TAAATTTTAA | AAAAGGCTTC | TAGTTAGCTG | 1740
| CTTTAAATCT | ATCTATATAA | TGTAGTATGA | TGTAAATGTT | TCTTTTCTTT | AGATTTTTGT | 1800
| CAGTTAATAC | TTAACATTTA | TTTATTTTCT | AATCATTTAA | ATATTAAATCA | ACTTTCCTTA | 1860
| AAATAAATAG | CCTCTTAGGT | AAAAATATAA | GAACCTGATA | TATTTCTATC | TCTTATATAG | 1920
| TATTCATTTT | CCTACCTATA | TTACACAAAA | AAGTATAGAA | AAGATTTAAG | TAATTTTGCC | 1980
| ATCTTAGGCT | TAAATGCAAT | ATTCTGGTGA | TTATTTACAA | TGCAGAAATT | TTTGAGTAAT | 2040
| TCTAGATTTT | AAAAATTAGT | GAAGTTCTTT | TACTGTAATT | GGTGACAATG | TCACATAATG | 2100
| AATGCTATTG | AAAAGGTTAA | CAGATACAGC | TCGGAGTTGT | GAGCACTCTA | CTGCAAGACT | 2160
| TAAATGTTCT | AGTATAAATT | GTCGTTTTTT | TCTGTGCTGT | ACTAATCTAT | AGCATGATCT | 2220
| TGTTAATGCA | TTTTGTATGG | GAAGAAAAGG | TACATGTTTA | CAAAGAGGTT | TTATGAAAAG | 2280
| AATAAAATTT | GACTTCTTGC | TTGTACATAT | AGGAGCAATA | CTATTATATT | ATGTAGTCCG | 2340
| TTAACACTAC | TTAAGGTTT | AGGGTTTCTT | CTGGTTGTA | GAGTGGCCCA | GAATTGCATT | 2400
| CTGAATGAAT | AAAGGTTAAA | AAAAAATCCC | CAGTGAAAAA | AAA
  
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SEQ ID NO:245 PBQ8 Protein sequence

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Protein Accession#: P16870

MAGRGSALL ALCGALAACG WILGAEAOEP GAPAAGMRRR RLQOEDGIS FEYHRYPELR 60
EALVSVWLQC TAISRIYTVG RSFEGRELLV IELSDNPGVH EPGEPEFYKI GNMHGNEAVG 120
RELLIFLAQY LCNEYQKGNE TIVNLHSTR IHIMPSLNDP GFEKAASQPG ELKDWVFGRS 180
NAQGDIDLNRN FPDLDRIYVY NEKEGGPNNH LLKNMKKJVD QNTKLAPETK AVIHWIMDIP 240
FVLSANLHGG DLVANYPYDE TRSGSAHEYS SSPDDAIRQS LARAYSSFN AMSPDNRPPC 300
RKNDDSSSFV DGTINGGAWY SVPGGMODFN YLSSNCFEIT VELSCEKFFP EETLKTYWED 360
NKNLSLISYLE QHHRGVKGFV RDLQGNPIAN ATISVEGIDH DVTSAKDGDY WRLLIPGNYK 420
LTASAPGYLA ITKKVAVPYS PAAGVDFELE SFSEKKEEEK EELMEWVKMM SETLNF
  
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SEQ ID NO:246 PB4 DNA sequence

Nucleic Acid Accession#: AF038966

Coding sequence:

91-1107 (undefined sequence corresponds to start and stop codon)

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1 11 21 31 41 51
| GGGGCGACGT | GAGCGCGCAG | GGGGGCGGCG | GCCTCGCCTC | GTCTCTCTCT | CTGCGCCTGG | 60
| GTCCGGTGGG | TGACGCCGAG | AGCCAGAGAG | ATGTCGGATT | TCGACAGTAA | CCCGTTTGCC | 120
| GACCCGGATC | TCAACAATCC | CTCAAGGAT | CCATCAGTTA | CACAAGTGAC | AAGAAATGTT | 180
| CCACCGAGG | TTGATGAATA | TAATCCATT | TCGGATTCTA | GAACACCTCC | ACCAGGCGGT | 240
| GTGAAGATGC | CTAATGTACC | CAATACACAA | CCAGCAATAA | TGAAACCAAC | AGAGGAACAT | 300
| CCAGCTTATA | CACAGATTGC | AAAGGAACAT | GCATTGGCCC | AAGCTGAAC | TCTTAAGCCC | 360
| CAAGAAGAAC | TAGAAGAAAA | AGCCGCAGAA | TTAGATCGTC | GGAACGAGA | AATGCAAAAC | 420
| CTCAGTCAAC | ATGTAGAAAA | AAATATTGCG | CCACCTCTTC | CTAGCAATTT | TCCTGTCCGA | 480
| CCTGTGTTCT | ATCAGGAATT | TTCTGTAGAC | ATTCTCTGTA | AATTCCAAAA | GACAGTAAAG | 540
| CTTATGTACT | ACTTGTGGAT | GTTCCATGCA | GTAACACTGT | TTCTAAATAT | CTTCGGATGC | 600
| TTGGCTTGGT | TTTGTGTTGA | TTCTGCAAGA | GCGGTTGATT | TTGGATTGAG | TATCCTGTGG | 660
| TTCTTGCTTT | TTACTCTCTG | TTCAATTGTC | TGTGGGTACA | GACCACTTTA | TGGAGCTTTC | 720
| AGGAGTGACA | GTCAATTTAG | ATTCCTTTGA | TTCTTCTTCG | TCTATATTGG | TCAGTTTGGT | 780
| GTACATGTAC | TCCAGCTGCG | AGGATTTCAT | AACTGGGGCA | ATTGTGGTTG | GATTTCATCC | 840
| CTTACTGGTC | TCAACCAAAA | TATTCCTGTT | GGAATCATGA | TGATAATCAT | AGCAGCACTT | 900
| TTACACGAT | CAGCAGTATT | CTCACTAGTT | ATGTTCAAAA | AAGTACATGG | ACTATATCCG | 960
| ACAACAGGTG | CTAGTTTGTG | GAAGGCCCAA | CAGGAGTTTG | CAACAGGTGT | GATGTCCAAC | 1020
| AAAACTGTCC | AGACCCGAGC | TGCAAAATGCA | GCTTCAACTG | CAGCATCTAG | TGCAGCTCAG | 1080
  
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AATGCTTTCA AGGTAACCA GATTTAAGAA TCCTCAACA ATACACTGTT ACCTTTTGAC 1140
TGTACCTTTT TCTCCAGTTA CTGTATTCTA CAAATATTTT TATGTTCAAA ACACACAGTA 1200
CAGACAGCAT GGATATTTCC TGTTCACTTG TGCATGGGCT AAAACCAGGA AAACCTTCCTT 1260
GTCTTATTAC TTTACCTAAT AGTTTCTTAA TATTTCACTG CCCCTTGCAG AAAAAATATT 1320
ACATGTCTAA TAAATATTCT CCATATTTTT GGGGGATGAC ATTCAGTGAA TTATTTTCAGT 1380
GGTGACCCAC TGAAAATTAA TAATGGTACT TATGATTAAA AACGCATTTA ATACTAACTG 1440
CAGTAGTTCT TTCAAGAATC TTAGAGATA AGGATTGCAC ATTGGAAGAAG TAAACCATGT 1500
TTCAATTCCTT TTTCCTTATT TATATTGAAA GAAATAGGCC AGCAGAGACT TAGGGATTTT 1560
AAATGGCTT GCTTTTTCAGC TGTTTCAGTC ACCAGTGAAG AGCCTATGTG CATTTTGTAG 1620
TAGATAATGT AAAATTGTGC ATCTTTTCTT TTCTTTTCTT TTAGAATAGC TGATATTTTG 1680
ATAACAATCT CTAATTTCGA TGGGCACCAC ATTTCTTTATA TTAAGAAGT TAGTGTTTTG 1740
GCTTCTGTAC TGCTTATGTT TGTAGGATTC AGGGGTAAAT GGAATCACAG AAATGATATT 1800
CTGCAAGAAAT TTCTTTTAAA TAAAAAGTTT GGGGGTGCAA TATAAGAAGT TTATATAATA 1860
TGCAGTACAT TATCCAAAAG AGAAGGTAGT TAATGCAGTA GAAAGTAGTG GTAATAATTC 1920
CTTTTTT
  
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SEQ ID NO: 247 PBH4 Protein sequence:

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Protein Accession #: none found

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MSDFDSNPFA DFDLNNPKFD PSVTQVTRNV PPGLEYNPF SDSRTPPPGG VKMPNVPNTQ 60
PAIMKPTTEH PAYTQIAKEH ALAQAEELKR QEELERKAAE LDRREREMQN LSQHGRKNIW 120
PPLPSNFPVG PCFYQFESVD IPVEFQKTVK LMYYLWMFHA VTLFLNIFGC LAWFCVDSAR 180
AVDFGLSLW FLLFTCSFV CWYRPLYGAF RSDSSFFV FFFVYICQFA VHVLAAGFH 240
NWGNCGWISS LTGLNQNPV GIMMIIAAL FTASAVISLV MFKKVHGLYR TTGASFEKAQ 300
QEFATGVMSN KTVQTAANA ASTAASSAAQ NAFKGNQI
  
```

SEQ ID NO: 248 PBH2 DNA sequence

30

Nucleic Acid Accession#: none found

Coding sequence: 1-613 (underlined sequence corresponds to start and stop codon)

35
 40
 45

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ATGAGAGACA ATAAATCGTG TGCTTTTTC ATGGGAAAGT TAAATGTTTG TTTGAAGGC 60
ACAGTAATAG CAGGCTATT AGTGTTTGGC ACTACCTGCA TCATTCACT GGCTGAGCT 120
AGTGCACTAC AATTTCCTAA AAAGTCTTCT CACCCTCACA GGACTGCTCT ACATCTGGCC 180
TCTGCCAATG GAAATTCAGA AGTAGTAAAT CTCTGCTGG ACAGACGATG TCAACTTAAT 240
ATCCTTGACA ACAAAAAGAG GACAGCTCTG ACAAGGCCG TACAATGCCA GGAAGATGAA 300
TGTCGGTTAA TGTTGCTGGA ACATGGCACT GATCCGAATA TTCCAGATGA GTATGGAAAT 360
ACCGCTCTAC ACTATGCTAT CTACAATGAA GATAAATTAA TGGCCAAAGC ACTGCTCTTA 420
TACGGTGCTG ATATCGAATC AAAAAACAAG CATGGCCTCA CACCACTGTT ACTTGGTGTA 480
CATGAGCAAA AACAGCAAGT GGTGAAATTT TTAATCAAGA AAAAAGCAAA TTAAATGCA 540
CTGGATAGAT ATGGAAGGTG TGTGACCTTG GGAACGTTAT TTACCACCAA ATATGTTGTC 600
ATATATGAAA AGTAG
  
```

SEQ ID NO: 249 PBH2 Protein sequence:

50

Protein Accession #: none found

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MRDNKSCAFF MGKLNVCPEG TVIAGYSVFA TTCIHLAVA SALQFPKKSS HPHRTALHLA 60
SANGNSEVVK LLLDRRCQLN ILDNKKRTAL TKA VQCQEDE CALMLLEHGT DPNIPDEYGN 120
TALHYAIYNE DKLMKAKALL YGADIESKNK HGLTPLLGV HEQKQVVKF LIKKKANLNA 180
LDRYGRCVL GTLFTTKYVV IYEK
  
```

SEQ ID NO: 250 PBH1 DNA sequence

55

Nucleic Acid Accession#: XM_005829

Coding sequence: 1-3043 (underlined sequence corresponds to start and stop codon)

60
 65
 70
 75

```

ATGGTGATCA TCTATCTTC TTCTGCAAT TATTACATGG AGTTCTACAG AGAAGAGCTT 60
CCCCACATTG ACTATTGAT TGACATTGAG TTGCAACAG GAAAGGTTAC TCAGCCGGGA 120
GAGGACACTT CCTACCATCA ATGCGCTCAG CTGGAAGCCA GAGACGAAG CACCGACAGT 180
TTATTATTAA ACAATGGCAG CAGCGCCACG CTGAAGACAC GAACGCGCTG TTATGGAACC 240
CCCAGAGGTC TCCCCATCG TAGCCTGCTC CAGCCGACTC CGCCACATG TAAAACGAAG 300
ATCAGGAGCA GATTGAAGA ATTACAAAGT GAATTTGGTG CAGTCAGCAT GTCAGAGACA 360
GACCACATAG CCTCTACTTC CTCTGATAAA AATGTTGGGA AAACACCTGA ATTAAAGGAA 420
GACTCATGCA ACTTGTTTC TGGCAATGAA AGCAGCAAA TAGAAAATGA GTCCAAACTA 480
TTGTCATTAA ACCTGATAA AACTTTATGT CAACCTAATG AGCATAATA TCGAATTGAA 540
GCCCAGGAAA ATTATATTC AGATCATGGT GGAGGTGAGG ATCTTGTGC CAAAACAGAG 600
ACAGGCTCAG AAAATTCTGA ACAAATAGCT AATTTTCTTA GTGGAATTT TGCTAAACAT 660
ATTTCAAAAA CAAATGAAAC AGAACAGAAA GTAACACAAA TATTGGTGA ATTAAGGTCA 720
TCTACATTTT CAGAATCAGC TAATGAAAAG ACTTATTCAG AAAGCCCTTA TGATACAGAC 780
TGCACCAAGA AATTATTTTC AAAAATAAAG AGCGTTTCAG CATCAGAGGA TTTGTTGGAA 840
GAAATAGAAAT CTGAGCTCTT ATCTACGGAG TTTCAGAAAC ATCGAGTACC AAATGGAATG 900
AATAAGGGAG AACATGCATT AGTTCTGTTT GAAAAGTGTG TGCAAGATAA ATATTTGCAG 960
CAGGAACATA TCATAAAAAA GTTAATTAAA GAAAATAAGA AGCATCAGGA GCTCTTCGTA 1020
GACATTTGTT CAGAAAAAGA CAATTTAAGA GAAGAACTAA AGAAAAGAAC AGAACTGAG 1080
AAGCAGCATA TGAACACAA TAAACAGTTA GAATCAAGAA TAGAAGAACT TAATAAGAA 1140
GTAAAGCTT CCAGAGATCA ACTAATAGCT CAAGACGTTA CAGCTAAAAA TGCAGTTGAG 1200
  
```

5 CAGTTACACA AAGAGATGGC CCAACGGATG GAACAGGCCA ACAAGAAATG TGAAGAGGCA 1260
 CGCCAAGAAA AAGAAGCAAT GGTAATGAAA TATGTAAGAG GTGAGAAGGA ATCTTTAGAT 1320
 CTTGCGAAGG AAAAAGAGAC ACTTGAGAAA AAACCTTAGAG ATGCAAAATA GGAACTTGAG 1380
 10 AAAAAACACTA ACAAAATTA CGACGTTTCT CAGGAGAAAG GACGGTTGCA CCAGCTGTAT 1440
 GAAACTAAGG AAGGCGAAAC GACTAGACTC ATCAGAGAAA TAGACAAATT AAAGGAAGAC 1500
 ATTAACCTC ACCTCATCAA AGTAAAGTGG GCACAAAACA AATTAAAGC TGAATGGAT 1560
 TCACACAAGG AAACCAAGA TAACTCAAA GAAACAACA CAAAATTAAC ACAAGCAAG 1620
 GAAGAGCAG ATCAGATACG AAAAACTGT CAGGATATGA TAAAAACATA TCAGGAGTCA 1680
 15 GAAGAAATTA AATCAATGA GCTTGATGCA AAGCTTAGAG TCACAAAAGG AGAACTTGAA 1740
 AAACAAATGC AAGAAAAATC TGACCAGCTA GAGATGCATC ATGCCAAAT AAAGGAACTA 1800
 GAAGATCTGA AGAGAACAT TAAGGAGGGT ATGGATGAGT TAAGAACT GAGAACAAG 1860
 GTGAAATGTC TAGAAGATGA ACGATTAAGA ACAGAAGATG AATTATCAAA ATATAAGGAA 1920
 ATTATTAATC GCCAAAAAGC TGAATTCAG AATTTATTGG ACAAGGTGAA AACTGCAGAT 1980
 CAGCTACAGG AGCAGCTTCA AAGAGGTAAG CAAGAAATTG AAAATTTGAA AGAAGAAGTG 2040
 20 GAAAGTCTTA ATCTTTGAT TAATGACCTA CAAAAAGACA TCGAAGGCAG TAGGAAAAGA 2100
 GAATCTGAGC TGCTGCTGTT TACAGAAAGG CTCAGTAGTA AGAATGCACA GCTTCAGTCT 2160
 GAATCCAATT CTTTCAGTC ACAATTTGAT AAAGTTTCT GTAGTGAAG TCAGTTACAA 2220
 AGCCAGTGTG AAAAAATGAA ACAGACAAAT ATTAATTTGG AAAGTAGGTT GTTGAAAGAG 2280
 GAAGAACTGC GAAAAAGGA AGTCCAACT CTGCAAGCTG AACTCGCTTG TAGACAAACA 2340
 25 GAAGTTAAAG CATTGATAC CCAGGTAGAA GAATTAAG ATGAGTTAGT AACTCAGAGA 2400
 CGTAAACATG CCTCTAGTAT CAAGGATCTC ACCAAACAAC TTCAGCAAGC ACGAAGAAAA 2460
 TTAGATCAGG TTGAGAGTGG AAGCTATGAC AAAGAAGTCA GCAGCATGGG AAGTCGTTCT 2520
 AGTTTCATCAG GGTCCCTGAA TGCTCGAAGC AGTGCAGAAG ATCGATCTCC AGAAAAACT 2580
 GGGTCTCAG TAGCTGTGGA TAACTTTCCA CAAGTAGATA AGGCCATGTT GATTGAGAGA 2640
 30 ATAGTTAGGC TGCAAAAAGC ACATGCCCGG AAAAAATGAA AGATAGAATT TATGGAGGAC 2700
 CACATCAAA ACCTGTGTGA AGAAATTAGG AAAAAACAA AAATAATICA AAGTTATATT 2760
 TTACGACAGG AATCAGAGCA ACTTTCTTCA GAGGCATCTG ATTTAACA AGTTCAATTA 2820
 AGTAGACGGG GTGCTCATCAT GGCATCTTTA TATACATCCC ATCCAGCTGA CAATGGATTA 2880
 ACATTGGAGC TCTCTTTGGA AATCAACCGA AAATTACAGG CTGTTTGGGA GGATACGTTA 2940
 35 CTAAAAATA TTACTTTGAA GGAATCTA CAAACACTTG GAACAGAAAT AGAACGTCTT 3000
 ATTAACACC AGCATGAACT AGAACAGAGG ACAAAGAAAA CCTAAAAACA GCCTCTTGCT 3060
 CAGTAAAGAG ACAAAGCCA CACAGGAGTA GGTGCCACTG ACCTCTATTG TTGGAGACTT 3120
 TGTTCACCTT TTTGTTTCAG CCAGTAAAAA TATTGTTTG CTTCATCTGT ACACAAAAA 3180
 ATACCCTTT ACAATATGAA TGCATTGCTG TATATCTGT AAGACTGAAA GCTTTGATGA 3240
 AATTGTTT TTGATGGTGC AATATGACAG CCGTTCATTG AATCTAAACA ACTTAATTG 3300
 CTTGATTICA TAAGAAGTGT TGAACATTAC AAGGGCTTTT AT

40 Protein Accession #: SEQ ID NO:251 PBJ1 Protein sequence:
 NP_060487

45 MVIYLSFNC YYMEFYREEL PHIDYLDIQ FATGKVTQPG EDTSYHQCAQ LEARDEGTD 60
 LLNNGSSAT LKTRTRYCYGT PRGLPHRSL QTPPTCKTK IRSRFEELQS ELVPVSMSET 120
 DHIATSSDK NVGKTPELKE DSCNLFSGNE SSKLENESKL LSLNTDKTLC QPNEHNNRIE 180
 AQENYIPDHG GGEDSCAKTD TGSENSEQIA NFPSGNFAKH ISKTNETEQK VTQILVELRS 240
 STFESANEK TYSESPYDID CTKKFISKIK SVSASEDLLE EIESELLSTE FAIEHRVPNGM 300
 NKGEHALVLF EKCVDQKYQ QEHIIKLIK ENKKHQELFV DICSEKDNLR BELKRTETE 360
 50 KQHMTNTKQL ESRIEELNKE VKASRDQLIA QDVTAKNVQ QLHKEMAQRM EQANKKCEEA 420
 RQEKEAMVMK YVRGEKESLD LRKEKETLEK KLRDANKLE KNTNLIKQLS QEKGRHLQLY 480
 ETKEGETTRL IREIDKLKED INSHVIKVKW AQNKLAEMD SHKETDKLXK ETTTKLTQAK 540
 EEADQIRKNC QDMIKTYQES EEEKSNELDA KLRVTKGELE KQMKEKSDQL EMHHAKIKEL 600
 EDLKRITKEG MDLRLTLRTK VKCLEDERLR TEDELSKYKE INRQKAEIQ NLLDKVKTAD 660
 55 QLQEQLRGKQ QEENLKEEV ESLNSLNDL OKDIEGSRKR ESELLLTER LTSKNAQLQS 720
 ESNLSQSQFD KVSCESEQLQ SQCEQMKQTN INLESRLKE EELRKEEVQT LQAEACRQT 780
 EVKALSTQVE ELKDELVTQR RKHASSIKDL TKQLQARRK LDQVESGSYD KEVSSMGSR 840
 SSSGSLNARS SAEDRSPENT GSSVAVDNFP QVDKAMLIER IVRLQKAHAR KNEKIEFMED 900
 HIKQLVEER KTKKIQSYI LREESGTLSS EASDFNKVHL SRRGGMASL YTSHPADNGL 960
 TLELSLEINR KLQAVLEDIL LKNITLKENL QTLGTEIERL IKHQHELEQR TKKT

60 SEQ ID NO:252 PBJ6 DNA sequence
 Nucleic Acid Accession#: D83760
 Coding sequence: 56-1459 (underlined sequence corresponds to start and stop codon)

65 1 11 21 31 41 51
 | | | | |
 TTGCGGTGAA GGGCTGTGCG GTTCCCGTGC GCGCCGGAGC CTGCTGTGGC CTCTTATGCA 60
 CTTCCACCACC CCCATCAGCT CCTCTTCTC CTTCCACCAG CCCGCACTGA AGAGACTGCT 120
 70 AGGCTGGAG CAAGGAGATG AAGAGGAAAA GTGGGCAGAG AAGGCACTGG ACTCTCTAGT 180
 AAGAAGTTTA AAGAAGAAGA AGGGAGCCAT GGACGAGCTG GAGAGGGCTC TCAGCTGCCC 240
 GGGGAGGCC AGCAATATGC TCACGATTCC CCGCTCCCTG GACGGGCGGC TGCAGGTGTC 300
 CCACCGCAAG GCGCTGCCCC ATGTGATTTA CTGTGCGCTG TGGCGCTGGC CGGATCTGCA 360
 GTCCACCAC GAGCTGAAGC CGCTGGAGTG CTGTGAGTTC CCATTGCTG CCAAGCAGAA 420
 AGAAGTGTGC ATTAACCTTT ACCACTACCG CCGGTGGAG ACTCCAGTAC TGCCCTCTGT 480
 75 GCTCGTGCCA AGACACAGT AATATAACCC CCAGCTCAGC CTCTGGCCA AGTTCCGCAG 540
 CGCCTCCCTG CACAGTGAAC CACTCATGCC ACACAACGCC ACCTATCCTG ACTCTTTCCA 600
 CGAGCCTCG TGCTCTGCAC TCCTCCCTC ACCCAGCCAC GCGTCTCCC AGTCCCGGTG 660
 CACGGCCAGC TACCTCACT CCCAGGAAG TCCTTCTGAG CCAGAGATGC CCTATCAACA 720
 CTCAGTTGAC ACACCAACCC TGCTTATCA TGCCACAGAA GCCTCTGAGA CCCAGAGTGG 780

5 CCAACCTGTA GATGCCACAG CTGATAGACA TGTAGTGCTA TCGATACCAA ATGGAGACTT 840
 TCGACCAAGT TGTACGAGG AGCCCCAGCA CTGGTGCTCG GTCCCTACT ATGAACTGAA 900
 CAACCGAGTT GGGGAGACAT TCCAGGCTTC CTCCCGAAGT GTGCTCATAG ATGGGTTCAC 960
 CGACCCCTCA AATAACAGGA ACAGATTCTG TCTTGGACTT CTTTCTAATG TAAACAGAAA 1020
 CTCAACGATA GAAATACCA GGAGACATAT AGGAAAGGGT GTGCACCTGT ACTACGTCGG 1080
 GGGAGAGGTT TATGCCGAGT GCGTGAGTGA CAGCAGCATC TTTGTGACAG GCCGGAACCTG 1140
 CAACATATCA CACGGCTTCC ACCCAGCTAC CGTCTGCAAG ATCCCCAGCG GCTGCAGCCT 1200
 CAAGGTCTTC AACAAACGAG TCTTCGCTCA GCTCCTGGCC CAGTCAGTTC ACCACGGCTT 1260
 10 TGAAGTCGTG TATGAATGTA CCAAGATGTG TACTATCCGG ATGAGTTTGT TTAAGGGTTG 1320
 GGGTGTCTAG TATCATCGCC AGGATGTAC CAGCACCCCC TGCTGGATTG AGATTTCATCT 1380
 TCATGGGCCA CTGCAGTGGC TGGACAAAGT TCTGACTCAG ATGGGCTCTC ACATAAACC 1440
 CATTCTCTCA GTGTCTAAC AGTCATGTCT TAAGCTGCAT TTCCATAGGA T

15 SEQ ID NO:253 PBj6 Protein sequence:
 Protein Accession #: NP_005896

16 MHSTTPISLL FSFTSPA VKR LLGWKQGDDE EKWAEKAVDS LVKKLKKKKG AMDELERALS 60
 17 CPQGSKCVT IPRSLDGRGQ VSHRKG LPHV IYCRVWRWPD LQSHHE LKPL ECCEFFPGSK 120
 18 QKEVCINPYH YRRVETPVL PVLVPRHSEY NPQLSLAKF RSASLHSEPL MPHINATYPDS 180
 19 FQPPPCALP PPSHAFS QS PCTASYPHSP GSPSESPY QHSVDITPLP YHATEASETQ 240
 20 SGQPV DATAD RHVVL SIFNG DFRPVCYEEP QHWC SVAYYE LNNRVGETFQ ASSRSVLIDG 300
 21 FIDFSNNRNR FCLGLLSNVN RNSTIENTRR HIGKGVHLYY VGGEVYAE CV SDSSIFVQSR 360
 22 NCNYQHGFHP ATVCKIPSGC SLKVFNNQLF AQLLAQSVHH GFEVYVELTK MCTIRMSFVK 420
 23 GWGA EYHRQD VTSTPCWIEI HLHGLPQLWLD KVLTMGSPH NPISSVS

24 SEQ ID NO:254 PBj8 DNA sequence
 Nucleic Acid Accession #: AB04684
 Coding sequence: 472-4377 (underlined sequence corresponds to start and stop codon)

30 1 11 21 31 41 51
 | | | | | |
 35 TGCAGGTTTG CAGGGTCTGA GATTACTTGG GCTTTTCTCG CCTTTTCTCT TTGCTTAAGG 60
 GATGGACAAG GAGCTGAGAT TTATGACCCCT TATTAGAGAA AAAAAATGTC CTTCCTAGGG 120
 TGGGGACACT TGTTGATGCG AGTCTCTCTC TCTCTTCTCT GGTGTTTATA AAAAAACAAA 180
 ACCAAAATGA ACTGAGGGGT TTGTAATGGT AGTTTGTGTT TTGCTGGAGA ATGCTACTTT 240
 GCATGCTTTT TTTCTCTTGC AGGGTATGTT CTGCTCTGTG CTTTCTCTTT TAGAAGCTAC 300
 TAAAGGGTGT TGGGATGCT TCTGACTATT ATGAAGGCCA AAAGGCTGTG TGAAGCTGGC 360
 40 TCCTTTTAACT CCTTCTCTAT TTGCTGAGAA TGCAGCCGTG TGACAGTAAC TGAACATTGG 420
 TCTAAAGTCT TTCCAAAAGG TCAAGGTTC AAGAACATC TGCTCAAAAT AATGACCATG 480
 GGGGATATGA AGACCCGAGA CTTTGTATGAC CTCTGGCAG CATTTGACAT CCCAGATATG 540
 GTCGATCTTA AAGCAGCTAT TGAGTCTGGA CACGATGACC ATGAAGGCCA CATGAAGCAG 600
 AATGCTCAGC GAGAGGATGA CTCCCACGCA CCATCATCTT CTGATGTGGG TGTACGCTT 660
 45 ATCGTCAAGA TGCTTCCGAA CATTGACTCT TCCGAGGGCG GGGAGAAAGA CGGCCACAAC 720
 CCCACTGGCA ATGGCTTACA TAATGGGTTT CTCACAGCAT CCTCCCTTGA CAGTTACAGT 780
 AAGAATGGAG CCAAGTCTAT GAAAGGAGAT GTGCTGCCT CTGAGGTGAC ACTGAAAGAC 840
 TCGACATTCA GCCAGTTTAG CCCGATCTCC AGTGTCTGAG AGTTTGTATG CAGCAGAGAAG 900
 ATTGAGGTGG ATGACCCCCC TGACAAGGAG GACATGCGAT CAAGCTTCAG GTCGAATGTG 960
 50 TTGACGGGGT CGCTTCCCA GCAGGACTAC GATAAGCTGA AGGCACCTCG AGGGGAAAAC 1020
 TCCAGCAAAA CTGGACTCTC TACGTGAGGC AATGTGGAGA AAAACAAAAG TGTTAAGAGA 1080
 GAAACAGTAC CCAAGTCTAT AAACCTGAGT GTTTATGAAC CTTTAAAGT CAGAAAAGCA 1140
 GAGGATAAAT TGAAGGAAAG CTCTGACAAG GTGCTGGAAA ACAGAGTCTC AGATGGGAAG 1200
 CTGAGCTCCG AGAAGAATGA CACGAGCTC CCCAGCGTTG CGCATCAAAA GACAAAGTCG 1260
 55 TCTTCCAAAG TCTCGTCTCG CATCGCTGCC ATCGCGGCTC TCAGCGCTAA AAAGCGCGCT 1320
 TCAGACTCCT GCAAGAAACC AGTGGCCAAT TCGAGGGAAT CCTCCCGGTT ACCAAAAGAA 1380
 GTAAATGACA GTCCGAGAGC CGCTGACAAG TCTCTGAAT CCCAGAAATC CATCGACGGG 1440
 ACCAAAAAAC CATCCCTGAA GCAACCGGAT AGTCCAGAAA GCATCTCAAG TGAGAACAGC 1500
 60 AGCAAAAGGAT CCCCGTCTC TCCCGCAGGG TCCACACCAG CAATCCCAA AGTCCGCATA 1560
 AAAAACCATT AGACATCTTC TGGGGAATC AAGAGAACAG TGACCAGGGT ATTGCCAGAA 1620
 GTGGATCTTG ACTCTGAAA GAAACCTTCC GAGCAGACAG CGTCCGTGAT GGCCTCTGTG 1680
 ACATCCCAAG TGTCTCTCT AGCATCAGCC GCCGTCTTTT CTTCTCCCCC CAGGGCGCCT 1740
 CTCAGTCTCG CGGTCTGTAC CAATGCAATT TCCCTGCGAG AGCTCACCCC CAAACAGGTC 1800
 65 ACAATCAAGC CTGTGGCTAC TGCTTTCTCT CCAGTGTCTG CTGTGAAGAC GGCAGGATCC 1860
 CAAGTCATTG ATTTGAAGCT CGCTAACAA ACCACGGTGA AAGCCACGCT CATATCTGCT 1920
 GCTCTGTGCC AGAGTGCCAG CAGCGCCATC ATTAAGAGCTG CCAACGCCAT CCAGCAGCAA 1980
 ACTGTCTGAG TGCCGGCATC CAGCCTGGCC AATGCCAAAC TCGTGCCAAA GACTGTGCAC 2040
 70 CTGTGCCAAC TTAACCTTTT GCCTCAGGGT GCCCAGGCCA CCTCTGAAC CCGCCAAGTG 2100
 TTAACCAAAC CTCAGCAACA AATAAGCAG GCAATAATCA ATGCAGCAGC CTGCGAACCC 2160
 CCCAAAAGGG TGCTCGAGT CCAGGTGGTG TCGTCTTTCG AGAGTTCTGT GTGGGAAGCT 2220
 TTCAACAAGG TGTGAGGACG TGTCATTCAC GTCCCTGTTT ACATCCAAA CCTCAGTCTC 2280
 CCGGCCAATG CAGGGATCAC GTTACCGACG CGTGCGTACA AGTGCTTGA GGTGTGGGAC 2340
 75 TCCTTTGCAC TTGAAAAGAG TCTGACCCAG CACTACGACA GACGGAGCGT GCGCATCGAA 2400
 GTAACGTGCA ACCATTGTAC AAAGAACCCT GTTTTTTACA ACAAATGCAG CCTCTTTTCC 2460
 CATGCCGTGG GGCATAAGGA GAAAGGGGTG GTAATGCAAT GCTCCCACTT AATTTTAAAG 2520
 CCAGTCCAGC CAGATCAAT GATAGTTTCT CCGTCAAGCA ATACTTCCAC TTCAACTTCC 2580
 ACTCTTTCAG GCCCTGTGGG AGCTGGCACA CACACTGTCA CAAAAATTC GCTGTGCATA 2640
 ACTGGGACAG TCATATCGGC TCCTTCAAGC ACTCCCATCA CCCAGCCAT GCCCTAGAT 2700
 80 GAAGACCCCT CCAACTGTG TAGACATAGT CTAAAAATGT TGGAGTGTAA TGAAGTCTTC 2760
 CAGGACGAGA CATCACTGGC TACACATTTC CAGCAGGCTG CAGATACGAG TGGACAAAAG 2820

	ACTTGCCTA	TCTGCCAGAT	GCTGCTTCCT	AACCAGTGCA	GTTATGCATC	ACACCAGAGA	2880
	ATCCATCAGC	ACAAATCTCC	CTACACCTGC	CCTGAGTGTG	GGGCCATCTG	CAGGTCCGGT	2940
	CACCTCCAGA	CCCACGTAC	CAAGAAGTGT	CTGCACTACA	CGAGGAGAGT	TGGTTTTCGA	3000
	TGTGTGCATT	GCAATGTTGT	GTAATCTGAT	GTGGCTGCTC	TGAAGTCTCA	CATTCAAGGT	3060
5	TCTCACTGTG	AAGTCTCTA	CAAGTGTCTT	ATTTGTCCAA	TGGCGTTTAA	GTCTGCCCCA	3120
	AGCACACATT	CCCACGCTA	CACACAGCAT	CCTGGCATCA	AGATAGGAGA	ACCAAAATA	3180
	ATATATAAGT	GTTCATGTG	CGACACTGTG	TTCACCTGTC	AAACCTTGCT	GTATCGCCAC	3240
	TTTGACCAAC	CAATTGAAAA	CCAGAAGGTG	TCTGTTTCA	AGTGTCCAGA	CTGTCTCTT	3300
10	TTATATGCAC	AGAAGCAACT	TATGATGGAC	CATATCAAGT	CTATGCATGG	AACATTGAAA	3360
	AGTATTGAAG	GGCCTCCAAA	CTTGGGTATA	AACCTGCCTT	TGAGCATTAA	GCCTGCAACT	3420
	CAAAATTCAG	CAAAATCAGAA	CAAAGAGGAC	ACCAAAATCCA	TGAATGGGAA	AGAGAAATTG	3480
	GAAGAAAGAT	CTCCATCTCC	TGTGAAAAAA	TCAATGGAAA	CAAAGAAAGT	GGCCAGTCCT	3540
	GGGTGGACGT	GTTGGGAGTG	TGACTGCCTG	TTCAATGCAGA	GAGATGTGTA	CATATCCAC	3600
15	GTGAGGAAGG	AGCACGGGAA	GCAAAATGAAG	AAACACCCCT	GGCCGCACTG	TGACAAGTCT	3660
	TTGAGCTCGT	CCCACAGCCT	GTGCGGGCAC	AACCGGATCA	AGCACAAAGG	CATCAGGAAA	3720
	GTGTACGCTT	GCTCGCCTT	CCCAGACTCC	AGACGTACCT	TTACCAAAAG	TTTGTAGCTG	3780
	GAGAAGCAGC	TCCAGCTGAT	GCATGGCATC	AAGGACCCCT	ACCTGAAAGA	AATGACAGAT	3840
	GCCACCAATG	AGGAGGAAAG	AGAAATAAAA	GAAGACACTA	AGTCCCCAG	TCCCAAGCGG	3900
20	AAGTTGGAAG	AACCAGTTCT	GGAGTTCAAG	CCTCCCGGAG	GAGCAATCAC	TCAACCACTG	3960
	AAAAAGCTGA	AAATCAATGT	TTTAAAGGTT	CACAAGTGTG	CGGTGTGTGG	CTTCACCACC	4020
	AAAAATCTGC	TGCAATTTCA	CGAACACATC	CCTCAGCACA	AATCGGATGG	TTCTTCTTAC	4080
	CAGTGGCCGG	AGTGTGGCCT	CTGTACACAG	TCTCACGTCT	CTCTGTCCAG	GCACCTCTTC	4140
	ATCGTACACA	AGTTAAAGGA	ACCTCAGCCA	GTGTCCAAAG	AAATGGGGC	TGGGGAAGAT	4200
25	AACCAACAGG	AGAACAACCC	CAGCCACGAG	GATGAATCCC	CTGATGGCGC	CGTGTACAGC	4260
	AGAAAGTGCA	AAGTGTGCGC	AAAAACTTTT	GAACTGAAG	CTGCCTTAAA	TACTCACATG	4320
	CGGACACACG	GCATGGCCTT	CATCAAAATCC	AAAAGGATGA	GCTCAGCCGA	GAAATAGCCA	4380
	CAGATGCTCC	ATGAGGAAAA	TCCCTGTCCA	CATTGGAATA	AAAAAGACAT	TTTTGTTACA	4440
	AAGTTTGCAG	TATAATAGAG	TTAACAGTAC	TGTCTAGGCT	GTTGCAATAT	ATTCTCTTTC	4500
30	AATGTACCTT	CCTTCACCTC	GTCGTATATA	TCCTCGATAA	GTAATTAAC	AGTATTTGAG	4560
	TTTAAAGAGG	TTTGTATATA	TTTAAATGAA	TAACCTTTTA	TACTCTTTGT	TACATGTTTG	4620
	TATCAGTATT	TAGTGGAAAA	CCATTGTAGT	TGTTTGGGT	TAGAAATTTT	CTTTTGTAC	4680
	TGTTCTCTTA	AAACAGAGTT	CTTAGTAACA	GGGGCAGTTC	CTGAATTCAA	ATAAACCAAT	4740
	TTGTATGTTT	GGATTTTGAA	TGGGTTAACT	AATTACAGGC	TAAATAAATG	CCTTTTITAG	4800
35	TGTTTITTAAT	TTTTAGAAAT	CACATACATA	ATTGTAAGTA	ATTGTGGGTC	TCAAAAACAC	4860
	TAGGAATCTT	TAAGTGTCTT	AGCACTTCCT	CGATGTGCCT	GGCCTGAGGG	AGTGAGTTCA	4920
	CATTTGAGAC	AACCTGCACCT	CAGTGTGGAC	GTGCTTTTGT	CTTCAGGCCA	TGCCGAAGGG	4980
	TGTTTAAAGC	AGTCTTGCAAG	GTCGCTCCTT	TCCAGCCGCT	GGATAAAAAC	TGAAGCTAGG	5040
	AACTCAATAA	GGAATGCTGA	TTTCTCTCAGT	TCCATTTTGA	GGAATGGGGA	AGGCTATTCT	5100
40	AAAGAAAAAA	ATGGGATTTC	TTTTCTCGGC	AGATCTGCAA	GGCTGGCTTT	AAGAGCACA	5160
	GGAGGAAAGG	TAACGAAAGG	GCTGGACTAC	TATAAAAGTT	ACAAATACGT	AGTTAGACCA	5220
	ATAGATTTAT	ATAGTCAGGT	TTTTGTCAAT	TAATTTATTA	ACTAATCTAT	ACAGAAACAC	5280
	AGCTAAGAAT	ATCAAGATAT	TCTCTGGCTC	TTGACAGAAA	AAATACAGTT	GACTTAACCC	5340
	TTTGTGTTCT	AAAGAGTTGG	CGTTTCTGT	TCTGGTGTCT	ACTGCCAAAC	GTTATGGTAC	5400
45	TTAGAGTCGG	GATGCACAAC	TTCAACCACC	GACTTATCAA	TGCAGCCGCC	TGTGTATTGC	5460
	AAATGGCCGT	TACCTTAAAG	ACTGAGCCAC	CGGGGTTTAG	TTGAGCCAT	TCAAGAAAGT	5520
	TATTTAACGT	CGGTAGTTCT	GCTTTATTTA	AATGCAGCAG	AGGTACTCTT	CTGTCCCTTC	5580
	CGTTTATAGT	TCTCTGAGAG	AGTTCTATT	TTTGGTTTGT	TTTTGTGTTT	TCTTTTGCAT	5640
	TTTGTATCTT	GTAATTTATCC	CTGAACATGT	TTTGTACCTT	TTTTTTTTTT	TTTTTTTTTA	5700
50	GAAGAGGAAT	TCTTTTGTGT	ATATATAGAT	ACTTGCATGA	TATACGTAGT	TCAATGTTTC	5760
	GTCTCTCAAA	AGGTCTTGCT	GCTGTACAGT	GTTATGCAC	CCATCCATCA	TAACGTGATG	5820
	AAACACATTT	CATATGTAAA	TAAACGTGGG	ACATTTG			

SEQ ID NO: 255 PB18 Protein sequence:

55	Protein Accession #:	BAB13455
	MKTPDFDILL	AAFDIPDMVD PKAAIESGHD DHESHMKQNA HGEDDSHAPS SSDVGVSVIV 60
	KNVRNIDSSE	GGEKDGHNPT GNGLHNGFLT ASSLDYSYKD GAKSLKGDVP ASEVTLKDST 120
60	FSQFSPISSA	EEFDDEKIE VDDPPDKEDM RSSFRSNVLT GSAPQQDYDK LKALGGENSS 180
	KTGLSTSGNV	EKNKAVKRET EASSINLSVY EPFKVRKAED KLKESDVKVL ENRVLDGKLS 240
	SEKNDTSLPS	VAPSKTKSSS KLSSCIAAIA ALSAKKAASD SKEPVSANR ESSPLPKEVN 300
	DSPPRAADKSP	ESQNLIDGDK KPSLKQPDSP RSISSENSSK GSPSPAGST PAIPKVRKLT 360
	IKTSSGEIKR	TVTRVLPEDV LDSGKKPSEQ TASVMASVTS LLSPASAAV LSPFPAPLQ 420
65	SAVVTNAVSP	AELTPKQVTI KPVATAFLPV SAVKTAGSQV INKLANNNT VKATVISAA 480
	VQSASSAIK	AANAQQQTV VYPASSLANA KLVPKTVHLA NLNLLPQGAQ ATSELRQVLT 540
	KPQQQIKQAI	INAAASQPPK KVSrvQVVSS LQSSVVEAFN KVLSSVNPVP VYIPNLSP 600
	NAGITLPTRG	YKLECGDSF ALEKSLTQHY DRRSVRIEVT CNHCTKNLVE YNKCSLLSHA 660
	RGHKEKGVM	QCSSLILKPV PADQMIVSPS SNTSTSTSL QSPVGAGTHT VTKIQSGITG 720
70	TVISAPSTIP	ITPAMPLED PSLKCRHSLK CLECNVFDQ ETSLATHFQQ AADTSQKTC 780
	TICQMLLPNQ	CSYASHQRIH QHKSPTYCPE CGAICRSVHF QTHVTKNCLH YTRRVGFRV 840
	HCNVISDVA	ALKSHIQGSH CEVFKCPC PMAFKSAFST HSHAYTQHPG IKIGEPKIY 900
	KSCMCDTVFT	LQTLRYRHFQ QHIENQKVSF FKPCDSCLLY AQKQLMMDHI KSMHGTLSI 960
	EGPPLNGLN	PLSIKPAQON SANQNKEDTK SMNGKEKLEK KSPSPVKSM ETKKVASPGW 1020
75	TCWECDCLEF	QRDVYISHVR KEHGKQMKKH PCRQCDKSF SSHSLCRHNR IKHGIRKVV 1080
	ACSHCPDSRR	TFTKRLMLEK HVQLMHGKID PDLKEMTDAT NEETEIKED TKVPSPKRKL 1140
	EEPVLFRPP	RGAATQPLKK LKINVFKVHK CAVCGFTTEN LQFHEHIPQ HKSDGSSYQC 1200
	RECGLCYTSH	VSLSRHLFTV HKLKEPQVVS KQNGAGEDNQ QENKPSHEDE SPDGA VSDRK 1260
80	CKVCAKTFET	EAALNTHMRT HGMAFIKSKR MSSAEK

SEQ ID NO:256 PBM1 DNA sequence

Nucleic Acid Accession#: AF111847

Coding sequence: 58-1608 (underlined sequence corresponds to start and stop codon)

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GTGTTCCTTT GCATTGATTG CTCAGGGTCC CACCGGTAC TGGTGTTCAT CTTGAGTTT 240
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AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760

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SEQ ID NO:257 PBM1 Protein sequence:

PBM1 Protein sequence: CAB76901

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ASQATRKHGT DLWLDSCVVP PLSPPKKEED FFASHVSPEV SDTAWASAI EPSSLTSRPV 180
ETLENNEGQ EQGQPSVEGL NVPTKATLEV SSIKKKPNQ AKKGLGAKKG SLGAQKLANT 240
CFNEIEKQAO AADKMKEQED LAKVVSKEES IVSSLRLAYK DLEIQMKKDE KMNISGKKNV 300
DSDRLGMGFG NCRSVISHSV TSDMQTIEQE SPIMAKPRKK YNDDSDSYF TSSSYFDEP 360
VELRSSFSF WDDSSDSYWK KETSKDTETV LKTTGYSDRP TARRKPDYEP VENTDEAQKK 420
FGNVKAISSD MYFRQSQAD YETRARLERL SASSSISSAD LFEEPRKQPA GNYSLSSVLP 480
NAPDMAQFKQ GVRSVAGKLS VFANGVVTSI QDRYGS

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SEQ ID NO:258 PBM4 DNA sequence

Nucleic Acid Accession#: D30891

Coding sequence: 1-4032 (underlined sequence corresponds to start and stop codon)

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GGAAACTCCA GAAATATAGA CCGTAGTG TGTTACAGCAT ATGGTAAACC CAGCGAGAGT 240
ATCTACTCAG CCTGAGTGC TAATGACTAT TTCAGTGAAG GGATAAGAA TCAGTTTAAT 300
AAGAACTATA TTGTTATGTA AGAAAAGCA ATAGATGGAC ATATAAATT AGGAATGCCT 360
CTCAAGTGCC TGCTTAGTGA TTCTCATTTT AAAATTACAT TTGGTCAAG AAAGAGTAGC 420

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5 AAAGAAGATG GACACATATT ACGCCAATGT GAAAAATCCAA ACATGGAATG CATTCTTTTT 480
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SEQ ID NO:259 PBM4 Protein sequence:
 PBM4 Protein sequence: BAB67788

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SEQ ID NO:260 PBQ1 DNA sequence

Nucleic Acid Accession#: NM_015642

Coding sequence: 489-2489 (underlined sequence corresponds to start and stop codon)

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AATTTACCTG	AAGAGTGACA	CCATTGATTT	TGAAACTACT	GAAGAAACCC	AAGACAGCTG	300
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CGGGCCTTCC	CTGCCGTAAC	TTTGAAGCTG	TTTGTCTCC	AGACCCAGCC	CTCATCCACT	420
CAACACATTC	ACTGACAAAC	TCTCAGCTC	ACACCGGGTC	ATCTGATTGT	GACATCAGTT	480
GCAAGGGGAT	ACCGAGCGCG	ATTACAGCA	TCAACCTTCA	CAACTTCAGC	AATTCGGTGC	540
TGCAGACCTC	CAACGAGCAG	CGCAACCGTG	GCCACTTCTG	TGACGTAAAC	GTGCGCATCC	600
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GCATCGTGTC	ACAGAACGTG	GGCGATGTGT	TCCCGGGGAT	CCAGGACTCG	GGCCAGGACA	900
CGCCCGGGGG	CACCTCCGAG	TCAGGCACGT	CAGGCCAGAG	CAGCGACACG	GAGTCGGGCT	960
ACCTGCAGAG	CCACCCACAG	CACAGCGTGG	ACAGGATCTA	CTCGGCACCTC	TACGCGTGCT	1020
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AGACTCGCGT	CGGCCTGCC	CGCGACCAAC	ACATGGGAAG	CCCCAGCTGG	ATCACACGCA	1140
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GCCGCAAGCA	AGCCCGGCT	GTGCGCATCC	AGACCTAGT	GGGCAACATC	CACATCAAGC	1260
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CAAGTACCAA	GCTTACTTTA	CGCCAGACAG	AAACCTTCAC	CAGCAACCTG	AGGATGCCTC	1740
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CCCTGGCAGG	CCAGCAGACC	CAGTTTGTGA	CAGTGTCCCA	GCCCGGTCTG	TCGACCTTTA	1920
CTGCACAGCT	GCCAGCGCCA	CAGCCCTTGG	CCTCATCCCG	AGGCCACAGC	ACAGCCAGTG	1980
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AGAACTACGT	CAAGCACATG	TTCTGTACCA	CAGGTGAGAA	GCCCCACCAA	TGCAGCATCT	2100
GTGGCGCTC	CTTCTCCTTA	AAGGATTACC	TTATCAAGCA	CATGGTGACA	CACACAGGAG	2160

5 TGAGGGCATA CCAGTGTAGT ATCTGCAACA AGCGCTTCAC CCAGAAGAGC TCCCTCAACG 2220
 TGCACATGCG CCTCCACCGG GGAGAGAAGT CCTACGAGTG CTACATCTGC AAAAAGAAGT 2280
 TCTCTCACA GACCTCTCTG GAGCGACACG TGGCCCTGCA CAGTGCACGC AATGGGACCC 2340
 CCCTGTCAGG CACACCCCA GGTGCCCGCG CTGCCCGCC AGGCGTGGTG GCCTGCACGG 2400
 10 AGGGGACCAC TTACGCTGCG TCCGCTCGCC CAGCAAAGTT TGACCAAATC GAGCAGTTCA 2460
 ACGACCACAT GAGGATGCAT GTGCTGACG GATAAGTAGT ATCTTTCTCT CTTCCTTATG 2520
 AACAAAAACA AACAAACA AAAAAACA AACAAAAA GCTATGGCAC TAGAATTTAA 2580
 GAAATGTTTT GGTTCATTTT TTACTTTCTG TTTTGTGTTT TGTTCGCTTT CATTTGTGAC 2640
 TACATGAAGA ACTGTTTTTT GCCTGCTGGT ACATTACATT TCCGAGGCT TGGGTGAATA 2700
 15 ATAGTTTTCC CAGTCTCCCT CGGATGGTGG CCTTAAGGCC TGGTAGTGCT TCAAGAGGTC 2760
 CACTGGTTGG ATCTCTAGCT ACTGGCTCTT AAATACAACC CTTCCTTACA AAAAAAAAAA 2820
 AAAAAAAAAA

15 SEQ ID NO:261 PBQ1 Protein sequence:

PBQ1 Protein sequence: NP_056457

120 MTERIHSINL HNFNSNVLET LNEQRNRGHF CDVTVRIHGS MLRAHRCVLA AGSPFFQDKL 60
 LLGYSDIEP SVVSVQSVQK LIDFMYSGVL RVSQSEALQI LTAASILQIK TVIDECTRIV 120
 20 SQNVGDVFPQ IQDSGQDTPR GTPESGTSQ SSDTESGYLQ SHPQHSVDRI YSALYACSMQ 180
 NGSERSFYFS GAVVSHIETA LGLPRDHME DPSWITRIHE RSQQMERYLS TTPETTHCRK 240
 QPRPVRIQTL VGNIIHKQEM EDDYDYGQO RVQILERNES EECTEDTDQA EGTESEPKGE 300
 SFDGVSSSI GTEPDSVEQO FGPGAARDSQ AEPTQPEQAA EAPAEQGPOT NQLETGASSP 360
 25 ERSNEVEMDS TVITVNSSD KSVLQQPSVN TSIGQPLPST QLYLRQTETL TSNLRMPLTL 420
 TSNTQVIGTA GNTYLPALFT TQPAAGSGPKP FLFSLPQLA GQQTQFVTVS QPGLSTFIAQ 480
 LPAPQPLASS AGHSTASGQG EKKPYECLC NKTFTAKQNY VKHMFVHTGE KPHQCSICWR 540
 SFLSKDYLIK HMTVHTGVRA YQCSICNKRK TQKSSLVNVM RLHRGEKSYE CYICKKKFSH 600
 30 KTLERHVAL HSASNGTPPA GTPPGARAGP PGVVACTEGT TYVCSVCPAK FDQIEQFNDH 660
 MRMHVSDG

SEQ ID NO: 262 PBQ6 DNA sequence

Nucleic Acid Accession#: AF654187

Coding sequence: 1-912 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51
 | | | | | |
 40 ATGGTGAAG AGGAAACAGG CATATCTTAC ATGGTGGCAG ACAAGGACA CCCTTCTACA 60
 AACTCTACCA CTTCGCGCC GTCTGTTTCA CCATATAAAA ACGACCTATG CGAACTGCGT 120
 CGGAAACTC CCTCAGCATG TAAAACGAAG ATCAGGAGCA GATTGAAGA ATTACAAAGT 180
 GAATGGTGC CAGTCAGCAT GTCAGAGACA GACCACATAG CCTCTACTTC CTCTGATAAA 240
 AATGTTGGGA AACACCTGA ATTAAAGGAA GACTCATGCA ACTTGTGTTT TGGCAATGAA 300
 AGCAGCAAT TAGAAAACTA GTCCAACTA TTGTCATTAA AACTGTATATG 360
 CAACCTAATG AGCATAATAA TCGAATTGAA GCCCAGGAAA ATTATATTCC AGATCATGGT 420
 45 GGAGGTGAGG ATCTCTGTGC CAAAACAGAC ACAGGCTCAG AAAATTCTGA ACAAAATAGCT 480
 AATTTCCTCA GTGGAATTTT TGCTAAACAT ATTTCAAAAA CAAATGAAC AGAACAGAAA 540
 GTAACACAA TATTGGTGA ATTAAAGTCA TCTACATTTC CAGAATCAGC TAATGAAAAG 600
 ACTTATTCAG AAAGCCCTTA TGATACAGAC TGCACCAAGA AATTATTTTC AAAAATAAAG 660
 AGCGTTTCAG CATCAGAGGA TTTGTTGGAA GAAATAGAAT CTGAGCTCTT ATCTACGGAG 720
 50 TTTGCAGAAC ATCGAGTACC AAATGGAATG AATAAGGGAG AACATGCATT AGTTCTGTTT 780
 GAAAGTGTG TCGAAGATAA ATATTTCAG CAGGAACATA TCATAAAAAA GGCCAGACTT 840
 GGTCTCTGTT ATTTGCCATC AAGAACCTCA ATTGACACGT TAATTCCGTT TATCCCAAAT 900
 TTATATAGAT AA

SEQ ID NO:263 PBQ6 Protein sequence:

Protein Accession #: NP_060170

60 MEPKEATGKE NMVTKKKKLA FLRSRLYMLE RRKTDTVVES SVSGDHSGLT RRSQSDRTEY 60
 NQKLQEKMTQ QGECVSAETL TPREEHHMKR MMAKREKIK ELIQTEKDYL NDLELCVREV 120
 65 VQPLRNKKTD RLDVDSLFSN IESVHQISAK LLSLLEAATT DVEPAMQVIG EVFLQIKOPL 180
 EDIYKYCYH HDEAHSILES YEKEELKEH LSHCIQSLK

SEQ ID NO:264 PBQ7 DNA sequence

Nucleic Acid Accession#: NM_014323

Coding sequence: 662-2725 (underlined sequence corresponds to start and stop codon)

70 1 11 21 31 41 51
 | | | | | |
 GGGCCTACTC TGCCGCCGCC GCCGCCGCC CGCTCCAGCC GCGGCCGCC CCGCCACCGC 60
 CCTCAGGCT CCGGAGCCCG GCCCGGCCA CCGCCCCCGT GCGCGCCCG CCGCCGCCGC 120
 CTTCGCTTC GCCTTTTGT TTCTCCGCTC CGGCGCCCG CCGCCGCCGC GCCTTTTGA 180
 75 GGGGACGCG CCGCGCCCG CAGCGGCCCG GGGAAAAGCC GCGCGCGCG CCGCGCGCTG 240
 CGCGCGGAC CCTCTCTT CTCTCCCGCG TCGCGGTGCC CTCTTGGCT GCGCGCGCG 300
 GCCGCTTGC GGGCGGAGG GGAGGTGCA GCGCGCTTG CAGGAGGGC GCACCTCTTC 360
 GCTCGCGAC CCGCCCGGA GGTAGACCG GAAGGGGAG CCGCGCGCG GAGAGGAGAG 420
 AGTGGCGCG AGTCCAGCA GCGCGGGGT TGGCTATGTG GGGGGTGGT CACCCGCGAG 480
 80 TCTAGACAG CTGATCCGG CTGGGGCGT GTACACTCG CGCACCTCG AGACTACAGA 540
 GCCTCGGGC GGCACGTGT GGGAGTGTG ACACGTCTG TCGCCCCCG TTCTCGCTGC 600

5	TGAGGGGAAG	GGAGGGGGCG	GGCAGGTGCA	GCGGCCGGGC	TAGTGGGAGG	GGGCGGCGGC	660
	CATGGAGCCG	GTGAAGACG	CTTCGTGCGG	CCGCTCTGGC	TGCTACACAT	ACCAGGTGAG	720
	CAGACACAGC	ACGGAGATGC	TGCACAACTT	GAACCAGCAG	CGCAAAAACG	GCGGGCGCTT	780
	CTGCGACGTG	CTCTTGCGGG	TAGGCGACGA	GAGCTTCCCA	GCGCACCGCG	CCGTGCTGGC	840
	CGCTGCAGC	GAGTACTTTG	AGTCGGTGTT	CAGCGCCACG	TTGGGCGACG	GCGGAGCTGC	900
	GGACGGGGGT	CCGGCTGATG	TAGGGGGGCG	GACGGCAGCA	CCAGGCGGCG	GGGCGGGGGG	960
	CAGCCGGGAG	CTGGAGATGC	ACACTATCAG	CTCCAAGGTA	TTTGGGGACA	TTCTGGACTT	1020
	CGCCTACACT	TCCCGCATCG	TGGTGGGCTT	GGAGAGCTTT	CCCGAACTCA	TGACGGGCCG	1080
10	CAAGTTCCGT	CTGATGAGGT	CGGTTATCGA	GATCTGCCAG	GAAGTCATCA	AACAGTCCAA	1140
	CGTACAGATC	CTGGTACCCC	CTGCGCCGCG	CGATATAATG	CTCTTTCCGC	CCCTGGGAC	1200
	CTCGGACTTG	GGCTTCCCTT	TGGACATGAC	CAACGGGGCA	GCCTTGGCAG	CCAACAGCAA	1260
	TGGCATCGCC	GGCAGCATGC	AGCCAGAGGA	GGAGGCAGCT	CGGGCGGCTG	GTGACGCCAT	1320
	TGCAGGCCAA	GCCTCTTTTG	CTGTGTTACC	TGGGGTGGAC	CGCTTGCCCA	TGGTGGCTGG	1380
15	ACCCCTATCC	CCCAACTCTG	TGACTTCCCC	ATTCCCCAGT	GTGGCATCCA	GTGCCCCCTC	1440
	CCTGACTGAT	AAGCGAGGCC	GGGGCCGCCC	AAGGAAGGCC	AACCTGCTGG	ACTCAATGTT	1500
	TGGGTCCCA	GGGGCCCTGA	GGGAGGACGG	CATCCTTCCA	TGCGGTCTAT	GTGGTAAGTT	1560
	GTTCACATGAT	GCCAAACCGC	TCCGGCAGCA	CGAGGCCACG	CACGGTGTC	CCAGCCTCCA	1620
	GCTGGGCTAC	ATGACCTTTC	CTCCTCCGAG	GCTGGGTGAG	AATGGGCTAC	CCATCTCTGA	1680
20	AGACCCCGAC	GGCCCCGAA	AGAGGAGCCG	GACCCAGGAG	CAGGTGGCTT	GTGAGATCTG	1740
	CGGCAAGATC	TTCCGTGATG	TGTATCATCT	TAACCGGCAC	AAGCTGTCCC	ACTCTGGGGA	1800
	GAAGCCCTTG	TGCTGCCCTG	TGTGTGGGTT	GCGGTTCAAG	AGAAAAGACC	GCAATGCTTA	1860
	CCATGTGCGG	TCCCATGATG	GCTCCGTGGG	CAAGCCTTAC	ATCTGCCAGA	GCTGTGGGAA	1920
	AGGCTTCTCC	AGGCTTGATC	ACTTGAACGG	ACATATCAAG	CAGGTGCACA	CTTCTGAGCG	1980
25	GCCTCACAA	TGTCAGACCT	GCAATGCTTC	TTTTCGCCAC	CGAGACCGTC	TGCGCTCCCA	2040
	CTTGGCTGTT	CATGAAGACA	AGGTGCCCTG	CCAGGTGTGT	GGGAAGTACT	TGCGGGCAGC	2100
	ATACATGGCA	GACCACTCTG	AGAAGCACAG	CGAGGGGCCC	AGCAACTTCT	GCAATATCTG	2160
	TAACCGAGGT	TTCTCCTCTG	CCTCCTACTT	AAAGGTCCAT	GTTAAAACCC	ACCACGGTGT	2220
	TCCCTTCCCC	CAGGTCTCCA	GGCACCAGGA	GCCCATCTCT	AATGGGGGAG	CAGCGTCCA	2280
30	CTGCGCCAGG	AGCTATGGGA	ACAAAGAAGG	CCAGAAATGC	TCACATCAGG	ATCCGATTGA	2340
	GAGCTCTGAC	TCTATGTTGG	ACCTCTCAGA	TGCCAGCGAC	CTGAAGACGC	CAGAGAAGCA	2400
	GAGTGGCAAT	GGCTCTTTCT	CCTGCACAT	GGCAGTCCCC	AAAAACAAAA	TGGAGTCTGA	2460
	TGGGGAGAAG	AAGTACCAT	GCCCTGAATG	TGGGAGCTTC	TTCCGCTCTA	AGTCTACTTT	2520
	GAACAAACAC	ATCCAGAAAG	TGCAATGTCCG	GGCTCTCGGG	GGCCCCCTGG	GGGACCTGGG	2580
35	CCCTGCCCTT	GGCTACCTTT	TCTCTCCTCA	GCAGAACATG	TCTCTCTCG	AGTCTTTTGG	2640
	GTTTCAGATT	GTTCAGTCCG	CATTTCGGTC	ATCTTTAGTA	GATCCTGAGG	TTGACCAGCA	2700
	GCCCATGGGG	CCTGAAGGGA	AATGAGGCAG	CTGCTGTGTC	CCCACGGAAA	CAACCATCTG	2760
	GGGACTGCTG	GGAAATGCTG	TGAATGCGGA	GGGAAGTGAT	GTTTGGGTTT	TGTAGCTGAG	2820
	AGATTTTAT	TCATTTTAA	CTGCCCCCA	ACCCCACTCC	AACCTCTTCT	CCACCACCCA	2880
40	TTCTCCCAAT	GGTCTTTAGA	AATAGATTTT	CATCTGATAT	TCTGCAGAAA	TATCAATGAG	2940
	ACTTGGTATG	GGACAGGGGG	AGAAAACACT	ACATAGGCTT	CCAAGGCCAA	ACCAGTCCCA	3000
	GTTTCTTTAA	TGGGAAGTCC	CTGGAATTCC	TGGTGCTCAA	TTCTTAGTGA	CCCCAATCCT	3060
	ATACCCAAAT	CTATGATATT	CTGGGACCTC	AGTGATTTTG	GTCCCCCTCC	ACTTCTCTAG	3120
	TTCTGTCATC	TCCCTTCCCA	TATCCTTCAA	AAGAACCACA	CTAGGGTCTC	CACCTACTTA	3180
45	TACAATGCGG	ATGCCCAACT	GTTTAAAGG	AAGCCAGAAG	CATCCCATGG	ACCATGGGGT	3240
	GAGTGTCTTC	CAAGAGCCCC	CTGAGCTCAG	CCCTCTGCCT	GGAGGGCTCC	AGACCTTTCT	3300
	GAGCCCTGCT	TGGAGGCGAG	CATTTTCACT	GCTAGGACAA	GCTCAGCTGT	TGAGGACACC	3360
	CCCAACCCAA	ATTTCAGTTC	TTACGTGATT	TTAACCATT	AACATGCTGT	TGGGTTTAA	3420
	TTCTCTAATT	ATTATATTAT	TGTGTATTAT	TTTTTAGGAC	CAGTTGTAGT	GAATTGCTAC	3480
50	TGAAAGTCCG	CCAGGTGAT	ACAGAGCTCT	TTGTAAACCG	CAGTCACACA	TTAGGGTTAG	3540
	TATTAACACT	TGTTTAGATG	TACCATAATT	AACCTGGGTA	GTTGATTTGT	TGAAGTCTAT	3600
	GGAGAGAAAT	GTTTATGCA	AAATTTTAAA	AAATGCCAGT	CTGGTCAGGG	AAGTAGGGGG	3660
	TTTCAATGCT	GTTGGGAACC	AGGAAGGTGG	CACAGCCGCG	AGGTAGGGAC	ATTGTGTACC	3720
	TCAGTTGTGT	CACATGTGAG	CAAGCCGAGG	TTGACCTTGT	GATGTGAATT	GATCTGATCA	3780
55	GACTGTATTA	AAATGTTAG	TACATTACTC	TA			

SEQ ID NO:265 PBY7 Protein sequence:

Protein Accession #: NP_114439

60	MERVNDASCG	PSGCIYTVQS	RHSTEMLHNL	NQQRKNNGRF	CDVLLRVGDE	SFPAHRAVLA	60
	ACSEYFESVF	SAQLDGGGAA	DGGPADVGG	TAAPGGGAGG	SRELEMHTIS	SKVFGDILDF	120
	AYTSRIVVRL	ESFPFLMTAA	KFLLMRSVIE	ICQEVIKQSN	VQILVPPARA	DIMLFRPQT	180
	SDLGFLPDMT	NGAALAANSN	GIAGSMQPEE	EAARAAGAAI	AGQASLPVLP	GVDRLPMVAG	240
65	PLSPQLLTSP	FPSVASSAPP	LTGKRGRGRP	RKANLLDSMF	GSPGGLREAG	ILPCGLCGKV	300
	FTDANRLRQH	EAHQGVTSIQ	LGIDLPFPR	LGENGLPISE	DPDGPKRKSR	TRKQVACEIC	360
	GKIFRDVYHL	NRHKLSHSGE	KPYSCPVCL	RFKRKDRMSY	HVRSHDGSVG	KPYICQSCGK	420
	GFSRPDHLNG	HIKQVHTSER	PHKCQTCNAS	FATRDRLRSH	LACHEDKVPC	QVCGKYLR	480
	YMADHLKKHS	EGPSNFCIS	NREGQKCSHQ	DPIESSDSYG	DLSDASDLKT	PEKQSANGSF	540
70	SCDMAVPKNK	MESDGEKKYP	CPECGSFFRS	KSYLNKHQK	VHVRALGGPL	GDLGPALGSP	600
	FSPQNMNSLL	ESFGQIVQS	AFASSLVDP	VDQPMGPEG	K		

SEQ ID NO:266 PBY9 DNA sequence

Nucleic Acid Accession#: NM_012429

Coding sequence: 174-1385 (underlined sequence corresponds to start and stop codon)

75	1	11	21	31	41	51	
	CCCTACTCCG	CCTCTCGGGA	TCCTTTAAGA	GCGGGGGCTT	GGCTGCCAGC	TCCGCGGCCC	60
80	GGGCAAAAGG	CTGGGACTTT	ACTCCGGGTG	GCGGCGAGGA	CGAGTCTGTG	CTCCATCAGC	120

5 TGCCGCACCC GCCGCCTCCC GCCCCCAAC CCCATCCCG CGGTTGAGCC ACGATGAGCG 180
 GCAGAGTCGG CGATCTGAGC CCCAGGCAGA AGGAGGCATT GGCCAAAGTTT CGGGAGAATG 240
 TCCAGGATGT GCTGCCGGCC CTGCCGAATC CAGATGACTA TTTTCTCCCTG CGTTGGCTCC 300
 GAGCCAGAG CTTCGACCTG CAGAAGTCGG AGGCCATGCT CCGGAAGCAT GTGGAGTTCC 360
 GAAGCAAAA GGACATGAC AACATCATTA GCTGGCAGCC TCCAGAGGTG ATCCAACAGT 420
 ATCTGTCCGG GGGTATGTGT GGCTATGACC TGGATGGCTG CCCAGTCTGG TACGACATAA 480
 TTGGACCTCT GGATGCCAAG GGTCTGCTGT TCTCAGCCTC CAACAGGAC CTGCTGAGGA 540
 CCAAGATGCG GGAGTGTGAG CTGCTTCTGC AAGAGTGTGC CCACAGACC ACAAGTTGG 600
 10 GGAGGAAGT GGAGACCATC ACCATAATTT ATGACTGCGA GGGGCTTGGC CTCAAGCATC 660
 TCTGGGAAGC TGCTGTGGAG GCCTATGGAG AGTTCTCTCT CATGTTTGAG GAAAAATTATC 720
 CCGAAACACT GAAGCGTCTT TTTGTGTGTA AAGCCCCAA ACTGTTTCTT GTGGCTTATA 780
 ACCTCATCAA ACCCTTCCCTG AGTGAGGACA CTCGTAAGAA GATCATGGTC CTGGGAGCAA 840
 ATTGGAAGGA GGTTTTACTG AAACATATCA GCCCTGACCA GGTGCCCTGTG GAGTATGGGG 900
 15 GCACCAAGT GTGCCCTGAA GGAAACCCCA AGTGCAAAAT CAAGATCAAC TACGGGGGTG 960
 ACATCCCCAG GAAGTATTAT GTGCGAGACC AGGTGAAACA CAGATATGAA CACAGCGTGC 1020
 AGATTTCCTG TGCTCTCTCC CACCAAGTGG AGTATGAGAT CCTCTTCCCT GGCTGTGTTC 1080
 TCAGGTGGCA GTTATATGTA GATGGAGCGG ATGTTGGTTT TGGGATTTCCT CTGAAGACCA 1140
 AGATGGGAGA GAGGCAGCGG GCAGGGGAGA TGACAGAGGT GCTGCCCAAC CAGAGGTACA 1200
 20 ACTCCACCTT GTGCCCTGAA GATGGGACCC TCACCTGCGA TGATCTTGGC ATCTATGTCC 1260
 TGCGGTTTGA CAACACCTAC AGCTTCAATC ATGCCAAGAA GGTCAATTTCT ACTGTGGAGG 1320
 TCTGTCTTGG AGCAAAAGCC TCAGAAGAGA AGATGAAACA GCTGGGGGCA GGCACCCCGA 1380
 AATAACACCT TCTCTTATAG CAGGCTTGGC CCCCTCAGTG TCTCCTGTCT AATTCTTACC 1440
 CCTTGTAGCA GTCATTTTCG CACAACCTTG AAGCCCAAG AAATCTGGCT GGAGGACAGA 1500
 25 CCTCAGGAGC TTTCAATTTCA GTTAGGCAGA GGAAGAGCGA CTGCAGTGGG TCTCCGTGTC 1560
 TATCAAAATC CTAAAGAGTG CCCAGGAGCT GGCTGGCCAT CGTGATAGGA TCTGCTGTCT 1620
 CTGTAACTTG TGCCAACTTC ACCTGTCCAG GGACAGCGAA GCTGGGGGTG GCGGGGGGCA 1680
 TGTACCACAG GGTGGCAGCA GGGAAAAAAA TTAGAAAAGG GTGAAAGATT GGGACTTAAC 1740
 ACTTCAGGGA AGTCAGCTGC CGGGGAGAAA CTGTCTCTTA AATGAACACA TAAGTTTAGA 1800
 30 TCGCAATGAG GAGTAGCAGG GTAGCTGGTT GCTAGAGTTA CGGTGGGGAT CAGAACTCT 1860
 TCCAAACATT TTAGCACTGA GGCTGGGGTA GCTTTTGGCT TTTCCAGGT CTCAAGAGGT 1920
 GGCTGAGTG AGCACACATC TTCCCACTCG GTAGACAGGC TGGCTCTCC CTCACTTTGA 1980
 GACTTTGGCA ACTCTGGGC CACACGGCCT GCCTCTTTGA TTAATAATGA TTGTACGTGA 2040
 CTCAGAGCTT CTTGGGACTT CGGGTACCCA CCCGCTGTTT TCCATGCAAA CAAAGCGCCA 2100
 35 GGGAAATGAC CACACGGGAT CGCAGCTGCA GGGAGGGCCA GGGAGGTGG GGGTGGGAGT 2160
 GAATGCTAAA AGCAGATCGT CCAGTGCCCT TTTCAAGTGT ACCGGCTCTT CACCAAGCAG 2220
 TCCCTCATGT GAGCAACCCC GAGACAAAAA TGCTAAGTGG GATCAAGAGA GCAGCACTCG 2280
 GAGAGGGTGT TTGCCAGTCT GAGTGTCCCG CGGTGCCCGC CAACCCGCTT CCTGACTGAC 2340
 CTGAGCAAGG TCTTACTAAG CAGTCCCATC TCTGTGGGAG GCATGCAACG CGTGACAGGA 2400
 40 GTTCAGGTGC CGGTGCGCGT AGCCAGGCTT GGAGGCCCCC CAGGCAGGAG GCCGCCCAAA 2460
 GGCAGGGGCG CGCTCTCGCA GACTAGGGGC TGGGGGGGCG CACAGACGGC CTCGAAACCA 2520
 CAGCCCTTAC CCAACCTCCA CGAGCCCGCG CAACGAACCA CAGGTGCTGG GCTTTAGAGA 2580
 ACATGGGAAG GCGGCCCCAG ACCTGGCCGG AACGCCCTTC CCTCAGAGCC AGGCCCCGGC 2640
 CCCGCTGCGG AAGCTCATCT TGCGAAGCTG AGGGAGCTCA GGGCAAGGCC CAGGCTAGCG 2700
 45 CGGACCGGAA GGGGCCGAGG CTGCACGGGC CTCTGCAGGA ACGCTCAGGA CATCCCGGCC 2760
 TGGGTTTACA ACCTGTTAG GAAAAATTA CAATGAATAA AGCAACGTTT AGTCCGCA

SEQ ID NO:267 PBX9 Protein sequence:

Protein Accession #: NP_036561

50 MSGRVGDLSR RQKEALAKFR ENVQDVLPAI PNPDDYFLLR WLRARSFDLQ KSEAMLRKHV 60
 EFRKQKDDN IISWQPPEVI QQYLSGGMCG YDLDCGPVWY DIHPLDAKG LLFSASKQDL 120
 LRTKMRECE LLQECAHQIT KLGRKVETIT IYDCEGLGL KHLWKPAVEA YGEFLCMFEE 180
 55 NYPETLKRLE VVKAPKLPV AYNLIKPLS EDTRKKIMVL GANWKEVLLK HISPDQVPVE 240
 YGGTMTDPDG NPKCKSKINY GGDIPRKYV RDQVKQYEH SVQISRGSSH QVEYELFPF 300
 CVLRWQFMSD GADVCGIFL KTKMGERQRA GEMTEVLPNQ RYNHSLVPED GTLTCSDPGI 360
 YVLRFDNTYS FIAKKVNFVT VEVLLPKAS EEMKQLGAG TPK

SEQ ID NO:268 PBH8 DNA sequence

Nucleic Acid Accession#: XM_009756

Coding sequence: 301-1440 (underlined sequence corresponds to start and stop codon)

65 1 11 21 31 41 51
 | | | | |
 GTGGGGACAG CCGAGCCGCG CCGGGCCCTT GGACGGCGTC GCCAAGGAGC TGGGATCGCA 60
 CTCTCTGCGAG ACTTTGGATG GATTGTGTTT TGTGGTAGCA TCTGATGGCA AAATCATGTA 120
 TATATCCGAG ACCGCTTCTG TCCATTTAGG CTATCCCGAG GTGAGCTCA CCGGCAACAG 180
 70 TATTATGAA TACATCCATC CTCTGACCA CGATGAGATG ACCGCTGTCC TCACGGGCCA 240
 CCAGCCGCTG CACCACCACC TGCTCCAAGG TATGAGATAG AGAGGTGCTT CTCTCTTCCA 300
 ATGAAATGTG TCTTGGCGAA AAGGAACGCG GGCCTGACCT GCAGCGGATA CAAGGTCATC 360
 CACTGCAAGT GCTACTTGA GATCAGGCAG TATATGCTGG ACATGTCCCT GTACGACTCC 420
 TGCTACCAGA TTGTGGGGCT GGTGGCCGTG GGCCAGTCCG TGCCACCCAG TGCCATCACC 480
 GAGATCAAGC TGTACAGTAA CATGTTTATG TTCAGGGCCA GCCTTGACCT GAAGCTGATA 540
 75 TTCTTGATT CCAGGGTGAC CGAGGTGACG GGTACGAGC GCAGGACCT GATCGAGAAG 600
 ACCCTATACC ATCAGCTGCA CGGCTGCGAC GTGTCCACC TCCGCTACCG ACACCACTC 660
 CTGTTGGTGA AGGGCCAGGT CACCACCAAG TACTACCGGC TCGTGTCCA GCGGGGCGGC 720
 TGGGTGTGGG TGCAGAGCTA CGCCACCGTG GTGCACAACA GCCGCTCTGC CCGGCCCTCC 780
 80 TGCACTGTA GTGTCAATTA TGTACTCAG GAGATTGAAT ACAAGGAAC TCAGCTGTCC 840
 CTGAGCAGG TGTCCACTGC CAAGTCCAG GACTCTTGA GGACCGCCTT GTCTACCTCA 900

5 CAAGAACTA GGAAATTAGT GAAACCCAAA AATACCAAGA TGAAGACAAA GCTGAGAACA 960
 AACCCCTTACC CCCCACAGCA ATACAGCTCG TTCCAAATGG ACAAACCTGGA ATGCGGCCAG 1020
 CTCGGAAACT GGAGAGCCAG TCCCTCTGCA AGCGCTGCTG CTCTCCAGA ACTGCAGCCC 1080
 CACTCAGAAA GCAGTGACCT TCTGTACAGC CCATCCTACA GCCTGCCCTT CTCTACCAT 1140
 TACGGCACT TCCCTCTGGA CTCTCAGCTC TTCAGCAGCA AAAAGCCAAT GTTGCCGGCC 1200
 AAGTTCGGGC AGCCCAAGG ATCCCTTGT GAGGTGGCAC GCTTTTCTCT GAGCACACTG 1260
 CCAGCCAGCG GTGAATGCCA GTGGCATTAT GCCAACCCCC TAGTGCCTAG CAGCTCCTCT 1320
 CCAGCTAAAA ATCTCCAGA GCCACCGCG AACACTGCTA GGCACAGCT GGTGCCAAGC 1380
 TACGAAGGCA AGCAGATGTC CTCTGCGGAG ATACCGCCAG CTCGCCAGGA CGCAGACTGA 1440
 CTCTGTGTTG CTCTGTGGAC CAAC

SEQ ID NO:269 PBH8 Protein sequence:
 Protein Accession #: NP_005060

15 MKEKSKNAAK TRREKENGEF YELAKLLPLP SAITSQLDKA SIURLTTSYL KMRAVFPEGL 60
 GDAWGQPSRA GPLDGVAKEL GSHLLQTLTG FVFVVASDGK IMYISETASV HLGSLQVELT 120
 GNSIYEYIHP SDHDEMTAVL TAHQPLHHHL LQYEIERSF FLRMKCVLAK RNAGLTCSGY 180
 KVIHCSGYLK IRQYMLDMSL YDSCYQIVGL VAVGQSLPPS ATEIKLYSN MFMFRASLDL 240
 20 KLIFLDSRVT EVTYEPQDL IEKTLYHHVH GCDVHFLRYA HILLLVKGQV TTKYRLLSK 300
 RGGVWVWQSY ATVHVNSRSS RPHCVSVNY VLTIEYKEL QLSLEQVSTA KSQDSWRTAL 360
 STSQETRLV KPKNTKMKTK LRTNPYPQO YSSFQMDKLE CGQLGNWRAS PPASAAAPPE 420
 LQPHSESSDL LYTPSYSLPF SYHYGHFPLD SHVFSSKKPM LPAKFGPQOG SPCEVARFFL 480
 25 STLPASGECQ WHYANPLVPS SSSPAKNPPE PPANTARHSL VPSYEAPAA VRRFGEDTAP 540
 PSFPCGHR EEPALGPAKA ARQAARDGAR LALARAPEC CAPPTPEAPG APAQLPFVLL 600
 NYHRVLARRG PLGGAAPAS GLACAPGGE AATGALRLRH PPAATSPPG APLPHYLGA 660
 VIITNGR

30 SEQ ID NO:270 PB19 DNA sequence:
 Nucleic Acid Accession#: AA760894

GGCACGAGGA GAAGATGTGG CTGTCTCATG CTGACTTCT GCCATGGTTG TGAGGCCTCC 60
 CCAGCCATGT GGAACGTGTT TCAGGTGCTG GTTCCATGGC TCTTCTGAG CCGAAATAA 120
 35 GGAAACTCCA GTAGTCTGT CCACTGGAAC TCGTTCCTAT CTACCCTCCA CTCTATCCAG 180
 GGTGATGGAT CTCTGCACTA AGTGGAGAG TTCTTCATGG CCCCCAAGGT TATATCCATC 240
 TAGAACTTCA GCACGTAAAT TCATCTGGAA ATAGTGCTT TGTGGATATA AGTTAGGTAA 300
 AACTGAAGAT GAGATCATA TGGATTAGGA TGGGATCTAA ATCCAATGAA AATGTCTCA 360
 40 TAAAAACAG GAAAGAACCC ATAGAAACAC AAGGAAGAAG GTCATGTGAA GATGGAGGCA 420
 GAGATTGGAG GGATGCAACC ACCGGCCCAG GAATGCCAGC AGCCACCCAG AAGCTGGAAG 480
 GAAATGAGGG ATCTCTCTCT AGAACCTTTA GAGAGACAT GGTCCTGTGA ACAGCTTGAT 540
 TTGGACTTG CCCATAGCT GTATACTCTT ACTTTGGATA CAATTTTATC CAAACTTGGC 600
 TAAACAGTTT CTCAGCCTAT GGAAAAATTA AAATGGAGAA GATTCAACTC GATTCTTACA 660
 GATTCAAAGC AAGAAAAATGA TGGGAACATA GGAGGAGACC AAGAAAGCCT ATAAAAAGCA 720
 45 AAAAATGAA GTGAACATTG TGGTAGCTTT AAGATGTTT GTGTAGCTGC AGGCACCTCA 780
 TACACATGAA AACCCCCAAG GGGAAATCCCC ATATCACAGT GTAGTGTGAT ATTTGACATT 840
 YGTGATCTG TAGATGTGA CAGAAAAGGT GAATCTGTGT TCTGTATATT CTGCTAAGG 900
 CAAAGAAATG TTAGCTYTC TTTAAATAG TTCCATAATT TTTTAAAAA AGCTTTGCTT 960
 GAAAACTGTA AGCTTCCAT ATCTGGAGCA TTTCACCTTA AATATTGGA TAAATATGTT 1020
 50 ATCTCTTAC TTGGACATTT CATGTGTTT GGGATGTGTT TYTAAATCT TCCTAATTCA 1080
 TATAGCTGCT AACACTTCCC GCAGAGCTAA ACCATTACAG ANTATGAAAT AAAGACCCTA 1140
 TTGATTGAA CTTAAAAAAA AAAAMAMAAA AAAAAAAAAA AAAAAAAT GA

55 SEQ ID NO:271 PBQ4 DNA sequence
 Nucleic Acid Accession#: AA149579
 Coding sequence: 1-1363 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 60 ATGGAATCAA TCCTATGAT GGAAGCCCT AAGAGCCTTA GTGAACTTG TTTACCTAAT 60
 GGCATAAATG GTATCAAAGA TGCAAGGAAG GTCAGTGTAG GTGTGATTGG AAGTGGAGAT 120
 TTTGCCAAAT CCTTGACCAT TCGACTTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180
 AGAAATCTTA AGTTGCTTC TGAATTTTTC CCTCATGTGG TAGATGTCAC TCATCATGAA 240
 65 GATGCTCTCA CAAAAACAAA TATAATATTT GTTGCTATAC ACAGAGAACA TTATACCTCC 300
 CTGTGGGACC TGAGACATCT GCTTGTGGGT AAAATCCTGA TTGATGTGAG CAATAACATG 360
 AGGATAAACCC AGTACCCAGA ATCCAATGCT GAATATTGCG CTTCATTATT CCCAGATTCT 420
 TTGATTGTCA AAGGATTAA TGTGTCTCA GCTTGGGCAC TTCAGTTAGG ACCTAAGGAT 480
 GCCAGCCGCG AGGTTTATAT ATGCAGCAAC AATATTCAG CGCGACAACA GGTATTGAA 540
 70 CTTGCCCGCC AGTTGAATTT CATTTCCATT GACTTGGGAT CCTTATCATC AGCCAGAGAG 600
 ATTGAAATTT TACCCCTACG ACTCTTACT CTCTGGAGAG GGCCAGTGGT GGTAGCTATA 660
 AGCTTGGCCA CATTTTTCCT CTTTATTCC TTTGTACAG AGTGATGTTA TCCATATGCT 720
 AGAAACCAAC AGAGTGACTT TTACAAAATT CCTATAGAGA TTGTGAATAA AACCTTACCT 780
 ATAGTTGCCA TTACTTTGCT CTCCCTAGTA TACCTGCGAG GTCTTCTGGC AGCTGCTTAT 840
 75 CAACCTTATT ACGGCACCAA GTATAGGAGA TTTCACCTT GGTGGAACCT CTGGTTACAG 900
 TGTAGAAATC AGCTTGGATT ACTAAGTTT TTCTTCGCTA TGGTCCATGT TGCCTACAGC 960
 CTCTGCTTAC CGATGAGAGG GTCAGAGAGA TATTTGTTTC TCAACATGGC TTATCAGCAG 1020
 GTTCATGCAA ATATTGAAA CTCTGGGAAT GAGGAAGAAG TTTGGAGAAAT TGAATGTAT 1080
 ATCTCTTTG GCATAATGAG CTTTGGCTTA CTTTCCCTCC TGGCAGTCAC TTCTATCCCT 1140
 TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTTA TTCAGTCTAC ACTTGGATAT 1200

GTCGCTCTGC TCATAAGTAC TTTCCATGTT TTAATTTATG GATGGAACG AGCTTTTGAG 1260
 GAAGAGTACT ACAGATTTTA TACACCACCA AACTTTGTTT TGTCTCTGT TTTGCCCTCA 1320
 ATTGTAATTC TGGATCTTTT GCAGCTTTCG AGATACCCAG ACTGA

5 SEQ ID NO:272 PBQ4 Protein sequence:
 Protein Accession #: none

10 1 11 21 31 41 51
 | | | | | |
 MESISMGSP KSLSETCLFN GINGIKDARK VTVGVIGSGD FAKSLTIRLI RCGYHVIGS 60
 RNPKFASEFF PHVVDVTHHE DALTKTNIIF VAIHREHYTS LWDLRHLLVG KILIDVSNM 120
 RINQVPESNA EYLASLFPDS LIVKGFNVVS AWALQLGPKD ASRQVYICSN NIQARQOVIE 180
 LARQLNFIPI DLGLSSSARE IENLPLRLFT LWRGPVVVAI SLATFFFLYS FVRDVIHPYA 240
 15 RNQSDDFYKI PIEIVNKTLP IVAITLLSLV YLAGLLAARY QLYYGTKYRR FPPWLETWLQ 300
 CRKQLGLLSF FFAMVHVAYS LCLPMRRSER YLFLNMAVQQ VHANIENSWN EEEVWRIEMY 360
 ISFGIMSLGL LSLLAVT SIP SVSNALNRE FSFIQSTLGY VALLISTFHV LIYGWKRAFE 420
 EYYRYFTTP NFVLALVLPS IVLDLLQLC RYPD

20 SEQ ID NO:273 PBQ5 DNA SEQUENCE
 Nucleic Acid Accession#: NM_001973
 Coding sequence: 150-1445 (underlined sequence corresponds to start and stop codon)

25 1 11 21 31 41 51
 | | | | | |
 CCGCCGCTT CTA^{CT}CCGCC GCGGGGGTCG CAGCGGCTCG CGCGCCGTCC TCGAGTTTCC 60
 AGCGTGAGGA GGAGGCTGAG GCGGAGAGG CGCATCGTGT TCGAGGCGGA GACCGAGGGG 120
 GAGCCCGCGG CGCGGCGTCG CTCA^{TT}GTCTA TGGACAGTGC TATCACCTCG TGGCAGTTCC 180
 TTCTTCAGCT CCTCAGAAAG CCTCAGAAC AGCACATGAT CTGTGGGACC TCTAATGATG 240
 30 GGCAGTTTAA GCTTTTTCAG GCAGAAGAGG TGGCTCGTCT CTGGGGGATT CGCAAGAACA 300
 AGCCTAATCT GAATATGAC AAAC^{TC}AGCC GAGCCCTCAG ATACTATTAT GTAAAGAATA 360
 TCATCAAAAA AGTGAATGGT CAGAAGTTTG TGTACAAGTT TGTCTCTTAT CCAGAGATT 420
 TGAACATGGA TCCAATGACA GTGGGCAGGA TTGAGGGTGA CTGTGAAAGT TTAAACTTCA 480
 GTGAAGTCAG CAGCAGTTCC AAAGATGTGG AGAATGGAGG GAAAGATAAA CCACCTCAGC 540
 35 CTGGTGCCAA GACCTCTAGC CGCAATGACT ACATACACTC TGGCTTATAT TCTTCATTTA 600
 CTCTCAACTC TTGAACCTC TCCAATGTAA AGCTTTTCAA ATTGATAAAG ACTGAGAATC 660
 CAGCCGAGAA ACTGGCAGAG AAAAAATCTC CTCAGGAGCC CACACCATCT GTCATCAAT 720
 TTGTCCAGAC ACCTTCCAAA AAGCCACCAG TTGAACCTGT TGTGCCACC ATTTCATTTG 780
 40 GCGCAAGTAT TTCTCCATCT TCAGAAGAAA CTATCCAAGC TTTCGAGACA TTGGTTTCCC 840
 CAAAACTGCC TTCCCTGGAA GCGCCCACTC CTGCTCTTAA CGTAATGACT GCTTTTGCCA 900
 CCACACCACT CATTTCTGCC ATACCCCTTT TGCAGGAACC TCCCAGAAC CTTTCACCAC 960
 CACTGAGTTC TCACCCAGAC ATCGACACAG ACATTTGATT AGTGGCTTCT CAGCCAATGG 1020
 AACTTCCAGA GAATTTGTCT CTGGAGCCTA AAGACCAGGA TTCACTCTTG CTAGAAAAGG 1080
 45 ACAAAGTAAA TAATTCATCA AGATCCAAGA AACCCAAAGG GTTAGGACTG GCACCCACCC 1140
 TTGTGATCAC GAGCAGTGAT CCAAGCCAC TGGGAATACT GAGCCCATCT CTCCCTACAG 1200
 TTCTCTTAC ACCAGCATTT TTTTCACAGA CACCCATCAT ACTGACTCCA AGCCCTTGC 1260
 TCTCCAGTAT CCATCTCTGG AGTACTCTCA GTCTGTGTC TCCCTTAAGT CCAGCCAGAC 1320
 TGAAGGGTC TAACACACTT TTCCAGTTTC CTCTGTACT GAACAGTCAT GGGCCATTCA 1380
 50 CTCTGTCTGG GCTGTATGGA CCTTCCACCC CTGCCCCATT TTCCCGACAC CTACAGAAGA 1440
 CATAACCTAT GCATCTTGGG AATGAGAGAA CCGAGGAACG AAGAAACAGA CATTCACAT 1500
 GATTGCATTT GAAGTGAGCA ATTGATAGTT CTACAATGCT GATAATAGAC TATTGTGATT 1560
 TTTGCCATT CCAATGTAAA ACATCTTTT AGGATCTCTT TTGAATAGGA CTCAAGTTGG 1620
 ACTATATGTA TAAAAATGCC TTAATTGGAG TCTAAACTCC ACCTCCCTCT GTCTTTTCTT 1680
 55 TTCTTTTTC TTCTCTCTCT TCCTTTCTT TTCTCTTTTA AAAATATTTT GAGCTTTGTG 1740
 CTGAAGAAGT TTTTGGTGGG CTTTAGTGAC TGTCTTTTGC AAAAGCAATT AAGAACAAG 1800
 TTACTCTTC TGGCTATTGG GACCTTTGG CCAGGAAAAA TTATGCTTAG AATCTATTAT 1860
 TAAAGAAGT ATTGTGAAA TGAATAAAAA AAAAAAATAA AAAAAAATAA AAAAAAATAA 1920
 AAAAAAATAA AAA

60 SEQ ID NO:274 PBQ5 Protein sequence:
 Protein Accession #: NP_001964

65 MDSAITLWQF LLQLLQKPQN KHMICWTSND GQFKLLQAE VRLWGIRKN KPNMNYDKLS 60
 RALRYYYVKN IIKVNGQKF VYKFVSYPEI LNMDPMTVGR IEGDCESLNF SEVSSSKDV 120
 ENGGKDKPPQ PGAKTSSRND YHSGLYSSF TLNSLNSSNV KLFKLIKTN PAEKLAEEKS 180
 PQEPTSPVIK FVTTIPSKPP VEPVAATISI GPSISPSSEE TQALETLSV PKLPSLEAPT 240
 SASNVMTAFA TTPPISIPP LQEPPTPSP PLSSHPDIDT DIDSVASQPM ELPENLSLEP 300
 70 KDQDSVLLK DKNVNSSRSK KPKGLGLAPT LVITSSDPSP LGILSPSLPT ASLTPAFFSQ 360
 TPILTPSPL LSSHFWSTL SPVAPLSPAR LQANTLFQF PSVLNSHGPF TSLGDLGPST 420
 PGPFSPDLQK T

75 SEQ ID NO:275 PBQ3 DNA SEQUENCE
 Nucleic Acid Accession#: AB040921
 Coding sequence: 131-2560 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 | | | | | |

5	AATCAGGAAC	AGATCATATA	TTGACCGAGA	TTCTGAGTAT	CTCTTGCAAG	AAAAATGAACC	60
	AGATGGAAC	TTAGACCAAA	AATTATTGGA	AGATTACAA	AAGAAAAAA	ATGACCTTCG	120
	GTATATTGAA	ATGCAGCATT	TCAGAGAAAA	GCTGCCTTCG	TATGGAATGC	AAAAGGAATT	180
	GGTAAATTAA	ATTGATAACC	ATCAGGTAAC	AGTAATAAGT	GGTGAACCTG	GTTGTGGCAA	240
	AACCACTCAA	GTTACTCAGT	TCATTTTGGA	TAACTACATT	GAAAGAGGAA	AAGGATCTGC	300
	TTGCAGAA	GTTTGTACTC	AGCCAAGAAG	AATTAGTGCC	ATTTTCAGTTG	CGGAAAGAGT	360
	AGCTGCAGAA	AGGGCAGAAT	CTTGTGGCAG	TGGTAATAGT	ACTGGATATC	AAATTCGTCT	420
	CCAGAGTCGG	TTGCCAAGGA	AACAGGGTTC	TATCTTATAC	TGTACAACAG	GAATCATCCT	480
10	TCAGTGGCTC	CAGTCAGACC	CGTATTGTTC	CAGTGTAGT	CATATCGTAC	TTGATGAAAT	540
	CCATGAAAGA	AATCTGCAGT	CAGATGTTTT	AATGACTGTT	GTTAAAGACC	TTCTCAATTT	600
	TCGATCTGAC	TTGAAAGTAA	TATTGATGAG	TGCAACATTG	AATGCAGAAA	AGTTTTCAGA	660
	ATATTTTGGT	AACITGTCCAA	TGATACATAT	ACCTGGTTTT	ACCTTTCCGG	TTGTGGAATA	720
	TCTTTTGAA	GATGTAATTG	AAAAAATAAG	GTATGTTCCA	GAACAAAAAG	AACACAGATC	780
15	CCAGTTTAAG	AGGGGTTTCA	TGCAAGGGCA	TGTAATAGA	CAAGAAAAAG	AAGAAAAAGA	840
	AGCAATATAT	AAAGAACGTT	GGCCAGATTA	TGTAAGGGAA	CTGCCAAGAA	GGTATTCTGC	900
	AAGTACTGTA	GATGTTATAG	AAATGATGGA	GGATGATAAA	GTTGATCTGA	ATTTGATTGT	960
	TGCCCTCATC	CGATACATTG	TTTGTGAAGA	AGAGGATGGT	GCGTACTTGG	TCTTTCTGCC	1020
	AGGCTGGGAC	AATATCAGCA	CTTTACATGA	TCTCTTGATG	TCACAAGTAA	TGTTTAAATC	1080
20	AGATAAATTT	TTAATTATAC	CTTTACATTC	ACTGATGCCT	ACAGTTAACC	AGACACAGGT	1140
	GTTTAAAGA	ACCCCTCCTG	GTGTTCCGAA	AATAGTAATT	GCTACCAACA	TTGCCGAGAC	1200
	TAGCATTACC	ATAGATGATG	TCGTTTATGT	GATAGATGGA	GGAAAAATAA	AAGAGACGCA	1260
	TTTGTATAGT	CAGAACATAA	TCAGTACAA	GTCCGCTGAG	TGGGTTAGTA	AAGCTAATGC	1320
	CAACACAGAG	AAAGGTCGAG	CTGGAAGAGT	TCAACCTGGT	CATTGCTATC	ATCTGTATAA	1380
25	TGGTCTTAG	GAAGTCTTC	TAGATGACTA	TCAACTGCCA	GAAATTTTGA	GAACCTCTTT	1440
	GGAAGAACTT	TGTTTACAAA	TAAAGATTTT	AAGGCTAGGT	GGAATTGCTT	ATTTTCTGAG	1500
	TAGATTAATG	GACCCACCAT	CAAAATGAGC	AGTGTACTC	TCCATAAGAC	ACCTGATGGA	1560
	GCTGAACGCT	TTGGATAAAC	AAGAAGAAAT	GACACCTCTT	GGAGTCCACT	TGGCACGATT	1620
30	ACCCGTTGAG	CCACATATTG	GAAAAATGAT	TCTTTTGGGA	GCACCTGTCT	GCTGCTTAGA	1680
	CCCACTACTC	GAATTTGCTG	CTAGTCTCAG	TTTCAAAGAT	CCATTGTGTA	TTCCACTGGG	1740
	AAAAGAAAG	ATTGAGATG	CAAGAAGAAA	GGAATTGGCA	AAGGATACTA	GAAGTGATCA	1800
	CTTAACAGTT	GTGAATGCGT	TTGAGGGCTG	GGAAGAGGCT	AGGCGACGTG	GTTTCAGATA	1860
	CGAAAGGAG	TAATGCTGGG	AATATTTTCT	GTCTTCAAAC	ACACTGCAGA	TGCTGCATAA	1920
35	CATGAAAGGA	CAGTTTGTCT	AGCATCTTCT	TGGAGCTGGA	TTTGTAAAGCA	GTAGAAATCC	1980
	TAAAGATCCA	GAATCTAATA	TAAATTCAGA	TAATGAGAAG	ATAATTAAAG	CTGTCACTCG	2040
	TGCTGGTTTA	TATCCCAAAG	TTGCTAAAT	TCGACTAAAT	TTGGGTAATA	AAAGAAAAAT	2100
	GGTAAAGT	TACACAAAAA	CCGATGGCCT	GGTTGCTGTT	CATCTTAAAT	CTGTTAATGT	2160
	GGAGCAACAA	GACTTTCACT	ACAACCTGGT	TATCTATCAC	CTAAAGATGA	GAACAAGCAG	2220
40	TATATACCTG	TATGACTGCA	CAGAGGTTTC	CCCATACTGT	CTCTGTGTTT	TTGGAGGTGA	2280
	CATTTCATCA	CAGAAAGATA	ACGATCAGGA	AACATATTGT	GTAGATGAGT	GGATTGTATT	2340
	TCAGTCTCCA	GCAAGAATTG	CCCATCTTGT	TAAGGAATTA	AGAAAGGAAC	TAGATATCTT	2400
	TCGTCAAGAG	AAGATTGAAA	GTCCATCATC	TGTAGACTGG	AATGACACTA	AATCCAGAGA	2460
	CTGTGCAATG	CTGTCACTCA	TTATAGACTT	GATCAAAACA	CAGGAAAGAG	CAACTCCAG	2520
45	GAACCTTCCG	CCACGATTCC	AGGATGGATA	TTACAGCTGA	CAGCTTTTCA	GGGGTGGTCT	2580
	GAAAGGCCAG	TTTGACAGCG	ATTCTTCATC	ATTGTTTAAA	TTTGGCTGGG	ATGCCAAACC	2640
	CTGGGACATG	AACAATTTTC	ATGTGTAAGG	TAGAAGCCTT	CAGTAGGTAG	TAAAGACTTA	2700
	ATGTGCATGA	CTTGATGTTA	TATGTAGAGA	TATATATATA	TATATATATA	CCATAAAAAGC	2760
	AATATGTTCT	CTGATCATAT	ACTCTGCTGT	GGTCATGCCC	ACTCTTTGGG	AGTATATTTCC	2820
	CTTTATATAT	ATTGAGTATT	GTACCACCTG	AGAAATTCCT	TTGTTCTGTT	ATACAAAAAT	2880
50	AATCTTCTCG	CTCAATATGA	TTGATGATAC	CACCAGTAAA	AATAGGATGT	TTACCCCAAA	2940
	ACAAGTGTC	ATTAAGAATT	TGAACACAAC	CACATTTTTT	AAAATGAAC	TTCTATCCGA	3000
	AGTAAATTA	TTTGTGTAA	TAAAGTCCAG	TATTTAATAA	AATGTACAAT	GTTAAATCTC	

SEQ ID NO:276 PB3 Protein sequence:

Protein Accession #: BAA96012

55	IRNRSYIDRD	SEYLLQENEP	DGTLQKLL	DLQKKNDLR	YIEMQHFREK	LPSYGMQKEL	60
	VNLIDNHQVT	VISGETGCGK	TTQVTQFILD	NYIERGKGS	CRIVCTQPRR	ISAISSAERV	120
	AAERAESCGS	GNSTGYQIRL	QSRLPRKQGS	ILYCTTGIL	QWLQSDPYLS	SVSHIVLDEI	180
60	HERNLQSDVL	MTVVKDILNF	RSDLKVLMS	ATLNAEKFS	YFGNCPMIHI	PGFTFFVVEY	240
	LLEDVIEKIR	YVPEQKEHRS	QFKRGFMQGH	VNRQEKEEKE	ATYKERWPDY	VRELRRRYSA	300
	STVDVIEHME	DDKVDNLNLI	ALIRYIVLEE	EDGAILVFLP	GWDNISTLHD	LLMSQVMFKS	360
	DKFLIPLHS	LMPTVNQTV	FKRTPPGVRK	IVIAITNIAET	SITIDDVVVV	IDGGKIKETH	420
	FDTONNISTM	SAEWSKANA	KQRKGRAGR	VQPHCYHLYN	GLRASLLDDY	QLPEILRTPL	480
65	EELCLQIKIL	RLGGIAYFLS	RLMDPPSNEA	VLLSIRHIME	LNALDKQEEL	TPLGVLHARL	540
	PVEPHIGKMI	LFGALFCCLD	PVLTAASLS	FKDPFVPLG	KEKIADARRK	ELAKDTRSDH	600
	LTVVNAFEGW	EEARRRGFRY	EKDYCWEIFL	SSNTLQMLHN	MKGQFAEHL	GAGFVSSRNP	660
	KDPESNNSD	NEKIKAVIC	AGLYPKVAKI	RLNLGKKRKM	VKVYTKTDGL	VAVHPKSVNV	720
	EQTDHFHYNL	IYHLKMRSS	IYLYDCTEVS	PYCLLFFGGD	ISIQKNDQ	ETIADVEWIVF	780
70	QSPARIAHLV	KLRKELDIL	LQEKIESPHP	VDWNTDKSRD	CAVLSAIDL	IKTQEKATPR	840
	NFPPRFQDGY	YS					

SEQ ID NO:277 PB6 DNA SEQUENCE

Nucleic Acid Accession#: AA454018

Coding sequence: 64-1669(underlined sequence corresponds to start and stop codon)

GATTTTATCC TGAACATTA CAGTGAAGAT GGCTATTTAT ATGAAGATGA AATTGCAGAT 60
 CTTATGATC TGAGACAAGC TTGTCGGACG CCTAGCCGGG ATGAGGCCGG GGTGGAACCTG 120

CTGATGACAT ACTTCATCCA GCTGGGCTTT GTCGAGAGTC GATTCTTCCC GCCACACGG 180
 CAGATGGGAC TCCTGTTCAC CTGGTATGAC TCTCTACCG GGGTCCCGT CAGCCAGCAG 240
 AACCTGCTGC TGGAGAAGGC CAGTGTCTTG TTCAACACTG GGGCCCTCTA CACCCAGATT 300
 GGGACCCGGT GTGATCGGCA GACGCAGGCT GGGCTGGAGA GTGCCATAGA TGCCTTTCAG 360
 AGAGCCGAG GGGTTTTAAA TTACCTGAAA GACACATTTA CCCATACTCC AAGTTACGAC 420
 ATGAGCCCTG CCATGCTCAG CGTGCTCGTC AAAATGATGC TTGCACAAGC CCAAGAAAGC 480
 GTGTTTGAGA AAATCAGCCT TCCTGGGATC CGGAATGAAT TCTCATGCT GGTGAAGGTG 540
 GCTCAGGAGG CTGCTAAGGT GGGAGAGGTC TACCAACAGC TACACGCAGC CATGAGCCAG 600
 GCGCCGGTGA AAGAGAACAT CCCCTACTCC TGGGCCAGCT TAGCCTGCGT GAAGGCCAC 660
 CACTACGCGG CCTTGGCCCA CTACTTCACT GCCATCTCC TCATCGACCA CCAGGTGAAG 720
 CCAGGCACGG ATCTGGACCA CCAGGAGAAG TGCCTGTCCC AGCTCTACGA CCACATGCCA 780
 GAGGGCTGA CACCCCTGGC CACACTGAAG AATGATCAGC AGCGCCGACA GCTGGGGAAG 840
 TCCCACTTGC GCAGAGCCAT GGCTCATCAC GAGGAGTCGG TCGCGGAGGC CAGCCTCTGC 900
 AAGAAGCTGC GGAGCATTTA GGTGCTACAG AAGTGCTGT GTGCCGACA GGAACGCTCC 960
 CGGCTCAGT ACGCCACGA CCAGGAGGAG GATGACCTGC TGAACCTGAT CGACGCCCC 1020
 AGTGTGTGT CTAAACTGA GCAAGAGGT GACATTATAT TGCCCCAGTT CTCCAAGCTG 1080
 ACAGTCACGG ACTTCTTCCA GAAGCTGGGC CCCTTATCTG TGTTCGGC TAACAAGCGG 1140
 TGGACGCTC CTGAAGCAT CCGCTTCACT GCAGAAGAAG GGGACTTGGG GTTCACTTG 1200
 AGAGGGAACG CCCCCTTCA GGTTCACITC CTGGATCCTT ACTGCTCTGC CTCGGTGGCA 1260
 GGAGCCCGG AAGGAGATTA TATTGTCTCC ATTCAGCTTG TGGATTGTA GTGGCTGACG 1320
 CTGAGTGAGG TTATGAAGCT GCTGAAGAGC TTTGGCGAGG ACAGAGTCGA GATGAAAGTC 1380
 GTGAGCCTCC TGGACTCCAC ATCATCCATG CATAATAAGA GTGCCACATA CTCGTGGGA 1440
 ATGCAGAAAA CGTACTCCAT GATCTGCTTA GCCATTGATG ATGACGACAA AACTGATAAA 1500
 ACCAAGAAAA TCTCAAGAA GCTTTCCTTC CTGAGTTGGG GCACCAACAA GAACAGACAG 1560
 AAGTCAGCA GCACCTTGTG CCTCCATCG GTCGGGGCTG CACGCCCTCA GGTCAAGAA 1620
 AAGTGCCCT CCCCTTCAG CCTTCTCAAC TCAGACAGTT CTTGGTACTA A

SEQ ID NO:278 PBYS Protein sequence:
 Protein Accession #: NP_149094

DFILEHYSYD GYLYEDELAD LMDLRQACRT PSRDEAGVEL LMTYFIQLGF VESRFFPPT 60
 QMGLLFTWYD SLTGVPVSQQ NLLLEKASVL FNTGALYTOI GTRCDRQTOA GLESAIDAFQ 120
 RAAGVLNLYLK DITHTPSYD MSPAMLSVLV KMMLAQAES VFEKISLPGI RNEFFMLVKV 180
 AQEAAKVGEV YQQLHAAMSQ APVKENIPYS WASLACVKAH HYAALAHYFT AILLDHQVK 240
 PGTDLDHQEK CLSOLYDHMP EGLTPLATLK NDQORRLGK SHLRRAAMAH EESVREASLC 300
 KKLRISIEVLQ KVLCAQERS RLTYAQHQEE DDLLNLIDAP SVVAKTEQEV DILPQFSKL 360
 TVTDFQKLG WTPFRSIRFT AEEGLGFTL RGNAPVQVHF LDPYCSASVA 420
 GAREGDYTVS IQLVDCKWLT LSEVMKLLKS FGEDEIEMKV VSLDSTSSM HNKSATYSVG 480
 MQKTYSMICL ADDDDKTDK TTKISKLLSF LSWGTNKNRQ KSATLCLPS VGAARFQVK 540
 KLPSPFSLN SDSSWY

SEQ ID NO:279 PBYS DNA SEQUENCE
 Nucleic Acid Accession#: AF107493
 Coding sequence: 125-556 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 50 GAATTCGGCA CGAGCCCTGT TGGAGGTTCT GGGGCGCAGA ACCGCTACTG CTGCTTCGGT 60
 CTCTCCTTGG GAAAAAATAA AATTGGAACC TTTTGGAGCT GTGTGCTAAA TCTTCAGTGG 120
 GACAAATGGT TCAGACAAAA GAGTGAGTAG AACAGAGCGT AGTGAAGAT ACGGTTCCAT 180
 CATAGACAGG GATGACCGTG ATGAGCGTGA ATCCCGAAGC AGGCGGAGGG ACTCAGATTA 240
 CAAAGATCTT AGTGATGATC GGAGGGGTGA TAGATATGAT GACTACCGAG ACTATGACAG 300
 55 TCCAGAGAGA GAGCGTGAAG GAAGGAACAG TGACCGATCC GAAGATGGCT ACCATTACAG 360
 TGGTGACTAT GGTGAGCAGC ACTATAGCCA TGACATCAGT GACGAGAGGG AGAGCAAGAC 420
 CATCATGCTG CGCGCCCTTC CCATCACCAT CACAGAGAGC GATATTTCAG AAATGATGGA 480
 GTCCTTCGAA GGCCCTCAGC CTGCGGATGT GAGGCTGATG AAGAGGAAAA CAGGTGAGAG 540
 60 CTTGCTTAGT TCCTGATATT ATGTGTCTCT TCCCATTTCC CACCTCAGTC CCTAAAGAAC 600
 ATCCTGATTC CCCAGTCTT CAAGCACATG AATTCAGAAT GAAAGGTTTG CCATGGCTAA 660
 GGAATGTGAC TCTTTGAAAA CCATGTTAGC ATCTGAGGAA CTTTTTAAAA CTTTGTTTTA 720
 GGGACTTTTT TTCTCTTAGG TAAGTAATGA TTTATAAACT CCTTTTTTTT TTTGACTATA 780
 GTCGGTTGCA TGGTTACTTT AAGCGTGGAA TCAAAATGGAG TGGCATTTAG TTCAGGCGGC 840
 65 TTGTTCTCTG CCATGGCAAA GTATCAAGAA GATCCCAAG TCAAGTCACA TTTGTAAAGC 900
 TGCTTCCCAA TTGGCTTTGT CACGCACTGT TGAAGCAGTG GGAGAGAGAT TCACCTGTTA 960
 TAAAGGAAC TACTAACACA AGTATCCCGT CTATATCTGA ATGCTGTCTC TAGGTGTAAG 1020
 CCGTGGTTTC GCCTTCGTGG AGTTTATCA CTTGCAAGAT GCTACCGACT GGATGGAAGC 1080
 CAATCAAGGT GCTTCACTCA CCAAGCTAG ATATTCATGA AAATGGAACA AGTCTGTACA 1140
 70 ATTTTAAAAA AAGGTGAAG GAGTGGTTTG TTCCAAAGGA GTGACTTTTT TTTAAAAAAA 1200
 AAGCTTTGTA TATATTAAAA TTGATGTTAC TAGAATAAGT ACAGTACCAA GCACTTCATT 1260
 ATAGAAATTT TTCTGCCTTT AAACATGGCT ACCTACCTGG CAGGCGCTTG TTAACACTG 1320
 AATACCTGTC TGGTAATCAC TAAACATCTT TTATGTTTCC CTTTTCCTTA GTTTGTTATA 1380
 TTCTATTAT GTCCATTGAG AGTAAGCTTA GTATATCAAA CTCTCCATT GACAGTGAAG 1440
 75 AGAATATAGT GAAAGTCTGT GCGCGCATTT TTATAAGTAA TTCTTATTT CTGCTGAAG 1500
 ACCACAAGC CTCTCTGAGG CGTAAGTCTC CAGACCGGTC TTCAGGGAAT ATTTAAGGAC 1560
 TTAGTGGAAT TTATGAACAA TAAGTCTGAT GAGATTAGCC TGGAGTGGT GTCTGACAG 1620
 TGCTTAATCT AGAGTGGCAT TAACATTCTA ATCTCCTTGA GAATGCCCTT TATAGTCTGT 1680
 TCAAGCAAG TCATTGATGT TTCTTCGAGG TAGTGTTAAC TGAAGTGTTC TTCAGTTTGT 1740
 CAAGATAATG TTCAGTGCTT GGCACTTAAA TAACATTTTT TGCAAGAACT CCAAGGCACA 1800

5 TTATTGAATG CCTTTAACCA AGTGCATTCT GGGAAAGTTG CTTGACTCAT TATCTTGCTT 1860
 TTCTGCAGCA TTCTGTGATT TGAGTCATCC ATGAATCCAT GAATAAAAGT TACATTCTTT 1920
 GATTGGTAAT ATTGCCATTT ATAACAAGAC TCACTAATGA GGGTATCACT TTGACTGACT 1980
 GATTGTGTTAA AGTTTTTAAG CCTCTCATTT TCCTAACCCA GAAATCACAG CCTGATTTTA 2040
 TTAAGTAG AGCTTCATTC ATTTTCATACC ATAGATACCA TCCTAGTAAA TCCAGAACAT 2100
 ATACAAGGTT CATGTGAGTC TGCTTTCTTG ACATGATAGC ATTGTTTGAT GCAGTGGATA 2160
 TGTCAAGATG ACTAACCTAG GAGTTTGAAA CTCTAAGAA ACTAAACCT GTAAGACATT 2220
 TAAAAGTCTC CACAATTTTA ATGTATACAA AGCTATGTTA CTGTGTAAAC CATTACAGTT 2280
 CAAATTCAC CTAGAAATAA AAGGCCAGTA GGATTAGGGA CTCACTGGTA GTTTGGAGTC 2340
 10 TCCAGCACA CATCCCTCCT AGTGGGATGA TCTATTACA TATCTCCAG CTTTTTTATT 2400
 TTTGCTCTG TATATCACAG TGAGTGGATG GCCCTTCAGC TTTTCTCTC CTGGCCAGAC 2460
 ATGCAGTCTT GCCTTTAGAT ATCGCAGAGA CAAAATTCAC AGCATGTCTT AAATCTTCCA 2520
 GGATTTCGAA GAACCAAAAT GCTCAACAGT ATGTATGTTT AGAGGGGTTA GACTCCTTTT 2580
 15 TAAAATCTGG ATATCTAACC ACCTACTTAA ATCTGTTTGA TAGTGTCAAA CCACCCCCAC 2640
 CCTTGATCCT CCCACCCCA AAAAAAAAAA AAAA

SEQ ID NO:280 PRY8 Protein sequence:

Protein Accession #: XP_003261

20 MGSDKRVSR ERSGRYSII DRDRDERES RSRRRSDYK RSSDDRRGDR YDDYRDYDSP 60
 ERERERNSD RSEDGYHSDG DYGEHDYRHD ISDERESKTI MLRGLPITIT ESDIREMMES 120
 FEGPQADV R LMKRKGTESL LSS

25

SEQ ID NO:281 PCI2 DNA SEQUENCE

Nucleic Acid Accession#: AF208291

Coding sequence: 109-3705 (underlined sequence corresponds to start and stop codon)

30 1 11 21 31 41 51
 CGGCCGCTTT TTTCTCAAGA TGGCAGATTC CCACTGAGGC TGAGGGGGCC GAGCTCGCGC 60
 GCGCGGTTC CTTCTCCGPT GCCATGAACC GCGGACACCC GGGCCCCGAT GGGCCCCGTG 120
 35 TACGAAGGTA TGGCCTCACA TGTGCAAGTT TTCCTCCCTC ACACCTTCA ATCAAGTGCC 180
 TTCTGTAGTG TGAAGAAACT AAAAGTAGAG CCAAGTTCCA ACTGGGACAT GACTGGGTAC 240
 GGCCTCCACA GCAAGGTGTA CAGCCAGAGC AAGAACATAC CACTTCTCA GCCAGCCTCC 300
 ACRAACGTCA GCACCTCTTT GCGCGTCCCA AACCCAAGCC TACCTTACGA GCAGACCATC 360
 GTCTTCCAG GAACACCCGG GCACATCGTG GTCACTCAG CAAGCAGCAC TTCTGTCAAC 420
 40 GGGCAAGTCC TCGCGGAGC ACACAACCTA ATGCGTCGAA GCACGTGAG CCTCCTTGAT 480
 ACCTACCAAA AATGTGGACT CAAGCGTAAG AGCGAGGAGA TCGAGAACAC AAGCAGCGTG 540
 CAGATCATCG AGGAGCATCC ACCCATGATT CAGAATAATG CAAGCGGGGC CACTGTCCGC 600
 ACTGCCACCA CGTCTACTGC CACCTCCAAA AACAGCGGCT CCAACAGCGA GGGCGACTAT 660
 CAGCTGGTGC AGCATGAGGT GCTGTGCTCC ATGACCAACA CCTACGAGGT CTTAGAGTTC 720
 45 TTGGCCGAG AGACGTTTGG ACAAGTGCTC AAGTGCTGGA AACGGGGCAC CAATGAGATC 780
 GTAGCCATCA GAATCTTGAA GAACCGCCCA TCCTATGCCC GACAAGGTCA GATTGAAGTG 840
 AGCATCCTGG CCCGGTTGAG CACGGAGAGT GCCGATGACT ATAACCTTCT CCGGGCTTAC 900
 GAATGTCTCA AGCACAAGAA CCACACGTGC TTGGTCTTCG AGATGTTGGA GCAGAACCTC 960
 TATGACTTTT TGAAGCAAAA CAAGTTTAGC CCCTTGCCCC TCAAAATACAT TCGCCAGTT 1020
 50 CTCCAGCAGG TAGCCACAGC CCTGATGAAA CTCAAAAGCC TAGGTCTTAT CCACGCTGAC 1080
 CTCAAACCTA AAAACATCAT GCTGGTGGAT CCATCTAGAC AACCATACAG AGCTCAAGGT 1140
 ATCGACTTTG TCTCAGCCAG CCACGCTTCC AAGGCTGTGT GCTCCACCTA CTTGCACTCC 1200
 AGATATTTCA GGGCCCTCGA GATCATCCTT GGTTTACCAT TTTGTGAGGC AATTGACATG 1260
 TGGTCCCTGG GCTGTGTTAT TGCAGAAATT TTCCTGGGTT GGCCGTATATA TCCAGGAGCT 1320
 55 TCGGAGTATG ATCAGATTCT GTATATTTCA CAAACACAGG GTTTGCTCTC TGAATATTTA 1380
 TTAAGCGCCG GGACAAAGAC AACTAGGTTT TTCAACCGTG ACACGGACTC ACCATATCCT 1440
 TTGTGGAGAC TGAAGACACC AGATGACCAT GAAGCAGAGA CAGGGATTAA GTCAAAAGAA 1500
 GCAAGAAAGT ACATTTTCAA CTGTTTAGAT GATATGGCCC AGGTGAACAT GACGACAGAT 1560
 TTGGAAGGGA GCGACATGTT GGTAGAAAAG GCTGACCGGC GGGAGTTTAT TGACCTGTTG 1620
 60 AAGAAGATGC TGACCATTTA TGCTGACAAG AGAATCACTC CAATCGAAAC CCTGAACCAT 1680
 CCTTTTGTC CATTGACACA CTTACTCGAT TTTCCTCACA GCACACACGT CAAATCATGT 1740
 TTCCAGAAAC TGGAGATCTG CAAGCGTCCG GTGAATATGT ATGACACGCT GAACAGAGC 1800
 AAAACCCCTT TCATCACGCA CGTGGCCCCC AGCACGTCCA CCAACCTGAC CATGACCTTT 1860
 AACAAACAGC TGACCACTGT CCACAACAG GCTCCCTCCT CTACAGTGC CACTATTTC 1920
 65 TTAGCCAATC CCGAAGTCTC CATACTAAAC TACCATCTA CACTTACCA GCCCTCAGCG 1980
 GCATCCATGG CTGCAGTGGC CCAGCGGAGC ATGCCCTCGC AGACAGGAAC AGCCAGATT 2040
 TGTGCCCGGC CTGACCGGTT CCAGCAAGCT CTCATCGTGT GTCCCCCGG CTTCCAAGGC 2100
 TTGCAGGCTT CTCCTCTTAA GCACGCTGGC TACTCGGTGC GAATGGAAAA TGCAGTTCCC 2160
 ATCGTCACTC AAGCCCGAGC AGCTCAGCCT CTTGATGATC AACAGGTCT GCTTGCCAG 2220
 70 CAGGCTTGGC CAAGTGGGAC CCAGCAGATC CTGCTTCCCC CAGCATGGCA GCAACTGACT 2280
 GGAGTGGCCA CCCCACATC AGTGCAGCAT GCCACCGTGA TTCCCGAGAC CATGGCAGGC 2340
 ACCCAGCAGC TGGCGGACTG GAGAAATACG CATGCTCAGC GAAGCCATTA TAATCCCATC 2400
 ATGCAGCAGC CTGCACTATT GACCGGTCA TGTACCCCTC CAGCAGCACA GCCCTTAAAT 2460
 GTGGGTGTGG CCCAGTGAT GCGGCAGCAG CCAACAGCA CCACCTCCTC CCGGAAGAGT 2520
 75 AAGCAGCACC AGTCATCTGT GAGAAATGTC TCCACCTGT AGGTGTCCTC CTCTCAGGCC 2580
 ATCAGCTCCC CACAGCGATC CAAGCGTGT CAGGAGAACA CACTCCCCCG CTGTGCCATG 2640
 GTGCACAGTA GCCCGGCTG CAGCACTTCG GTACCTGTG GGTGGGGCGA CGTGGCCTCC 2700
 AGCACCACCC GGGAAACGGA GCGGCAGACA ATTGTCAAT CCGACACTCC CAGCCCCAGC 2760
 GTACGGGTCA TCACATCAG CAGTGACAGC GACGAGGAG AGGAACAGAA ACACGCCCCC 2820
 80 ACCAGCATCT TCTCAAGCA AAGAAAAAC GTCATCAGCT GTGTCAAGT CCACGACTCC 2880
 CCTACTCCG ACTCTCCAG CAACACCAGC CCTACTCCG TGCAGCAGC TGCTGGGCAC 2940

5 AACAAATGCCA ATGCTTTTGA CACCAAGGGG AGCCTGGAGA ATCACTGCAC GGGGAACCCC 3000
 CGAACCATCA TCGTGCCACC CCTGAAACCC CAGGCCAGCG AAGTATTGGT GGAGTGTGAT 3060
 AGCCTGGTGC CAGTCAACAC CAGTCACCAC TCGTCTCTCT ACAAGTCCAA GTCCTCCAGC 3120
 AACGTGACCT CCACCAAGCG TCACTCTTCA GGGAGCTCAT CTGGAGCCAT CACCTACCGG 3180
 CAGCAGCGCG CGGGCCCCCA CTTCACAGAG CAGCAGCCAC TCAATCTCAG CCAGGCTCAG 3240
 CAGCACATCA CCACGGACCG CACTGGGAGC CACCGAAGGC AGCAGGCCCTA CATCACTCCC 3300
 ACCATGGCCC AGGCTCCGTA CTCTTCCCG CACAACAGCC CCAGCCACGG CACTGTGCAC 3360
 CCGCATCTGG CTGCAGCCGC TGCCGCTGCC CACCTCCCCA CCCAGCCCCA CCTCTACACC 3420
 TACACTGCGC CGGCGGCCCT GGGCTCCACC GGCACCGTGG CCCACCTGGT GGCCCTCGCA 3480
 GGCTCTGCGC GCCACACCGT GCAGCACACT GCCTACCCAG CCAGCATCGT CCACCAGGTC 3540
 CCGGTGAGCA TGGGCCCCCG GGTCTGCCC TCGCCACCA TCCACCCGAG TCAGTATCCA 3600
 GCCCCAATTG CCCACAGAC CTACATCAGC GCCTCGCAG CCTCCACCGT CTACATGGA 3660
 TACCCACTGA GCCCCGCCAA GGTCAACCAG TACCTTACA TATAAACA CTGGAGGGAGG 3720
 GAGGAGGGA GGGAGGAGA GAATGGCCCG AGGAGGAGG GAGAGAAGGA GGGAGGCGCT 3780
 15 CCTGGGACCG TGGGCGCTGG CCTTTTATAC TGAAGATGCC GCACACAAAC AATGCAAAACG 3840
 GGGCAGGGCG GGGGGGGGGG GGGGCAGAGG GCAGGGGAGG GGTTCGGGAC ACCAGTGAAA 3900
 CTTGAACCGG GAAGTGGGAG GACGTAGAGC AGAGAAGAGA ACATTTTAA AAGGAAGGGA 3960
 TTAAAGAGGG TGGGAATCT ATGGTTTTTA TTTTAAAAA

20

SEQ ID NO:282 PCI2 Protein sequence:
 Protein Accession #: NP_073577

25 MAPVYEGMAS HVQVFSPTL QSSAFCSVKK LKVEPSSNWD MTGYGSHSKV YSQSKNIPPS 60
 QPASTTVYST LPVNPFSLPY EQTVFPGST GHVVTSSASS TSVTGQVLGG PHNLMRRSTV 120
 SLLDTYQKCG LKRXKEEIH TSSVQIEEH PPMIQNNASG ATVATATTST ATSKNSGSNS 180
 EGDYQLVQHE VLCSMTNTYE VLEFLGRGTF GQVVKCWKRG TNEIVAIIK KNRPSYARQG 240
 QIEVSILARL STESADDYFN VRA YECFQHK NHTCLVFEML EQNLVDFLKQ NKFSPLPKY 300
 IRPVLQQVAT ALMKLKSGL IHADLKPENI MLVDPSPRPY RVKVIDFGSA SHVSKAVCST 360
 30 YLQSRYYRAP EILGLPFCF AIDMWSLGCV IAEFLGWPL YPGASEYDQI RYISQTQGLP 420
 AEYLLSAGTK TTRFFNRD TD SPYPLWRLKT PDDHEAETGI KSKEARKYIF NCLDDMAQVN 480
 MTDLLEGSDM LVEKADRRF IDLLKKMLTI DADKRITPIE TLNHPFVTMT HLLDFPHSTH 540
 VKSCFQNM EI CKRRVNM YDT VNQSKTFFIT HVAPSTSTNL TMITFNQLTT VHNQAPSSTS 600
 ATISLANPEV SILNYPSTLY QPSAASMAAV AQRSMPLQTG TAQICARPDF FQALIVCPP 660
 35 GFQGLQASPS KHAGYSVRME NAVPIVTPAQ GAQPLQIQPG LLAQQA WPSG TQQLLPPAW 720
 QQLTGVAHTI SVQHATVPE TMAGTQQLAD WRNTHAGSH YNPIMQPAL LTGHVTLPA 780
 QPLNVGVAVH MRQQPTSTTS SRKSKHQHSS VRNVSTCEVS SSQAISPPQR SKRVKENTPP 840
 RCAMVHSSPA CSTSVTCGWG DVASSTTRER QRQTIVIPDT PSPTSVVITI SSDTDEEEEQ 900
 KHAPTSTVSK QRKNVISCVT VHDSPYSDSS SNTSPYSVQQ RAGHNNANAF DTKGSLEHNC 960
 40 TGNPRTIJVP PLKTOASEVL VECDLVPVN TSHHSSSYKS KSSSNVTSTS GHSSGSSSGA 1020
 ITYRQQRPGF HFQQQQLNL SQAQQHITTD RTGSHRRQA YITPTMAQAP YSFPHNSPSH 1080
 GTVHPHLAAA AAAAHLPTQP HLYTYTAPAA LGSTGTVAHL VASQGSARHT VQHTAYPASI 1140
 VHQPVMGMP RVLPSFTIHP SQYPAQFAHQ TYISASPAST VYTGYPPLSPA KVNQYPYI

45

SEQ ID NO:283 PBY1 DNA SEQUENCE

Nucleic Acid Accession #: NM_017700
 Coding sequence: 147-806 (underlined sequence corresponds to start and stop codon)

50 1 11 21 31 41 51
 | | | | |
 AGTCACAGCC AGGTAACCCCT GGAGTGAAGC GGTTTAGTTA GAAGGGAGCA GATAAACTCG 60
 TCACTCTAGT AGCTTTAACC CTCACCCCTGA GGCACCTTAG CAATCAGCCA TTGCTGCAA 120
 GCCTCCAAAG CTGTCTTTTG CCTAATATGG AGCCCAAAGA AGCCACTGGG AAAGAAAACA 180
 TGGTCACCAA GAAAAAGAA TCGGCCCTCT TGAGGTCTAG ACTCTATATG CTGGAGAGAA 240
 55 GGAAGACTGA CACTGTGGTT GAGAGCAGTG TTTCTGGGGA CCACTCTGGC ACCTTGAGGA 300
 GGAGCCAATC TGACAGGACC GAAATACAAC AGAAATTACA AGAAAAGATG ACTCCACAGG 360
 GTGAGTGTTC TGAGCTGAG ACCTTAACCC CAGAGGAAGA GCATCATATG AAGAGGATGA 420
 TGGCAAGCGG GAAAAGATC ATTAAGGAGC TGATACAGAC AGAAAAGGAT TATCTCAATG 480
 ATCTAGAGCT GTGTGTTAGG GAAGTGGTTC AGCCCTGAG AATAAAAAAG ACTGATAGGC 540
 60 TGGATGTGGA TAGCTTGTIT AGCAACATTG AGTCGTGCA TCAGATATCA GCCAAGCTGC 600
 TGTCATGTGT GGAAGAGGCC ACAACAGACG TGAACCCGCC CATGCAAGTA ATTGGAGAAG 660
 TATTCTPGCA GATTAAAGGG CCACTGGAAG ATATTATATA AATCTACTGC TATCACCATG 720
 ATGAAGCACA TAGTATACTG GAGTCCTATG AAAAGGAAGA AGAGCTGAAG GAACATTTGA 780
 GCCACTGTAT CCAGTCCTTA AAGTAAGGCC TTTTCAAATG ATGATTCCTA TCTCTCTCA 840
 65 GTTGCCCTAGC AGGGAACATT TTAAATGGAT GTAGATGAAA GGTCTCACAT AAATCCTATG 900
 TTTTATGAGA CTGTCTGGGA GCTCTGCTTT GCATTCCTTT TATAAAAAGC TGACATGCCA 960
 GAAGCCCTGA TTGACTTTTT TTCCCCCTGC GAGAATGACT AAAAAATAACA TGGAGAAGA 1020
 TTTAGAGCTC TGCAGCGATT GAAAAATGCA ATATCAAAT ATAAATGTG GAAGAAAAGC 1080
 CTCTTCTTAA AGCTATTGTA ACTTGCCTGG CCCCACGTAG TTCAAGGATT ATGTGAGATA 1140
 70 ACACGTGGCC CCATGACCAC TGGAGCACAT GGGTTAATGG AGTTAGGGGA ATGGCCTACA 1200
 ACTCTGCATG GCCCTCTTCT TTCCCCAAC TCACTGTGGG GAGATGGGTG AAGACAAGTC 1260
 AGGCCTGTGT AAAGTTAGTT TCAGAACAAAT TACTCATGCC TTCTTTTCTC ATCCCTAAAA 1320
 CATGTGTGGG GGAGCTACAC AATGTACTTT TTCTTTTCTA GAGGAAGTAT CTATTCACTG 1380
 75 TGAATACTCG AAAAAATATA CAAAGTATGT GTAAGATAAA AACCCCTGTC TATTTCAAAA 1440
 AAAAAAAAAA AAAAAAAAAA AAAA

SEQ ID NO:284 PBY1 Protein sequence:
 Protein Accession #: NP_060170

80 1 11 21 31 41 51

MEPKEATGKE NMVTKKKNLA FLRSRLYMLE RRKTDTVVES SVSGDHSGLT RRSQSDRTEY 60
 NQKLQEKMTF QGECVAETL TPEEHHMKR MMAREKIIK ELIQTEKDYI NDLELCVREV 120
 VQPLRNKRTD RLVDLSLPSN IESVHQISAK LLSLLEEATT DVEPANQVIG EVFLQIKGFL 180
 EDIYKIYCYH HDEAHSILES YEKEELKEH LSHCIQSLK

SEQ ID NO:285 PBQ9 DNA SEQUENCE

Nucleic Acid Accession#: X66534
 Coding sequence: 523-2676 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 15 CCCTTATGGC GATTGGGCGG CTGCAGAGAC CAGGACTCAG TTCCCTTGCC CTAGTCTGAG 60
 CCTAGTGGGT GGGACTCAGC TCAGAGTCAG TTTTCAGAAG CAGGTTTCAG TTGCAGAGTT 120
 TTCCTTACTT TTTCTTGGCG TAGAGCAGCG AGCAGCTTGG AACAGACCCA GCGGAGGAC 180
 ACCTGTGGGG GAGGGAGCGC CTGGAGGAGC TTAGAGACCC CAGCCGGGCG TGATCTCACC 240
 ATGTGCGGAT TTGCGAGGCG CGCCCTGGAG CTGCTAGAGA TCCGGAAGCA CAGCCCCGAG 300
 20 GTGTGCGAAG CCACCAAGAC TCGGCTCTTT GGAGAAAGCG TGAGCAGGGG GCCACCGCGG 360
 TCCTCGGCGT GTCTGCACCC TGTCGCTTGA GCTGCTGCAC AGTGACAATG ACATCCCACT 420
 TACCACTGTC CTGGAATTGA TAGTGGCTTC TGTTTGTCTG TCTCATATAA GAACCTACAGC 480
 TCATCAGGAG GAGATCGCAG CAGGGTAAGA GACACCAACA CCATGTTCTG CACGAAGCTC 540
 AAGGATCTCA AGATCACAGG AGAGTGTCTT TTCTCTTAC TGGCACCAGG TCAAGTTCTT 600
 25 AACGAGTCTT CAGAGGAGGC AGCAGGAAGC TCAGAGAGCT GCAAAGCAAC CGTGCCCATC 660
 TGTCAGAGCA TTCTTGAGAA GAACATACAA GAAAGTCTTC CTCAAAGAAA AACCACTCGG 720
 AGCCGAGTCT ATCTTCACAC TTGGCAGAG AGTATTGTGA AACTGATTTT CCCAGAGTTT 780
 GAACGGCTGA ATGTGCACT TCAGAGAACA TTGGCAAAAC ACAAAATAAA AGAAAGCAGG 840
 AAATCTTTGG AAGAGAAGA CTTTGAAAAA ACAATTGCAG AGCAAGCAGT GCAGCAGAGT 900
 30 CCACTGGAGT TATCAAGAA TCTCTTGGTG AAGAGGTTT TAAATATATG TACGAGGAAG 960
 ATGAAACCAT CTCTGGGGTG GTTGGAGGCA CCCTTAAAGA TTTTAAACA GCTTCAGTAC 1020
 CCTCTGAAA CAGAGCAGCC ATTGCCAAGA AGCAGGAAAA AGGGGCAGCT TGAGGACGCC 1080
 TCCATCTCAT GCCTGGATAA GGAGGATGAT TTTCTACATG TTTACTACTT CTCCCTAAG 1140
 AGAACCACTG CCTGATTTCT TCCCGCATC ATAAAGGCAG CTGCTCACGT ATTATATGAA 1200
 35 ACGGAAGTGG AAGTGTCTGT AATGCTCTCC TGCTTCCATA ATGATTGCAG CGAGTTTGTG 1260
 AATCAGCCCT ACTTGTGTGA CTCCGTTTAC ATGAAAGACA CCAAGCCATC CTGTCTCCCC 1320
 AGCAAAACCC AGTCTCTGCT GGTGATTCCC ACATCGCTAT TCTGCAAGAC ATTTCCATTC 1380
 CATTTCATGT TTGACAAGA TATGACAAAT CTGCAATTGT GCAATGGCAT CAGAAGGCTG 1440
 ATGAACACCT CCTGATTTCA AGGAAAGCCT AATTTTGAAT ACTTTGAAAT TCTGACTCCA 1500
 40 AAAATCAACC AGACCTTTAG CCGGATCATG ACTATGTTGA ATATGCAGTT TGTGTACGA 1560
 GTGAGGAGAT GGGACAACCT TGTGAAGAAA TCTTCAAGGG TTATGGACCT CAAAGGCCAA 1620
 ATGATCTACA TTGTGGAAT CAGTGCAATC TTGTTTGTGG GGTCAACCTG TGTGGACAGA 1680
 TTAGAAGATT TTACAGGACG AGGGCTCTAC CTCTCAGACA TCCCAATTCA CAATGCACCTG 1740
 45 AGGGATGTGAC CTTTAATAGG GGAACAAGCC CGAGCTCAAG ATGGCCTGAA GAAGAGGCTG 1800
 GGGAAAGCTGA AGGCTACCTT TGAGCAAGCC CACCAAGCCC TGGAGGAGGA GAAGAAAAAG 1860
 ACAGTAGACC TTCTGTGCTC CATATTTCCC TGTGAGGTTG CTCAGCAGCT GTGGCAAGGG 1920
 CAAGTTGTGC AAGCAAGAAA GTTCAGTAAT GTCAACATGC TCTTCTCAGA CATCGTTGGG 1980
 TTCACTGCCA TCTGTCTCCA GTGCTCACCG CTGCAAGTCA TCACCATGCT CAATGCACCTG 2040
 50 TACACTCGCT TCGACACAGA GTGTGGAGAG CTGGATGTCT ACAAGGTGGA GACCATTGCG 2100
 ATGCTTATTTG TGTGGCTTGG GGGATTACAC AAAGAGAGTG ATACTCATGC TGTTCAGATA 2160
 GCGCTGATGG CCTTGAAGAT GATGGAGCTC TCTGATGAAG TTATGTCTCC CCATGGAGAA 2220
 CCTATCAAGA TCGGAATTGG ACTGCACTCT GGATCAGTTT TTGCTGGCGT CGTTGGAGTT 2280
 AAAATGCCCC GTTACTGTCT TTTTGGAAAC AATGTCACTC TGGCTAACAA ATTTGAGTCC 2340
 55 TGCAGTGTGAC CAGCAAAAT CAATGTACGC CCAACAACCT ACAGATTACT CAAAGACTGT 2400
 CCTGGTTTCG TGTATTACCC TCGATCAAGG GAGGAACCTC CACCAAACTT CCCTAGTGAA 2460
 ATCCCGGAAA TCTGCCATT TCTGGATGCT TACCAACAAG GAACAAACTC AAAACCATGC 2520
 TTCCAAAAGA AAGATGTGGA AGATGCAAGC CAATTTTATA GGCAAGCAT CAGGAATAGA 2580
 TTAGCAACCT ATATACCTAT TTATAAGTCT TTGGGGTTTG ACTCATTGAA GATGTGTAGA 2640
 60 GCCTCTGAAA GCACCTTAGG GATTGTAGAT GGCTAACAAG CAGTATTAAA ATTTGAGGAG 2700
 CCAAGTCACA ATCTTTCTCC TGTTTAATAT GACAAAATGT ACTCACTTCA GTACTTCAGC 2760
 TCTTCAAGAA AAAAAAATA ACCTTAAAAA GCTACTTTTG TGGGAGTATT TCTATTATAT 2820
 AACCAGCACT TACTACCTGT ACTCAAAATT CAGCACCTTG TACATATATC AGATAATTGT 2880
 AGTCAATTGT ACAAACGAT GGAGTCACCT GCAATCTCAT ATCTGGTGG AATGCCATGG 2940
 65 TTATTAAGT GTGTTTGTGA TAGTTGTCTG CAAAAAATAA AAAAAAATAA AAAAAAATAA 3000
 AAAA

SEQ ID NO:286 PBQ9 Protein sequence:
 Protein Accession #: Q02108

70 1 11 21 31 41 51
 MFCTKLKDLK ITGECFFSLL APGQVFNES EEAAGSSESC KATVPICQDI PEKNIQESLP 60
 QRKTSRSRVY LHTLAESICK LIPFEFERLN VALQRTLAKH KIKESRKSLE REDFEKTIAE 120
 75 QAVAAGVPVE VIKESLGEV FKICYEEDN ILGVVGGTLK DFLNSPSTLL KQSSHQCEAG 180
 KRGRLEDASI LCILDKEDDFL HVYFFPKRT TSLILPGIHK AAAHVLYETE VEVSLMPPCF 240
 HNDCESEFVNQ PYLLYSVHMK STKPSLSPSK PQSSSLVPTS LFCKTTPPFHF MFDKDHITLQ 300
 FGNIGIRRLMN RRFQKKNPF EEFYFELTPK INQTFSGIMT MLNMQPVVRV RRWDNSVKKS 360
 SRVMDLKGPM IYIVESSAIL PLGSPCVDR L EDPFTRGLYL SDIPIHNALR DVVLIGEQR 420
 80 AQDGLKRLGL KKLKLEQAH QALEEEKKKT VDLCSIFPC EVAQQLWQGO VQQAQKFSNV 480
 THLFSDIVGF TAICSQCSPL QVITMLNALY TRFDQCCGEL DVYKVTETGD AYCVAAGLHK 540

ESDTHAVQIA LMALIOMMELS DEVMSPHGEP IKMRIGLHSG SVFAGVVGK MPRYCLFGNN 600
VTLANKEPESC SVPRKINVSF TTYRLLKDCP GFVFTPRSRE ELPPNFPSEI PGICHFLDAY. 660
QQGTNSKPCF QKQDVEDGNA NPLGKASGID

SEQ ID NO:287 PFD2 DNA SEQUENCE

Nucleic Acid Accession#: NM_000720

Coding sequence: 119-6664 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
| | | | |
AGAATAAGGG CAGGACCCG GGCTCCTATC TCTTGGTGAT CCCCTTCCCC ATTCGCGCCC 60
CGCCTCAACG CCACGACACG TGCCCTGCAC ACAGTAGTCG CTCAATAAAT GTTCGTGGAT 120
GATGATGATG ATGATGATGA AAAAAATGCA GCATCAACGG CAGCAGCAAG CGGACCACGC 180
GAACGAGGCA AACTATGCAA GAGGCACCAG ACTTCTCTTT TCTGGTGAAG GACCAACTTC 240
TCAGCCGAAT AGCTCCAAGC AAATGTCTCT GTCTTGGCAA GCTGCAATCG ATGCTGCTAG 300
ACAGGCCAAG GCTGCCCAAA CTATGAGCAC CTCTGCACCC CCACCTGTAG GATCTCTCTC 360
CCAAAGAAA CCGTACGCAAT ACGCCAAGAG CAAAAACAG GGTAACCTCGT CCAACAGCCG 420
ACCTGCCCGC GCCCTTTTCT GTTTATCACT CAATAACCCC ATCCGAAGAG CCGTCAATTAG 480
TATAGTGGAA TGGAAACCAT TTGACATATT TATATTATTG GCTATTTTGG CCAATTGTGT 540
GGCCTTAGCT ATTTACATCC CATTCCCTGA AGATGATTCT AATTCAACAA ATCATAACTT 600
GGAAAAAGTA GAATATGCCT TCCTGATTAT TTTTACAGTC GAGACATTTT TGAAGATTAT 660
AGCGTATGGA TTATTGCTAC ATCCTAATGC TTATGTTAGG AATGGATGGA ATTTACTGGA 720
21 TTTTGTATA GTAATAGTAG GATTGTTTAG TGTAAATTTG GAACAATTAA CCAAAGAAAC 780
AGAAGGCGGG AACCACTCAA CGGCAAAATC TGGAGGCTTT GATGTCAAAG CCTCCGTGTC 840
CTTTGAGATG TTGCGACCAC TTCCGACTAGT GTCAGGGGTG CCGAGTTTAC AAGTTGTCTC 900
GAATCCCATT ATAAAAAGCA TGGTTCCCTT CCTTCACATA GCCCTTTTGG TATTATTTGT 960
AATCATAATC TATGCTATTA TAGGATTGGA ACTTTTATT GGAAAAATG ACAAACATG 1020
31 TTTTGTGCT GACTCAGATA TCGTAGCTGA AGAGGACCCA GCTCCATGTG CGTCTCAGG 1080
GAATGGAAGC CAGTGTACTG CCAATGGCAC GGAATGTAGG AGTGGCTGGG TTGGCCCGAA 1140
CGGAGGCATC ACCAACTTTG ATAACTTTGC CTTTGCCATG CTACTGTGT TTCAGTGCA 1200
CACCATGGAG GGCTGGACAG ACGTGCTCTA CTGGGTAAAT GATGCGATAG GATGGGAATG 1260
GCCATGGGTG TATTTTGTTA GTCTGATCAT CCTTGGCTCA TTTTTCGTCC TTAACCTGGT 1320
35 TCTTGGTGCT CTAGTGGAG AATTCCTAAA GGAAAGAGAG AAGGCAAAAG CACGGGGAGA 1380
TTCCCAAGAG CTCCGGGAGA AGCAGCAGCT GGAGGAGGAT CTAAAGGGCT ACTTGGATTG 1440
GATCACCCAA GCTGAGGACA TCGATCCGGA GAATGAGGAA GAAGGAGGAG AGGAAGGCAA 1500
ACGAAATACT AGCATGCCCA CCAGCGAGAC TGAGTCTGTG AACACAGAGA ACGTCAGCGG 1560
40 TGAAGGGGAG AACCGAGGCT GCTGTGGAAG TCTCTGGTGC TGGTGGAGAC GGAGAGCGGC 1620
GGCCAAAGGG GGGCCCTCTG GGTGTGCGCG GTGGGGTCAA GCCATCTCAA AATCCAAACT 1680
CAGCGGACAG TGGCGTCTGT GGAACCGATT CAATCGCAGA AGATGTAGGG CCGCCCGTAA 1740
GTCTGTACAG TTTTACTGGC TGGTTATCGT CCTGGTGTGT CTGAACACCT TAACCATTTT 1800
CTCTGAGCAC TACAATCAGC CAGATTGGTT GACACAGATT CAAGATATTG CCAACAAAGT 1860
45 CCTCTGGCTG CTGTTTCACT GCGAGATGCT GGTAAAAATG TACAGCTTGG GCCTCCAAGC 1920
ATATTTCGCT TCTCTTTTCA ACCGGTTTGA TTGCTCTGTG GTGTGTGTGT GAATCACTGA 1980
GACGATCTG TCGGAACCTG AAATCATGTC TCCCTGGGG ATCTCTGTGT TTGGTGTGT 2040
GCGCTCTTAA AGAATCTTCA AAGTGACCAG GCATGGACT TCCCTGAGCA ACTTAGTGGC 2100
ATCCTTATTA TACCTCCATGA AGTCCATCGC TTCGCTGTG CTCTGCTTT TTCTCTTCAT 2160
50 TATCATCTTT TCTTGTCTTG GGATGACGCT GTTGGCGGCA AAGTTTAAAT TTGATGAAC 2220
GCAAAACCAAG CGGAGCAGCT TTGACAAATT CCCTCAAGCA CTCTCAGAG TGTTCAGAT 2280
CCTGACAGGG GAAGACTGGA ATGCTGTGAT GTACGATGGC ATCATGGCTT ACGGGGGCCC 2340
ATCCTCTTCA GGAATGATCG TCTGCATCTA CTTCATCATC CTCTTCAATT GTGGTAACTA 2400
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55 GAACACTGCT CAGAAAGAAG AAGCGGAAGA AAAGGAGAGG AAAAAAGATT CCAGAAAAGA 2520
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SEQ ID NO:288 PFD2 Protein sequence:
 Protein Accession #: A38198

55
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 A P R V L R P L R L V S G V P S L Q V V L N S I I K A M V P L L H I A L L V L F V I I I A I I G L E L F I G K M H K T 300
 65 C F F A D S D I V A E E D P A P C A F S G N G R Q C T A N G T E C R S G W V G F N G G I T N F D N F A F A H L T V F Q C 360
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 D F Q K L R E K Q Q L E E D L K G Y L D W I T Q A E D I D P E N E E G G E E G K R N T S M P T S E T E S V N T E N V S 480
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 K S V T F Y W L V I V L V F L N T L T I S S E H Y N Q P D W L T Q I Q D I A N K V L L A L P T C E M L V K M Y S L G L Q 600
 70 A Y F V S L F N R F D C F V V C G G I T E T I L V E L I M S P L G I S V F R C V R L L R I P K V T R H W T S L S N L V 660
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 C D V F V G E E E E E E D E P E V P A G P R P R R I S E L N M K E I A P I P E G S A F F I L S K T N P I R V G C H 900
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 80 K A R P L R R Y I P K N P Y Q V K F Y M V N S S P F E Y M M F V L I L M A T L C L A M Q H Y E Q S K M F N D A M D I L 1260
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	CDPESDYNPG	EETTCGSNFA	IVYFISFYML	CAFLIINLFV	AVIMDNFDYL	TRDWSILGPH	1500
	HLDEFKRIWS	EYDPEAKGRI	KHLDVVTLRL	RIQPLGPGK	LCPHRVACKR	LVAMNMPLNS	1560
	DGTVMFNATL	FALVRTALKI	KTEGNLEQAN	EELRAVIKKI	WKRTSMKLLD	QVVPFAGDDE	1620
	VTVGKFYATP	LIQDYFRKFK	KRKEQGLVGK	YPAQMTTIAL	QAGLRTLHDI	GPEIRRAISC	1680
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	GEQEYFSSEE	CYEDDSSPTW	SRQNYGYYSR	YPGRNIDSER	PRGYHHPQGF	LEDDDSPVCY	1920
	DSRRSPRRRL	LPPTPASHRR	SSFNFECLRR	QSSQEEVPS	PIFPHRTALP	LHLMQQQIMA	1980
	VAGLSSSKAQ	KYSPSHSTRS	WATPPATPPY	RDWTPCYTPL	IQVEQSEALD	QVNGSLFSLH	2040
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15	VSATKHEIAD	ACDLTIDEME	SAASTLLNGN	VRPRANGDVG	PLSHRQDYEL	QDFGPGYSDE	2160
	EPDPGRDEED	LADEMICTTT	L				

SEQ ID NO:289.OB16 DNA SEQUENCE

Nucleic Acid Accession#: NM_002812

Coding sequence: 150-3362 (underlined sequence corresponds to start and stop codon)

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	CCCGCCGGTT	GCCTCTGCTC	AGCGTCTTGC	TGCTGCCCGT	GCTGGGCGGT	ACCCAGACAG	240
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	GCAGCCAGAA	CTTCAACCTTG	AGCATTGCTG	ATGAAAGCTT	TGCCAGGGTG	GTGCTGGCAC	840
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	AGCCACGCCC	GCTGCTGAG	TGGCTCTTTG	AGGATGAGAC	TCCCATCACT	AACCGCAGTC	960
40	GCCTCCACCA	CCTCCGACGA	GCCACAGTGT	TTGCCAACGG	GTCTCTGCTG	CTGACCCAGG	1020
	TCCGGCCAGC	CAATGACGGG	ATCTACCGCT	GCATTGGCCA	GGGGCAGAGG	GGCCACCCCA	1080
	TCATCTGAGA	AGCCACACTT	CACCTAGCAG	AGATTGAAGA	CATCCCGCTA	TTTGAGCCAC	1140
	GGGTGTTTAC	AGCTGGCAGC	GAGGAGCGTG	TGACCTGCCT	TCCCCCCAAG	GGTCTGCCAG	1200
	AGCCACGCGT	GCTGTGGGAG	CACGCGGAG	TCCGGCTGCC	CACCATGGC	AGGGTCTACC	1260
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	AGCAGTGCAT	GGAGTTTGAC	AAGGAGGCCA	CGGTGCCCTG	TTCAGCCACA	GGCCGAGAGA	1740
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	ACGCTGGGAC	CTGTCATTTT	GCCCCGGTGA	CTCGAGATGA	CGCTGGCAAC	TACACTTGCA	1860
55	TTGCCCTCAA	CGGGCCGCGG	GGCCAGATTG	GTGCCCATGT	CCAGCTCACT	GTGGCAGTTT	1920
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	TCCATGACGT	GGCCCTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAGGC	AACAGCTGCA	2160
60	ACATCAAGCA	CACGGAGGCC	CCCCCTCTAT	TCGTGGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
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	TCAGCACTGA	TGTGTACAA	AGTGAGTACT	ACCACTTCCG	CCAGGCCTGG	GTGCCGCTCG	3060
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	CAGATGATGA	AGTACTTGCA	GATTTCAGG	CTGGGAAGGC	TAGACTTCTC	CAGCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCTTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCGCT	3360
80	GAGGAGGGAG	CCCCCTCAGG	ATGGCTTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420

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SEQ ID NO:290 ORF6 Protein sequence:
 Protein Accession #: NP_002812

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1 11 21 31 41 51
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SEQ ID NO:291 AAB1 DNA SEQUENCE

Nucleic Acid Accession #: NM_002205
 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

45
50
55
60
65
70
75
80

1 11 21 31 41 51
 | | | | |
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 20 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAGTTGCA TTTCCGAGTC 2820
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SEQ ID NO:292 AAB1 Protein sequence:

Protein Accession #: NP_002196

25 1 11 21 31 41 51
 MGSRTPEPSL HAVQLRWGPR RRPPLLPLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
 30 GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL 120
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 DNFRILLEYA PCRSDFSWAA GQGYCQGGFS AEPTKTRGVV LGGPGSYFWQ GQILSATQEQ 240
 IAESYYPEVL INLVQGLQQT RQASSIYDDS YLGYSVAVGE FSGDDTDEFV AGVPKGNLTY 300
 35 GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360
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 QQGVVVFPG GPGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGG YPDILVGSFG 480
 VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNFV ACINLSFCLN ASGKHVADSI 540
 GFTVELQLDW QKQGGVRRRA LFLASRQATL TQTLIIQNGA REDCREMKIY LRNESEFRDK 600
 40 LSPHIALNF SLDPQAFVDS HCLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
 GEQNHVYLDG KNALNLTFHA QNVGEGGAYE AELRVTAPEE AEYSGLVRHP GNFSSLSCDY 720
 FAVNQSRLLV CDLGNPKKAG ASLWGGRLPT VFHLRDTKRT IQPDFQILSK NLNNSQSDVV 780
 SFRLSVEAQA QVTNLGVSKP EAVLFPVSDW HFRDQPKQEE DLGPAVHHVY ELINQGPSSI 840
 SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINFKGL ELDPEGLSHH QOKREAPSR 900
 45 SASSGPQILK CPEAECFLR CELGPLHQRE QSLSQLHFRV WAKTFLOREH QPFSLQCEAV 960
 YKALKMYYRI LPRQLPKER QVATAVQWTK AEGSYGVPLW IILAILFLGL LLLGLLIYIL 1020
 YKLGFFKRSL PYGTAMEKAQ LKPPATSDA

SEQ ID NO:293 LBH4 DNA SEQUENCE

Nucleic Acid Accession #: BC001291

Coding sequence: 44-541 (start and stop codons are underlined)

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 55 GGGGGCGCCG CGCGCTGACC CTCCTGGGC ACCGCTGGGG ACGATGGGCG TGCTCGCCTT 60
 GCTGCTGGTC GTGGCCCTAC CGCGGGTGTG GACAGACGCC AACCTGACTG CGAGACAAAG 120
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 60 TGAGAGAGAA AACACTTTTC AGTGCCAGAA CCCAAGGAGG TGCAATGGA CAGAGCCATA 240
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 CGCTGTTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA 360
 GCCCATGGCC TCTTTTTACC TCAAGTGTG TAAATTCGC TACTGCAAT TAGAGGGGCC 420
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 GCTGTGGCTG GCCATCTCTC TGCTGCTGGC CTCCATTGCA GCCGGCTCA GCCTGTCTTG 540
 65 AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC 600
 ACCTGTTGCA TTAACATTGT TTCTGTTGA TTACCTCTTG GTTGTACTTC CCAGGGTCTT 660
 GGGATGGGAG ATGGGGGAGT AGGTGCAGTT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC 720
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 70 AAATCAAACC TTGTAATCA TTTATTGCTG ATGGCCACTC TTTTCTTGA CTCCCTCTG 840
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 TGCTGAGATG CTTCGACCT TACAGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG 960
 GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGAGTGG GGCACACGTT 1020
 AGGGCTGCCC CCATTCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTCC TCAACCTTTC 1080
 CTACCAAGAT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCACCC 1140
 75 ACCAGCTGGC CTTCAGTATC AGATTCATAA ATTCACACAC GTGTGTGTTT AACATCTGAA 1200
 ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTCTCTGTTT AAGATGCAGC 1260
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCACCC AAAAAAAT ACAAGGGGAC 1320
 TTCAAAAGTT CACGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA

SEQ ID NO: 294 LBH4 Protein sequence:
Protein Accession #: AAH01291

5 1 11 21 31 41 51
 | | | | | |
10 MALLALLLVV ALPRVWTDAN LTARQDPED SORTDEGDNR VWCHVCEREN TFECQNPRRC 60
 KWTEPYCVIA AVKIFPRFFM VAKQCSAGCA AMERPKPEEK RFLLEPMPPF FYLKCKKIRY 120
 CNLEGGPPINS SYFKEYAGSM GESCGGLWLA ILLLLASIAA GLSL

15 It is understood that the examples described above in no way serve to limit the
true scope of this invention, but rather are presented for illustrative purposes. All
publications, sequences of accession numbers, and patent applications cited in this
specification are herein incorporated by reference as if each individual publication or patent
20 application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a prostate cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat prostate cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having
2 prostate cancer.

- 1 13. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16,
8 thereby monitoring the efficacy of the therapy.
- 1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated transcript to a level of the prostate cancer-
3 associated transcript in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 15. The method of claim 13, wherein the patient is a human.
- 1 16. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated antibody in the
6 biological sample by contacting the biological sample with a polypeptide encoded by a
7 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
8 as shown in Tables 1-16, wherein the polypeptide specifically binds to the prostate cancer-
9 associated antibody, thereby monitoring the efficacy of the therapy.
- 1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated antibody to a level of the prostate cancer-
3 associated antibody in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 18. The method of claim 16, wherein the patient is a human.

- 1 19. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1-16, thereby monitoring
9 the efficacy of the therapy.
- 1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated polypeptide to a level of the prostate cancer-
3 associated polypeptide in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 21. The method of claim 19, wherein the patient is a human.
- 1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-16.
- 1 23. The nucleic acid molecule of claim 22, which is labeled.
- 1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label
- 1 25. An expression vector comprising the nucleic acid of claim 22.
- 1 26. A host cell comprising the expression vector of claim 25.
- 1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-16.
- 1 28. An antibody that specifically binds a polypeptide of claim 27.
- 1 29. The antibody of claim 28, further conjugated to an effector component.

- 1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.
- 1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.
- 1 32. The antibody of claim 29, which is an antibody fragment.
- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a prostate cancer cell in a biological sample
2 from a patient, the method comprising contacting the biological sample with an antibody of
3 claim 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to prostate cancer in a
2 patient, the method comprising contacting a biological sample from the patient with a
3 polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-16.
- 1 38. A method for identifying a compound that modulates a prostate cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a prostate cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.

- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.
- 1 44. A method of inhibiting proliferation of a prostate cancer-associated
2 cell to treat prostate cancer in a patient, the method comprising the step of administering to
3 the subject a therapeutically effective amount of a compound identified using the method of
4 claim 38.
- 1 45. The method of claim 44, wherein the compound is an antibody.
- 1 46. The method of claim 45, wherein the patient is a human.
- 1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having prostate cancer or a
3 cell isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of prostate cancer.
- 1 48. The assay of claim 47, wherein the control is a mammal with prostate
2 cancer or a cell therefrom that has not been treated with the test compound.
- 1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having prostate cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having prostate
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.

1 52. The method according to claim 1, wherein said biological sample is
2 contacted with a plurality of polynucleotides comprising a first polynucleotide that
3 selectively hybridizes to a sequence at least 80% identical to a first sequence as shown in
4 Tables 1-16; and a second polynucleotide that selectively hybridizes to a second sequence at
5 least 80% identical to a second sequence as shown in Tables 1-16.

1 53. A method according to claim 52, wherein the plurality of
2 polynucleotides comprises a third polynucleotide that selectively hybridizes to a sequence at
3 least 80% identical to a third sequence as shown in Tables 1-16..

1 54. A method of detecting a prostate cancer associated transcript, the
2 method comprising contacting a biological sample from the patient with a plurality of
3 polynucleotides wherein at least two of said polynucleotides selectively hybridize to a
4 difference sequence at least 80% identical to a sequence as shown in Tables 1-16.

1 55. A method of detecting a prostate cancer, the method comprising the
2 steps of:
3 (i) providing a biological sample from a patient;
4 (ii) contacting the biological sample with a first polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a first sequence as shown in Tables 1-16 to
6 determine the level of a prostate cancer-associated transcript in the biological sample; and
7 with a second polynucleotide that selectively hybridizes to a second sequence at least 80%
8 identical to a sequence not shown in Tables 1-16; wherein the expression of said second
9 sequence is not substantially changed in prostate cancer, to determine the level of expression
10 of a control transcript in the biological sample;

11 (iii) comparing the level of the prostate cancer-associated transcript to a level
12 of the normal tissue associated transcript in the biological sample.

1 56. A method of quantitating a prostate cancer-associated transcript in a
2 cell from a patient, the method comprising contacting a biological sample from the patient
3 with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a
4 sequence as shown in Tables 1-16.

1 57. The method of claim 56, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.

1 58. The method of claim 56, wherein the biological sample is a tissue
2 sample.

1 59. The method of claim 56, wherein the biological sample comprises
2 isolated nucleic acids.

1 60. The method of claim 56, wherein the nucleic acids are mRNA.

1 61. The method of claim 59, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.

1 62. The method of claim 56, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-16.

1 63. The method of claim 56, wherein the polynucleotide is labeled.

1 64. The method of claim 63, wherein the label is a fluorescent label.

1 65. The method of claim 56, wherein the polynucleotide is immobilized on
2 a solid surface.

1 66. The method of claim 56, wherein the patient is undergoing a
2 therapeutic regimen to treat metastatic prostate cancer.

1 67. The method of claim 56, wherein the patient is suspected of having
2 metastatic prostate cancer.

1 68. A biochip comprising a plurality of polynucleotides that selectively
2 hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

1 69. A method of screening drug candidates comprising:
2 i) providing a cell that expresses an expression profile gene selected from the
3 group consisting of an expression profile gene set forth in Tables 1-16 or fragment thereof;
4 ii) adding a drug candidate to said cell; and
5 iii) determining the effect of said drug candidate on the expression of said
6 expression profile gene.

1 70. A method according to claim 59 wherein said determining comprises
2 comparing the level of expression in the absence of said drug candidate to the level of
3 expression in the presence of said drug candidate.

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